PRINT DATE: 2024-04-01 19:44:11 +0200

JOB ID: 122c278b-05ec-46db-9fc5-374c8a5c9480

RESULT PAGE: https://tygs.dsmz.de/user_results/show?guid=122c278b-05ec-46db-9fc5-374c8a5c9480

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_030329025.1_ASM3032902v1_genomic'	belongs to known species	*Thiopseudomonas alkaliphila*	
'GCF_030328955.1_ASM3032895v1_genomic'	belongs to known species	*Thiopseudomonas alkaliphila*	
'GCF_001267315.1_ASM126731v1_genomic'	belongs to known species	*Thiopseudomonas alkaliphila*	
'GCF_001267295.1_ASM126729v1_genomic'	belongs to known species	*Thiopseudomonas alkaliphila*	
'GCF_001267275.1_ASM126727v1_genomic'	belongs to known species	*Thiopseudomonas alkaliphila*	
'GCF_001267255.1_ASM126725v1_genomic'	belongs to known species	*Thiopseudomonas alkaliphila*	
'GCF_001267215.1_ASM126721v1_genomic'	belongs to known species	*Thiopseudomonas alkaliphila*	
'GCF_001267195.1_ASM126719v1_genomic'	belongs to known species	*Thiopseudomonas alkaliphila*	
'GCF_001267175.1_ASM126717v1_genomic'	belongs to known species	*Thiopseudomonas alkaliphila*	
'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'	*Thiopseudomonas alkaliphila* B4199	100.0	[100.0 - 100.0]	100.0	[100.0 - 100.0]	100.0	[100.0 - 100.0]	0.0
'GCF_001267215.1_ASM126721v1_genomic.fna'	'GCF_001267195.1_ASM126719v1_genomic.fna'	94.3	[91.8 - 96.1]	96.7	[95.4 - 97.6]	96.5	[94.9 - 97.6]	0.05
'GCF_001267255.1_ASM126725v1_genomic.fna'	'GCF_001267215.1_ASM126721v1_genomic.fna'	95.0	[92.7 - 96.6]	94.5	[92.8 - 95.8]	96.7	[95.2 - 97.7]	0.08
'GCF_001267255.1_ASM126725v1_genomic.fna'	'GCF_001267195.1_ASM126719v1_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'	*Thiopseudomonas alkaliphila* B4199	89.7	[86.5 - 92.3]	93.7	[91.8 - 95.1]	92.9	[90.5 - 94.7]	0.14
'GCF_001267215.1_ASM126721v1_genomic.fna'	'GCF_001267175.1_ASM126717v1_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'	*Thiopseudomonas alkaliphila* B4199	85.2	[81.4 - 88.2]	93.1	[91.2 - 94.6]	89.3	[86.4 - 91.6]	0.1
'GCF_001267195.1_ASM126719v1_genomic.fna'	'GCF_001267175.1_ASM126717v1_genomic.fna'	85.2	[81.4 - 88.2]	93.1	[91.2 - 94.6]	89.3	[86.4 - 91.6]	0.1
'GCF_001267255.1_ASM126725v1_genomic.fna'	'GCF_001267175.1_ASM126717v1_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'	*Thiopseudomonas alkaliphila* B4199	86.2	[82.5 - 89.2]	92.7	[90.7 - 94.2]	90.0	[87.3 - 92.2]	0.07
'GCF_030329025.1_ASM3032902v1_genomic.fna'	'GCF_001267315.1_ASM126731v1_genomic.fna'	83.1	[79.3 - 86.4]	91.1	[88.9 - 92.9]	87.4	[84.3 - 89.9]	0.1
'GCF_001267275.1_ASM126727v1_genomic.fna'	'GCF_001267215.1_ASM126721v1_genomic.fna'	90.6	[87.4 - 93.0]	89.6	[87.2 - 91.5]	92.9	[90.6 - 94.7]	0.12
'GCF_001267275.1_ASM126727v1_genomic.fna'	'GCF_001267195.1_ASM126719v1_genomic.fna'	87.5	[84.0 - 90.3]	89.6	[87.3 - 91.6]	90.6	[87.9 - 92.7]	0.08
'GCF_001267275.1_ASM126727v1_genomic.fna'	'GCF_001267255.1_ASM126725v1_genomic.fna'	89.4	[86.1 - 92.0]	89.5	[87.1 - 91.5]	92.0	[89.6 - 94.0]	0.04
'GCF_001267275.1_ASM126727v1_genomic.fna'	*Thiopseudomonas alkaliphila* 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_001267175.1_ASM126717v1_genomic.fna'	83.1	[79.3 - 86.3]	89.2	[86.8 - 91.2]	87.0	[84.0 - 89.6]	0.02
'GCF_001267295.1_ASM126729v1_genomic.fna'	'GCF_001267275.1_ASM126727v1_genomic.fna'	85.5	[81.8 - 88.5]	89.1	[86.7 - 91.1]	88.9	[86.1 - 91.3]	0.06
'GCF_001267295.1_ASM126729v1_genomic.fna'	'GCF_001267215.1_ASM126721v1_genomic.fna'	90.8	[87.6 - 93.2]	88.6	[86.1 - 90.6]	92.9	[90.6 - 94.7]	0.06
'GCF_001267295.1_ASM126729v1_genomic.fna'	'GCF_001267255.1_ASM126725v1_genomic.fna'	89.1	[85.7 - 91.7]	88.6	[86.1 - 90.7]	91.7	[89.1 - 93.6]	0.02
'GCF_001267295.1_ASM126729v1_genomic.fna'	'GCF_001267195.1_ASM126719v1_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'	*Thiopseudomonas alkaliphila* 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_001267295.1_ASM126729v1_genomic.fna'	'GCF_001267175.1_ASM126717v1_genomic.fna'	91.0	[87.9 - 93.3]	88.3	[85.9 - 90.4]	93.0	[90.7 - 94.8]	0.08
'GCF_001267315.1_ASM126731v1_genomic.fna'	'GCF_001267255.1_ASM126725v1_genomic.fna'	84.2	[80.4 - 87.4]	86.8	[84.2 - 89.0]	87.5	[84.5 - 90.0]	0.22
'GCF_030329025.1_ASM3032902v1_genomic.fna'	'GCF_001267255.1_ASM126725v1_genomic.fna'	82.9	[79.1 - 86.2]	86.7	[84.1 - 88.9]	86.5	[83.4 - 89.1]	0.32
'GCF_030329025.1_ASM3032902v1_genomic.fna'	'GCF_001267195.1_ASM126719v1_genomic.fna'	79.7	[75.8 - 83.2]	86.7	[84.1 - 88.9]	83.8	[80.6 - 86.6]	0.36
'GCF_001267315.1_ASM126731v1_genomic.fna'	'GCF_001267215.1_ASM126721v1_genomic.fna'	87.8	[84.3 - 90.6]	86.6	[84.0 - 88.9]	90.4	[87.7 - 92.6]	0.3
'GCF_030329025.1_ASM3032902v1_genomic.fna'	'GCF_001267215.1_ASM126721v1_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'	'GCF_001267175.1_ASM126717v1_genomic.fna'	84.1	[80.3 - 87.3]	86.5	[83.8 - 88.7]	87.4	[84.4 - 89.9]	0.16
'GCF_001267315.1_ASM126731v1_genomic.fna'	*Thiopseudomonas alkaliphila* B4199	84.1	[80.3 - 87.3]	86.5	[83.8 - 88.7]	87.4	[84.4 - 89.9]	0.16
'GCF_001267315.1_ASM126731v1_genomic.fna'	'GCF_001267195.1_ASM126719v1_genomic.fna'	85.0	[81.3 - 88.1]	86.4	[83.7 - 88.6]	88.1	[85.2 - 90.5]	0.26
'GCF_030329025.1_ASM3032902v1_genomic.fna'	'GCF_001267275.1_ASM126727v1_genomic.fna'	82.0	[78.1 - 85.3]	85.9	[83.2 - 88.2]	85.6	[82.4 - 88.2]	0.28
'GCF_001267315.1_ASM126731v1_genomic.fna'	'GCF_001267275.1_ASM126727v1_genomic.fna'	84.0	[80.2 - 87.2]	85.9	[83.2 - 88.2]	87.3	[84.2 - 89.8]	0.18
'GCF_030329025.1_ASM3032902v1_genomic.fna'	*Thiopseudomonas alkaliphila* B4199	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'	'GCF_001267175.1_ASM126717v1_genomic.fna'	77.8	[73.8 - 81.3]	85.7	[83.0 - 88.0]	82.0	[78.7 - 85.0]	0.26
'GCF_001267315.1_ASM126731v1_genomic.fna'	'GCF_001267295.1_ASM126729v1_genomic.fna'	84.8	[81.0 - 87.9]	85.4	[82.7 - 87.7]	87.8	[84.8 - 90.2]	0.24
'GCF_030329025.1_ASM3032902v1_genomic.fna'	'GCF_001267295.1_ASM126729v1_genomic.fna'	83.3	[79.4 - 86.5]	85.2	[82.5 - 87.5]	86.5	[83.4 - 89.1]	0.34
'GCF_030328955.1_ASM3032895v1_genomic.fna'	'GCF_001267315.1_ASM126731v1_genomic.fna'	81.2	[77.3 - 84.6]	80.4	[77.5 - 83.1]	84.0	[80.8 - 86.8]	0.4
'GCF_030329025.1_ASM3032902v1_genomic.fna'	'GCF_030328955.1_ASM3032895v1_genomic.fna'	76.7	[72.7 - 80.2]	79.7	[76.8 - 82.4]	80.0	[76.6 - 83.1]	0.5
'GCF_030328955.1_ASM3032895v1_genomic.fna'	'GCF_001267215.1_ASM126721v1_genomic.fna'	78.4	[74.4 - 81.9]	79.0	[76.0 - 81.7]	81.4	[78.0 - 84.3]	0.1
'GCF_030328955.1_ASM3032895v1_genomic.fna'	'GCF_001267255.1_ASM126725v1_genomic.fna'	76.5	[72.5 - 80.1]	78.7	[75.7 - 81.4]	79.7	[76.3 - 82.7]	0.18
'GCF_030328955.1_ASM3032895v1_genomic.fna'	*Thiopseudomonas alkaliphila* B4199	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'	'GCF_001267175.1_ASM126717v1_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'	'GCF_001267195.1_ASM126719v1_genomic.fna'	74.4	[70.5 - 78.1]	78.1	[75.1 - 80.8]	77.8	[74.3 - 80.9]	0.15
'GCF_030328955.1_ASM3032895v1_genomic.fna'	'GCF_001267275.1_ASM126727v1_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_030328955.1_ASM3032895v1_genomic.fna'	'GCF_001267295.1_ASM126729v1_genomic.fna'	75.6	[71.6 - 79.1]	77.4	[74.4 - 80.2]	78.7	[75.2 - 81.7]	0.16
'GCF_030328995.1_ASM3032899v1_genomic.fna'	'GCF_030328955.1_ASM3032895v1_genomic.fna'	77.7	[73.7 - 81.2]	65.7	[62.8 - 68.5]	78.1	[74.7 - 81.2]	0.55
'GCF_030328995.1_ASM3032899v1_genomic.fna'	'GCF_001267315.1_ASM126731v1_genomic.fna'	77.3	[73.3 - 80.8]	65.4	[62.4 - 68.2]	77.7	[74.2 - 80.8]	0.96
'GCF_030329025.1_ASM3032902v1_genomic.fna'	'GCF_030328995.1_ASM3032899v1_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'	'GCF_001267175.1_ASM126717v1_genomic.fna'	71.5	[67.5 - 75.1]	64.3	[61.4 - 67.1]	72.4	[68.9 - 75.6]	0.8
'GCF_030328995.1_ASM3032899v1_genomic.fna'	*Thiopseudomonas alkaliphila* B4199	71.5	[67.5 - 75.1]	64.3	[61.4 - 67.1]	72.4	[68.9 - 75.6]	0.8
'GCF_030328995.1_ASM3032899v1_genomic.fna'	'GCF_001267275.1_ASM126727v1_genomic.fna'	76.3	[72.4 - 79.9]	63.9	[61.0 - 66.8]	76.5	[73.1 - 79.7]	0.77
'GCF_030328995.1_ASM3032899v1_genomic.fna'	'GCF_001267295.1_ASM126729v1_genomic.fna'	75.6	[71.6 - 79.2]	63.8	[60.9 - 66.6]	75.9	[72.4 - 79.1]	0.71
'GCF_030328995.1_ASM3032899v1_genomic.fna'	'GCF_001267215.1_ASM126721v1_genomic.fna'	77.7	[73.7 - 81.3]	63.8	[60.9 - 66.6]	77.7	[74.2 - 80.8]	0.65
'GCF_030328995.1_ASM3032899v1_genomic.fna'	'GCF_001267255.1_ASM126725v1_genomic.fna'	78.2	[74.2 - 81.7]	63.7	[60.8 - 66.6]	78.0	[74.6 - 81.1]	0.73
'GCF_030328995.1_ASM3032899v1_genomic.fna'	'GCF_001267195.1_ASM126719v1_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'	*Acinetobacter towneri* 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'	*Acinetobacter rongchengensis* 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'	*Nitrosomonas stercoris* 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'	*Acinetobacter defluvii* 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'	*Nitrosomonas stercoris* 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'	*Acinetobacter seohaensis* 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'	*Advenella alkanexedens* LAM0050	12.7	[10.1 - 16.0]	45.6	[43.1 - 48.2]	13.2	[10.8 - 15.9]	2.6
'GCF_030328995.1_ASM3032899v1_genomic.fna'	*Acinetobacter rongchengensis* 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'	*Nitrosomonas stercoris* ATCC BAA-2718	12.7	[10.0 - 15.9]	43.9	[41.4 - 46.5]	13.1	[10.8 - 15.8]	2.81
'GCF_030328955.1_ASM3032895v1_genomic.fna'	*Advenella alkanexedens* LAM0050	12.6	[9.9 - 15.8]	41.7	[39.2 - 44.3]	13.0	[10.7 - 15.7]	2.19

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'	*Ignatzschineria cameli* 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'	*Nitrosomonas stercoris* ATCC BAA-2718	12.6	[9.9 - 15.9]	40.9	[38.4 - 43.4]	13.0	[10.7 - 15.8]	2.31
'GCF_030329025.1_ASM3032902v1_genomic.fna'	*Advenella alkanexedens* LAM0050	12.6	[9.9 - 15.8]	39.9	[37.4 - 42.5]	13.0	[10.7 - 15.7]	2.69
'GCF_030328955.1_ASM3032895v1_genomic.fna'	*Acinetobacter defluvii* WCHA30	12.6	[9.9 - 15.9]	39.6	[37.2 - 42.2]	13.0	[10.7 - 15.8]	9.62
'GCF_030328995.1_ASM3032899v1_genomic.fna'	*Advenella alkanexedens* LAM0050	12.6	[9.9 - 15.9]	39.1	[36.6 - 41.6]	13.0	[10.7 - 15.8]	1.64
'GCF_030329025.1_ASM3032902v1_genomic.fna'	*Acinetobacter rongchengensis* 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'	*Citrobacter tructae* 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'	*Acinetobacter rongchengensis* 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'	*Acinetobacter defluvii* 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'	*Nitrosomonas stercoris* 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'	*Citrobacter tructae* SNU WT2	12.7	[10.0 - 15.9]	35.3	[32.8 - 37.8]	13.1	[10.7 - 15.8]	4.34
'GCF_030328995.1_ASM3032899v1_genomic.fna'	*Citrobacter tructae* 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'	*Nitrosomonas stercoris* ATCC BAA-2718	12.7	[10.0 - 15.9]	33.2	[30.8 - 35.7]	13.1	[10.8 - 15.8]	2.65
'GCF_001267315.1_ASM126731v1_genomic.fna'	*Citrobacter tructae* SNU WT2	12.7	[10.0 - 15.9]	30.8	[28.4 - 33.3]	13.1	[10.7 - 15.8]	4.75
'GCF_001267315.1_ASM126731v1_genomic.fna'	*Enterobacter cloacae* ATCC 13047	12.8	[10.1 - 16.0]	30.4	[28.0 - 32.9]	13.2	[10.8 - 15.9]	7.38
'GCF_001267315.1_ASM126731v1_genomic.fna'	*Shigella flexneri* ATCC 29903	12.8	[10.1 - 16.0]	30.4	[28.0 - 32.9]	13.2	[10.8 - 15.9]	3.46
'GCF_001267295.1_ASM126729v1_genomic.fna'	*Acinetobacter rongchengensis* 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'	*Ignatzschineria cameli* 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'	*Ignatzschineria cameli* 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'	*Acinetobacter rongchengensis* 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'	*Acinetobacter rongchengensis* 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'	*Acinetobacter rongchengensis* WCHAc060115 T	12.6	[9.9 - 15.8]	28.9	[26.5 - 31.4]	13.0	[10.6 - 15.7]	9.81

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_001267195.1_ASM 126719v1_genomic.fna'	*Acinetobacter rongchengensis* 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_ASM 126719v1_genomic.fna'	*Citrobacter tructae* 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_ASM 126731v1_genomic.fna'	*Acinetobacter defluvii* WCHA30	12.6	[9.9 - 15.9]	28.2	[25.8 - 30.7]	13.0	[10.7 - 15.8]	9.22
'GCF_001267175.1_ASM 126717v1_genomic.fna'	*Citrobacter tructae* SNU WT2	12.6	[10.0 - 15.9]	27.6	[25.3 - 30.1]	13.1	[10.7 - 15.8]	4.59
'GCF_001267215.1_ASM 126721v1_genomic.fna'	*Citrobacter tructae* SNU WT2	12.7	[10.0 - 15.9]	27.6	[25.3 - 30.1]	13.1	[10.7 - 15.8]	4.44
'GCF_030329025.1_ASM 3032902v1_genomic.fna'	*Ignatzschineria cameli* 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_ASM 126725v1_genomic.fna'	*Citrobacter tructae* SNU WT2	12.6	[10.0 - 15.9]	27.5	[25.2 - 30.0]	13.0	[10.7 - 15.8]	4.52
'GCF_001267275.1_ASM 126727v1_genomic.fna'	*Nitrosomonas stercoris* ATCC BAA-2718	12.6	[9.9 - 15.9]	27.5	[25.1 - 29.9]	13.0	[10.7 - 15.7]	2.59
'GCF_001267275.1_ASM 126727v1_genomic.fna'	*Citrobacter tructae* SNU WT2	12.6	[10.0 - 15.9]	27.5	[25.1 - 30.0]	13.0	[10.7 - 15.8]	4.56
'GCF_001267255.1_ASM 126725v1_genomic.fna'	*Nitrosomonas stercoris* ATCC BAA-2718	12.6	[9.9 - 15.9]	27.5	[25.1 - 30.0]	13.0	[10.7 - 15.7]	2.63
'GCF_001267175.1_ASM 126717v1_genomic.fna'	*Nitrosomonas stercoris* ATCC BAA-2718	12.6	[10.0 - 15.9]	27.5	[25.1 - 29.9]	13.0	[10.7 - 15.8]	2.56
'GCF_001267195.1_ASM 126719v1_genomic.fna'	*Advenella alkanexedens* LAM0050	12.6	[9.9 - 15.9]	27.4	[25.0 - 29.9]	13.0	[10.7 - 15.7]	2.34
'GCF_030328955.1_ASM 3032895v1_genomic.fna'	*Enterobacter cloacae* ATCC 13047	12.7	[10.0 - 15.9]	27.2	[24.8 - 29.7]	13.1	[10.7 - 15.8]	6.98
'GCF_001267255.1_ASM 126725v1_genomic.fna'	*Advenella alkanexedens* LAM0050	12.6	[9.9 - 15.9]	27.2	[24.9 - 29.7]	13.0	[10.7 - 15.8]	2.37
'GCF_001267315.1_ASM 126731v1_genomic.fna'	*Acinetobacter towneri* DSM 14962	12.6	[9.9 - 15.8]	27.2	[24.9 - 29.7]	13.0	[10.7 - 15.7]	6.03
'GCF_030329025.1_ASM 3032902v1_genomic.fna'	*Enterobacter cloacae* ATCC 13047	12.7	[10.0 - 15.9]	27.2	[24.9 - 29.7]	13.1	[10.7 - 15.8]	7.48
'GCF_001267295.1_ASM 126729v1_genomic.fna'	*Acinetobacter seohaensis* 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_ASM 126731v1_genomic.fna'	*Acinetobacter seohaensis* DSM 16313	12.6	[9.9 - 15.9]	26.9	[24.6 - 29.4]	13.0	[10.7 - 15.8]	5.86
'GCF_030328955.1_ASM 3032895v1_genomic.fna'	*Shigella flexneri* ATCC 29903	12.6	[10.0 - 15.9]	26.6	[24.3 - 29.1]	13.0	[10.7 - 15.8]	3.06
'GCF_030328995.1_ASM 3032899v1_genomic.fna'	*Enterobacter cloacae* ATCC 13047	12.7	[10.0 - 16.0]	26.6	[24.2 - 29.1]	13.1	[10.8 - 15.8]	6.42
'GCF_001267295.1_ASM 126729v1_genomic.fna'	*Advenella alkanexedens* LAM0050	12.6	[9.9 - 15.9]	26.6	[24.2 - 29.1]	13.0	[10.7 - 15.7]	2.35
'GCF_001267175.1_ASM 126717v1_genomic.fna'	*Acinetobacter seohaensis* DSM 16313	12.6	[9.9 - 15.9]	26.5	[24.1 - 29.0]	13.0	[10.7 - 15.8]	6.02
'GCF_001267215.1_ASM 126721v1_genomic.fna'	*Acinetobacter seohaensis* DSM 16313	12.6	[9.9 - 15.9]	26.5	[24.1 - 29.0]	13.0	[10.7 - 15.8]	6.17
'GCF_001267215.1_ASM 126721v1_genomic.fna'	*Advenella alkanexedens* LAM0050	12.6	[9.9 - 15.9]	26.4	[24.0 - 28.8]	13.0	[10.7 - 15.8]	2.29
'GCF_001267275.1_ASM 126727v1_genomic.fna'	*Advenella alkanexedens* LAM0050	12.6	[9.9 - 15.9]	26.4	[24.0 - 28.9]	13.0	[10.7 - 15.8]	2.41

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_ASM 126717v1_genomic.fna'	*Advenella alkanexedens* LAM0050	12.6	[9.9 - 15.9]	26.3	[24.0 - 28.8]	13.0	[10.7 - 15.8]	2.44
'GCF_001267195.1_ASM 126719v1_genomic.fna'	*Ignatzschineria cameli* UAE-HKU57	12.6	[9.9 - 15.8]	26.2	[23.9 - 28.7]	13.0	[10.7 - 15.7]	5.76
'GCF_001267295.1_ASM 126729v1_genomic.fna'	*Citrobacter tructae* 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_ASM 126721v1_genomic.fna'	*Nitrosomonas stercoris* 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_ASM 126725v1_genomic.fna'	*Acinetobacter seohaensis* 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_ASM 126727v1_genomic.fna'	*Acinetobacter seohaensis* 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_ASM 126727v1_genomic.fna'	*Acinetobacter rongchengensis* 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_ASM 126717v1_genomic.fna'	*Ignatzschineria cameli* UAE-HKU57	12.6	[9.9 - 15.9]	25.6	[23.2 - 28.0]	13.0	[10.7 - 15.8]	5.66
'GCF_001267215.1_ASM 126721v1_genomic.fna'	*Ignatzschineria cameli* UAE-HKU57	12.6	[9.9 - 15.9]	25.5	[23.2 - 28.0]	13.0	[10.7 - 15.8]	5.81
'GCF_030328995.1_ASM 3032899v1_genomic.fna'	*Shigella flexneri* ATCC 29903	12.7	[10.0 - 15.9]	25.5	[23.1 - 27.9]	13.1	[10.7 - 15.8]	2.51
'GCF_001267295.1_ASM 126729v1_genomic.fna'	*Shigella flexneri* 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_ASM 3032902v1_genomic.fna'	*Shigella flexneri* 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_ASM 126729v1_genomic.fna'	*Acinetobacter towneri* 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_ASM 126721v1_genomic.fna'	*Acinetobacter towneri* 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_ASM 126717v1_genomic.fna'	*Acinetobacter towneri* 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_ASM 126719v1_genomic.fna'	*Acinetobacter seohaensis* 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_ASM 126725v1_genomic.fna'	*Ignatzschineria cameli* 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_ASM 126717v1_genomic.fna'	*Shigella flexneri* 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_ASM 126721v1_genomic.fna'	*Shigella flexneri* 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_ASM 3032895v1_genomic.fna'	*Acinetobacter towneri* DSM 14962	12.6	[9.9 - 15.8]	24.7	[22.3 - 27.1]	13.0	[10.6 - 15.7]	6.43
'GCF_001267255.1_ASM 126725v1_genomic.fna'	*Shigella flexneri* ATCC 29903	12.7	[10.0 - 15.9]	24.7	[22.4 - 27.2]	13.1	[10.7 - 15.8]	3.24
'GCF_001267195.1_ASM 126719v1_genomic.fna'	*Enterobacter cloacae* ATCC 13047	12.6	[10.0 - 15.9]	24.7	[22.4 - 27.2]	13.0	[10.7 - 15.8]	7.12
'GCF_001267215.1_ASM 126721v1_genomic.fna'	*Acinetobacter defluvii* WCHA30	12.6	[9.9 - 15.9]	24.6	[22.3 - 27.1]	13.0	[10.7 - 15.7]	9.52
'GCF_001267295.1_ASM 126729v1_genomic.fna'	*Enterobacter cloacae* ATCC 13047	12.7	[10.0 - 15.9]	24.6	[22.3 - 27.1]	13.1	[10.7 - 15.8]	7.14
'GCF_001267215.1_ASM 126721v1_genomic.fna'	*Enterobacter cloacae* ATCC 13047	12.7	[10.0 - 15.9]	24.6	[22.3 - 27.1]	13.1	[10.7 - 15.8]	7.08
'GCF_001267175.1_ASM 126717v1_genomic.fna'	*Enterobacter cloacae* ATCC 13047	12.7	[10.0 - 15.9]	24.6	[22.3 - 27.1]	13.1	[10.7 - 15.8]	7.22

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_001267275.1_ASM126727v1_genomic.fna'	*Enterobacter cloacae* 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'	*Enterobacter cloacae* ATCC 13047	12.7	[10.0 - 15.9]	24.4	[22.1 - 26.9]	13.1	[10.7 - 15.8]	7.15
'GCF_001267295.1_ASM126729v1_genomic.fna'	*Acinetobacter defluvii* WCHA30	12.6	[9.9 - 15.9]	24.3	[22.0 - 26.8]	13.0	[10.7 - 15.7]	9.46
'GCF_001267175.1_ASM126717v1_genomic.fna'	*Acinetobacter defluvii* WCHA30	12.6	[9.9 - 15.9]	24.3	[22.0 - 26.8]	13.0	[10.7 - 15.7]	9.38
'GCF_001267275.1_ASM126727v1_genomic.fna'	*Acinetobacter towneri* DSM 14962	12.6	[9.9 - 15.8]	24.2	[21.9 - 26.7]	13.0	[10.6 - 15.7]	6.21
'GCF_001267255.1_ASM126725v1_genomic.fna'	*Acinetobacter towneri* DSM 14962	12.6	[9.9 - 15.8]	24.2	[21.9 - 26.7]	13.0	[10.6 - 15.7]	6.25
'GCF_030328995.1_ASM3032899v1_genomic.fna'	*Acinetobacter towneri* DSM 14962	12.5	[9.9 - 15.8]	23.9	[21.6 - 26.4]	12.9	[10.6 - 15.7]	6.98
'GCF_001267275.1_ASM126727v1_genomic.fna'	*Shigella flexneri* ATCC 29903	12.7	[10.0 - 15.9]	23.9	[21.6 - 26.4]	13.1	[10.7 - 15.8]	3.28
'GCF_001267195.1_ASM126719v1_genomic.fna'	*Shigella flexneri* 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'	*Ignatzschineria cameli* UAE-HKU57	12.6	[9.9 - 15.9]	23.7	[21.4 - 26.2]	13.0	[10.7 - 15.8]	5.69
'GCF_001267275.1_ASM126727v1_genomic.fna'	*Acinetobacter defluvii* WCHA30	12.6	[9.9 - 15.8]	23.6	[21.3 - 26.1]	13.0	[10.7 - 15.7]	9.4
'GCF_030329025.1_ASM3032902v1_genomic.fna'	*Pseudomonas yangonensis* JCM 33396	12.8	[10.1 - 16.1]	23.6	[21.3 - 26.0]	13.2	[10.9 - 16.0]	15.81
'GCF_001267195.1_ASM126719v1_genomic.fna'	*Pseudomonas sessilinigenes* CMR12a	12.8	[10.1 - 16.0]	23.5	[21.2 - 25.9]	13.2	[10.8 - 15.9]	15.34
'GCF_001267255.1_ASM126725v1_genomic.fna'	*Acinetobacter defluvii* WCHA30	12.6	[9.9 - 15.8]	23.5	[21.2 - 26.0]	13.0	[10.7 - 15.7]	9.44
'GCF_030328995.1_ASM3032899v1_genomic.fna'	*Chryseomonas asuensis* JCM 13501	12.7	[10.1 - 16.0]	23.4	[21.1 - 25.8]	13.1	[10.8 - 15.9]	5.42
'GCF_001267295.1_ASM126729v1_genomic.fna'	*Pseudomonas sessilinigenes* CMR12a	12.8	[10.1 - 16.1]	23.3	[21.0 - 25.8]	13.2	[10.9 - 16.0]	15.36
'GCF_001267175.1_ASM126717v1_genomic.fna'	*Pseudomonas sessilinigenes* CMR12a	12.8	[10.1 - 16.1]	23.3	[21.0 - 25.7]	13.2	[10.9 - 16.0]	15.44
'GCF_001267195.1_ASM126719v1_genomic.fna'	*Acinetobacter towneri* DSM 14962	12.6	[9.9 - 15.8]	23.3	[21.0 - 25.8]	13.0	[10.6 - 15.7]	6.28
'GCF_001267215.1_ASM126721v1_genomic.fna'	*Pseudomonas sessilinigenes* CMR12a	12.8	[10.1 - 16.1]	23.2	[20.9 - 25.7]	13.2	[10.9 - 16.0]	15.3
'GCF_001267195.1_ASM126719v1_genomic.fna'	*Acinetobacter defluvii* WCHA30	12.6	[9.9 - 15.8]	23.1	[20.8 - 25.5]	13.0	[10.6 - 15.7]	9.48
'GCF_001267315.1_ASM126731v1_genomic.fna'	*Pseudomonas sessilinigenes* CMR12a	12.8	[10.1 - 16.1]	23.0	[20.8 - 25.5]	13.2	[10.9 - 16.0]	15.6
'GCF_001267175.1_ASM126717v1_genomic.fna'	*Pseudomonas tensinigenes* ZA 5.3	12.9	[10.2 - 16.1]	23.0	[20.8 - 25.5]	13.2	[10.9 - 16.0]	11.81
'GCF_001267195.1_ASM126719v1_genomic.fna'	*Pseudomonas tensinigenes* ZA 5.3	12.8	[10.1 - 16.1]	23.0	[20.7 - 25.5]	13.2	[10.9 - 16.0]	11.71
'GCF_001267315.1_ASM126731v1_genomic.fna'	*Thiopseudomonas acetoxidans* CY1220	13.6	[10.8 - 16.9]	23.0	[20.7 - 25.4]	13.9	[11.5 - 16.7]	1.37
'GCF_001267215.1_ASM126721v1_genomic.fna'	*Pseudomonas tensinigenes* ZA 5.3	12.9	[10.2 - 16.1]	22.9	[20.6 - 25.3]	13.2	[10.9 - 16.0]	11.66
'GCF_001267275.1_ASM126727v1_genomic.fna'	*Pseudomonas sessilinigenes* CMR12a	12.8	[10.1 - 16.1]	22.9	[20.6 - 25.4]	13.2	[10.8 - 16.0]	15.42

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_001267295.1_ASM126729v1_genomic.fna'	*Chryseomonas asuensis* JCM 13501	12.7	[10.0 - 16.0]	22.9	[20.6 - 25.3]	13.1	[10.8 - 15.9]	6.13
'GCF_001267315.1_ASM126731v1_genomic.fna'	*Pseudomonas yangonensis* JCM 33396	12.9	[10.2 - 16.2]	22.9	[20.6 - 25.4]	13.3	[10.9 - 16.0]	15.71
'GCF_001267215.1_ASM126721v1_genomic.fna'	*Chryseomonas asuensis* JCM 13501	12.7	[10.0 - 16.0]	22.8	[20.5 - 25.3]	13.1	[10.8 - 15.9]	6.07
'GCF_001267315.1_ASM126731v1_genomic.fna'	*Chryseomonas asuensis* JCM 13501	12.7	[10.0 - 16.0]	22.8	[20.5 - 25.3]	13.1	[10.8 - 15.9]	6.37
'GCF_001267175.1_ASM126717v1_genomic.fna'	*Chryseomonas asuensis* 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'	*Pseudomonas indoloxydans* JCM 14246	12.8	[10.1 - 16.1]	22.8	[20.5 - 25.2]	13.2	[10.8 - 16.0]	15.04
'GCF_001267175.1_ASM126717v1_genomic.fna'	*Pseudomonas matsuisoli* 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'	*Acinetobacter seohaensis* DSM 16313	12.5	[9.9 - 15.8]	22.7	[20.4 - 25.2]	13.0	[10.6 - 15.7]	6.82
'GCF_001267255.1_ASM126725v1_genomic.fna'	*Pseudomonas sessilinigenes* CMR12a	12.8	[10.1 - 16.1]	22.7	[20.4 - 25.1]	13.2	[10.9 - 16.0]	15.37
'GCF_001267295.1_ASM126729v1_genomic.fna'	*Pseudomonas tensinigenes* ZA 5.3	12.9	[10.2 - 16.2]	22.6	[20.3 - 25.0]	13.3	[10.9 - 16.0]	11.73
'GCF_001267215.1_ASM126721v1_genomic.fna'	*Pseudomonas matsuisoli* JCM 30078	12.8	[10.1 - 16.0]	22.6	[20.4 - 25.1]	13.2	[10.8 - 15.9]	11.97
'GCF_001267295.1_ASM126729v1_genomic.fna'	*Pseudomonas indoloxydans* 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'	*Pseudomonas indoloxydans* JCM 14246	12.8	[10.1 - 16.1]	22.6	[20.3 - 25.0]	13.2	[10.9 - 16.0]	14.74
'GCF_030328995.1_ASM3032899v1_genomic.fna'	*Thiopseudomonas acetoxidans* CY1220	13.7	[10.9 - 17.1]	22.6	[20.3 - 25.1]	14.0	[11.6 - 16.8]	0.41
'GCF_001267255.1_ASM126725v1_genomic.fna'	*Pseudomonas tensinigenes* 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'	*Pseudomonas indoloxydans* JCM 14246	12.8	[10.1 - 16.1]	22.5	[20.3 - 25.0]	13.2	[10.9 - 16.0]	14.89
'GCF_001267315.1_ASM126731v1_genomic.fna'	*Pseudomonas tensinigenes* ZA 5.3	12.9	[10.2 - 16.2]	22.4	[20.1 - 24.8]	13.3	[10.9 - 16.0]	11.97
'GCF_001267295.1_ASM126729v1_genomic.fna'	*Pseudomonas perfectomarina* CCUG 16156	12.8	[10.1 - 16.1]	22.4	[20.1 - 24.8]	13.2	[10.9 - 16.0]	13.94
'GCF_001267175.1_ASM126717v1_genomic.fna'	*Pseudomonas perfectomarina* CCUG 16156	12.8	[10.1 - 16.1]	22.3	[20.1 - 24.8]	13.2	[10.9 - 16.0]	14.02
'GCF_001267275.1_ASM126727v1_genomic.fna'	*Pseudomonas tensinigenes* 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'	*Pseudomonas perfectomarina* CCUG 16156	12.8	[10.1 - 16.1]	22.3	[20.0 - 24.7]	13.2	[10.9 - 16.0]	14.18
'GCF_001267315.1_ASM126731v1_genomic.fna'	*Pseudomonas sediminis* PI11	12.8	[10.1 - 16.1]	22.3	[20.1 - 24.8]	13.2	[10.9 - 16.0]	15.28
'GCF_001267295.1_ASM126729v1_genomic.fna'	*Pseudomonas indica* NBRC 103045	12.8	[10.1 - 16.0]	22.3	[20.0 - 24.8]	13.1	[10.8 - 15.9]	16.69
'GCF_001267215.1_ASM126721v1_genomic.fna'	*Pseudomonas perfectomarina* CCUG 16156	12.8	[10.1 - 16.1]	22.3	[20.1 - 24.8]	13.2	[10.9 - 16.0]	13.87
'GCF_001267275.1_ASM126727v1_genomic.fna'	*Chryseomonas asuensis* JCM 13501	12.7	[10.0 - 16.0]	22.2	[19.9 - 24.6]	13.1	[10.8 - 15.9]	6.19

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'	*Pseudomonas yangonensis* JCM 33396	12.8	[10.1 - 16.1]	22.2	[19.9 - 24.6]	13.2	[10.9 - 16.0]	15.31
'GCF_001267295.1_ASM126729v1_genomic.fna'	*Ignatzschineria cameli* UAE-HKU57	12.6	[10.0 - 15.9]	22.2	[19.9 - 24.6]	13.0	[10.7 - 15.8]	5.75
'GCF_001267215.1_ASM126721v1_genomic.fna'	*Pseudomonas indica* NBRC 103045	12.8	[10.1 - 16.0]	22.2	[19.9 - 24.7]	13.2	[10.8 - 15.9]	16.62
'GCF_001267175.1_ASM126717v1_genomic.fna'	*Pseudomonas indica* 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'	*Pseudomonas matsuisoli* JCM 30078	12.8	[10.1 - 16.1]	22.2	[20.0 - 24.7]	13.2	[10.8 - 15.9]	12.27
'GCF_001267255.1_ASM126725v1_genomic.fna'	*Chryseomonas asuensis* JCM 13501	12.7	[10.0 - 16.0]	22.2	[19.9 - 24.6]	13.1	[10.8 - 15.9]	6.15
'GCF_001267215.1_ASM126721v1_genomic.fna'	*Atopomonas hussainii* JCM 19513	12.9	[10.2 - 16.1]	22.1	[19.9 - 24.6]	13.2	[10.9 - 16.0]	11.32
'GCF_001267195.1_ASM126719v1_genomic.fna'	*Pseudomonas indoloxydans* JCM 14246	12.8	[10.1 - 16.0]	22.1	[19.8 - 24.5]	13.1	[10.8 - 15.9]	14.79
'GCF_001267175.1_ASM126717v1_genomic.fna'	*Pseudomonas pseudoalcaligenes* NBRC 14167	12.8	[10.2 - 16.1]	22.1	[19.8 - 24.6]	13.2	[10.9 - 16.0]	14.88
'GCF_001267315.1_ASM126731v1_genomic.fna'	*Pseudomonas pseudoalcaligenes* NBRC 14167	12.8	[10.2 - 16.1]	22.0	[19.8 - 24.5]	13.2	[10.9 - 16.0]	15.04
'GCF_030328955.1_ASM3032895v1_genomic.fna'	*Acinetobacter seohaensis* DSM 16313	12.6	[9.9 - 15.8]	22.0	[19.7 - 24.4]	13.0	[10.6 - 15.7]	6.27
'GCF_001267315.1_ASM126731v1_genomic.fna'	*Pseudomonas indica* NBRC 103045	12.8	[10.1 - 16.0]	22.0	[19.8 - 24.5]	13.2	[10.8 - 15.9]	16.93
'GCF_001267275.1_ASM126727v1_genomic.fna'	*Pseudomonas matsuisoli* JCM 30078	12.8	[10.1 - 16.0]	22.0	[19.7 - 24.4]	13.1	[10.8 - 15.9]	12.09
'GCF_001267275.1_ASM126727v1_genomic.fna'	*Pseudomonas indoloxydans* JCM 14246	12.8	[10.1 - 16.1]	22.0	[19.8 - 24.5]	13.2	[10.8 - 15.9]	14.86
'GCF_001267295.1_ASM126729v1_genomic.fna'	*Pseudomonas sediminis* 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'	*Pseudomonas indoloxydans* JCM 14246	12.8	[10.1 - 16.1]	22.0	[19.8 - 24.5]	13.2	[10.8 - 16.0]	14.82
'GCF_001267215.1_ASM126721v1_genomic.fna'	*Pseudomonas pseudoalcaligenes* NBRC 14167	12.9	[10.2 - 16.1]	22.0	[19.8 - 24.5]	13.2	[10.9 - 16.0]	14.74
'GCF_001267215.1_ASM126721v1_genomic.fna'	*Pseudomonas sediminis* 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'	*Halopseudomonas sabulinigri* JCM 14963	12.9	[10.2 - 16.2]	22.0	[19.7 - 24.4]	13.3	[10.9 - 16.0]	12.41
'GCF_001267175.1_ASM126717v1_genomic.fna'	*Pseudomonas sediminis* PI11	12.9	[10.2 - 16.1]	22.0	[19.8 - 24.5]	13.2	[10.9 - 16.0]	15.12
'GCF_001267255.1_ASM126725v1_genomic.fna'	*Pseudomonas matsuisoli* JCM 30078	12.8	[10.1 - 16.0]	22.0	[19.7 - 24.4]	13.1	[10.8 - 15.9]	12.05
'GCF_001267175.1_ASM126717v1_genomic.fna'	*Pseudomonas xionganensis* 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'	*Pseudomonas sediminis* PI11	12.8	[10.1 - 16.1]	21.9	[19.6 - 24.3]	13.2	[10.8 - 15.9]	15.02
'GCF_001267315.1_ASM126731v1_genomic.fna'	*Pseudomonas xionganensis* 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_001267295.1_ASM126729v1_genomic.fna'	*Pseudomonas yangonensis* JCM 33396	12.8	[10.1 - 16.1]	21.9	[19.6 - 24.3]	13.2	[10.9 - 16.0]	15.47

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_001267195.1_ASM126719v1_genomic.fna'	*Pseudomonas pseudoalcaligenes* NBRC 14167	12.8	[10.1 - 16.1]	21.9	[19.6 - 24.3]	13.2	[10.8 - 15.9]	14.78
'GCF_001267215.1_ASM126721v1_genomic.fna'	*Pseudomonas yangonensis* 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'	*Pseudomonas yangonensis* 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'	*Pseudomonas xionganensis* 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'	*Pseudomonas xionganensis* 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'	*Pseudomonas pseudoalcaligenes* NBRC 14167	12.9	[10.2 - 16.1]	21.9	[19.6 - 24.3]	13.2	[10.9 - 16.0]	14.8
'GCF_030328995.1_ASM3032899v1_genomic.fna'	*Pseudomonas tensinigenes* ZA 5.3	12.8	[10.1 - 16.1]	21.8	[19.6 - 24.3]	13.2	[10.9 - 16.0]	11.01
'GCF_001267315.1_ASM126731v1_genomic.fna'	*Pseudomonas abyssi* 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'	*Pseudomonas matsuisoli* JCM 30078	12.7	[10.0 - 16.0]	21.8	[19.6 - 24.3]	13.1	[10.8 - 15.9]	12.02
'GCF_001267175.1_ASM126717v1_genomic.fna'	*Pseudomonas abyssi* MT5	12.8	[10.1 - 16.0]	21.8	[19.6 - 24.3]	13.1	[10.8 - 15.9]	13.9
'GCF_001267295.1_ASM126729v1_genomic.fna'	*Pseudomonas abyssi* MT5	12.8	[10.1 - 16.0]	21.8	[19.5 - 24.2]	13.2	[10.8 - 15.9]	13.81
'GCF_001267195.1_ASM126719v1_genomic.fna'	*Pseudomonas xionganensis* 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_001267195.1_ASM126719v1_genomic.fna'	*Pseudomonas yangonensis* 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'	*Pseudomonas matsuisoli* JCM 30078	12.8	[10.1 - 16.1]	21.7	[19.5 - 24.2]	13.2	[10.8 - 15.9]	12.03
'GCF_001267275.1_ASM126727v1_genomic.fna'	*Pseudomonas abyssi* MT5	12.7	[10.0 - 16.0]	21.7	[19.5 - 24.2]	13.1	[10.8 - 15.9]	13.87
'GCF_001267315.1_ASM126731v1_genomic.fna'	*Atopomonas hussainii* JCM 19513	12.9	[10.2 - 16.2]	21.7	[19.5 - 24.1]	13.3	[10.9 - 16.0]	11.62
'GCF_001267215.1_ASM126721v1_genomic.fna'	*Pseudomonas abyssi* 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'	*Chryseomonas asuensis* JCM 13501	12.7	[10.0 - 16.0]	21.7	[19.4 - 24.1]	13.1	[10.8 - 15.9]	6.12
'GCF_001267295.1_ASM126729v1_genomic.fna'	*Atopomonas hussainii* JCM 19513	12.9	[10.2 - 16.2]	21.6	[19.3 - 24.0]	13.3	[10.9 - 16.1]	11.38
'GCF_030328995.1_ASM3032899v1_genomic.fna'	*Pseudomonas sessilinigenes* CMR12a	12.8	[10.1 - 16.1]	21.6	[19.3 - 24.0]	13.2	[10.8 - 15.9]	14.64
'GCF_001267275.1_ASM126727v1_genomic.fna'	*Pseudomonas indica* NBRC 103045	12.8	[10.1 - 16.0]	21.6	[19.3 - 24.0]	13.1	[10.8 - 15.9]	16.75
'GCF_001267175.1_ASM126717v1_genomic.fna'	*Pseudomonas toyotomiensis* JCM 15604	12.8	[10.1 - 16.1]	21.6	[19.3 - 24.0]	13.2	[10.8 - 15.9]	15.25
'GCF_001267175.1_ASM126717v1_genomic.fna'	*Halopseudomonas sabulinigri* JCM 14963	12.9	[10.2 - 16.2]	21.6	[19.3 - 24.0]	13.3	[10.9 - 16.0]	12.55
'GCF_030329025.1_ASM3032902v1_genomic.fna'	*Pseudomonas sessilinigenes* CMR12a	12.8	[10.1 - 16.1]	21.6	[19.4 - 24.1]	13.2	[10.8 - 15.9]	15.7

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'	*Pseudomonas toyotomiensis* JCM 15604	12.8	[10.1 - 16.1]	21.6	[19.4 - 24.1]	13.2	[10.8 - 15.9]	15.16
'GCF_030328995.1_ASM3032899v1_genomic.fna'	*Pseudomonas yangonensis* JCM 33396	12.8	[10.1 - 16.1]	21.6	[19.4 - 24.1]	13.2	[10.9 - 16.0]	14.76
'GCF_001267275.1_ASM126727v1_genomic.fna'	*Pseudomonas perfectomarina* CCUG 16156	12.8	[10.1 - 16.1]	21.6	[19.3 - 24.0]	13.2	[10.9 - 16.0]	14.0
'GCF_001267255.1_ASM126725v1_genomic.fna'	*Pseudomonas perfectomarina* CCUG 16156	12.8	[10.1 - 16.1]	21.6	[19.3 - 24.0]	13.2	[10.9 - 16.0]	13.95
'GCF_001267295.1_ASM126729v1_genomic.fna'	*Pseudomonas indica* 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'	*Pseudomonas subflava* YIM B01952	12.8	[10.1 - 16.1]	21.6	[19.3 - 24.0]	13.2	[10.8 - 15.9]	19.1
'GCF_001267315.1_ASM126731v1_genomic.fna'	*Pseudomonas toyotomiensis* JCM 15604	12.8	[10.1 - 16.1]	21.6	[19.3 - 24.0]	13.2	[10.8 - 15.9]	15.41
'GCF_001267315.1_ASM126731v1_genomic.fna'	*Pseudomonas pharmacofabricae* ZYSR67-Z	13.1	[10.4 - 16.4]	21.6	[19.3 - 24.0]	13.4	[11.1 - 16.2]	15.42
'GCF_001267195.1_ASM126719v1_genomic.fna'	*Pseudomonas perfectomarina* CCUG 16156	12.8	[10.1 - 16.1]	21.6	[19.3 - 24.0]	13.2	[10.8 - 15.9]	13.92
'GCF_001267195.1_ASM126719v1_genomic.fna'	*Pseudomonas toyotomiensis* JCM 15604	12.7	[10.0 - 16.0]	21.6	[19.4 - 24.1]	13.1	[10.8 - 15.9]	15.15
'GCF_001267255.1_ASM126725v1_genomic.fna'	*Pseudomonas pseudoalcaligenes* NBRC 14167	12.8	[10.1 - 16.1]	21.6	[19.3 - 24.0]	13.2	[10.9 - 16.0]	14.82
'GCF_030328955.1_ASM3032895v1_genomic.fna'	*Chryseomonas asuensis* JCM 13501	12.6	[9.9 - 15.9]	21.5	[19.3 - 23.9]	13.0	[10.7 - 15.8]	5.97
'GCF_001267315.1_ASM126731v1_genomic.fna'	*Azomonas agilis* DSM 375	12.9	[10.2 - 16.2]	21.5	[19.2 - 23.9]	13.3	[11.0 - 16.1]	4.57
'GCF_001267215.1_ASM126721v1_genomic.fna'	*Pseudomonas toyotomiensis* JCM 15604	12.8	[10.1 - 16.1]	21.5	[19.3 - 24.0]	13.2	[10.8 - 15.9]	15.1
'GCF_001267195.1_ASM126719v1_genomic.fna'	*Pseudomonas subflava* YIM B01952	12.7	[10.0 - 16.0]	21.5	[19.3 - 24.0]	13.1	[10.8 - 15.9]	19.0
'GCF_001267255.1_ASM126725v1_genomic.fna'	*Pseudomonas sediminis* PI11	12.8	[10.2 - 16.1]	21.5	[19.3 - 24.0]	13.2	[10.9 - 16.0]	15.05
'GCF_001267275.1_ASM126727v1_genomic.fna'	*Pseudomonas sediminis* PI11	12.8	[10.1 - 16.1]	21.5	[19.2 - 23.9]	13.2	[10.9 - 16.0]	15.1
'GCF_001267295.1_ASM126729v1_genomic.fna'	*Halopseudomonas sabulinigri* JCM 14963	12.9	[10.2 - 16.2]	21.5	[19.2 - 23.9]	13.3	[10.9 - 16.0]	12.47
'GCF_001267195.1_ASM126719v1_genomic.fna'	*Pseudomonas flexibilis* ATCC 29606	12.8	[10.1 - 16.1]	21.5	[19.3 - 24.0]	13.2	[10.8 - 15.9]	18.35
'GCF_001267315.1_ASM126731v1_genomic.fna'	*Pseudomonas subflava* YIM B01952	12.8	[10.1 - 16.1]	21.5	[19.3 - 24.0]	13.2	[10.8 - 15.9]	19.26
'GCF_001267195.1_ASM126719v1_genomic.fna'	*Pseudomonas abyssi* MT5	12.7	[10.0 - 16.0]	21.5	[19.3 - 23.9]	13.1	[10.8 - 15.8]	13.8
'GCF_001267175.1_ASM126717v1_genomic.fna'	*Atopomonas hussainii* JCM 19513	12.9	[10.2 - 16.2]	21.5	[19.3 - 23.9]	13.3	[10.9 - 16.0]	11.46
'GCF_001267315.1_ASM126731v1_genomic.fna'	*Halopseudomonas sabulinigri* 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'	*Pseudomonas subflava* YIM B01952	12.8	[10.1 - 16.1]	21.5	[19.2 - 23.9]	13.2	[10.8 - 15.9]	18.96

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'	*Pseudomonas subflava* YIM B01952	12.8	[10.1 - 16.1]	21.5	[19.3 - 24.0]	13.2	[10.8 - 15.9]	19.02
'GCF_001267215.1_ASM126721v1_genomic.fna'	*Pseudomonas indica* JCM 21544	12.8	[10.1 - 16.1]	21.5	[19.2 - 23.9]	13.2	[10.8 - 16.0]	16.61
'GCF_001267275.1_ASM126727v1_genomic.fna'	*Pseudomonas pseudoalcaligenes* NBRC 14167	12.8	[10.1 - 16.1]	21.5	[19.2 - 23.9]	13.2	[10.9 - 16.0]	14.86
'GCF_001267175.1_ASM126717v1_genomic.fna'	*Pseudomonas indica* JCM 21544	12.8	[10.1 - 16.1]	21.5	[19.2 - 23.9]	13.2	[10.8 - 15.9]	16.75
'GCF_001267275.1_ASM126727v1_genomic.fna'	*Atopomonas hussainii* 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'	*Pseudomonas indica* NBRC 103045	12.8	[10.1 - 16.0]	21.4	[19.2 - 23.9]	13.1	[10.8 - 15.9]	16.7
'GCF_001267255.1_ASM126725v1_genomic.fna'	*Pseudomonas yangonensis* JCM 33396	12.8	[10.1 - 16.1]	21.4	[19.1 - 23.8]	13.2	[10.9 - 16.0]	15.49
'GCF_001267255.1_ASM126725v1_genomic.fna'	*Pseudomonas xionganensis* 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_001267315.1_ASM126731v1_genomic.fna'	*Pseudomonas indica* 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'	*Pseudomonas xionganensis* 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_001267195.1_ASM126719v1_genomic.fna'	*Pseudomonas indica* NBRC 103045	12.7	[10.0 - 16.0]	21.3	[19.1 - 23.8]	13.1	[10.8 - 15.9]	16.67
'GCF_001267295.1_ASM126729v1_genomic.fna'	*Thiopseudomonas denitrificans* DSM 28679	13.0	[10.3 - 16.3]	21.3	[19.1 - 23.8]	13.4	[11.0 - 16.2]	11.53
'GCF_001267315.1_ASM126731v1_genomic.fna'	*Thiopseudomonas denitrificans* DSM 28679	13.1	[10.3 - 16.4]	21.3	[19.1 - 23.8]	13.4	[11.1 - 16.2]	11.77
'GCF_001267175.1_ASM126717v1_genomic.fna'	*Thiopseudomonas denitrificans* DSM 28679	13.0	[10.3 - 16.3]	21.3	[19.0 - 23.7]	13.4	[11.0 - 16.2]	11.61
'GCF_001267275.1_ASM126727v1_genomic.fna'	*Pseudomonas yangonensis* JCM 33396	12.8	[10.1 - 16.1]	21.3	[19.1 - 23.8]	13.2	[10.8 - 16.0]	15.53
'GCF_001267255.1_ASM126725v1_genomic.fna'	*Halopseudomonas sabulinigri* JCM 14963	12.9	[10.2 - 16.2]	21.3	[19.1 - 23.8]	13.3	[10.9 - 16.0]	12.49
'GCF_001267315.1_ASM126731v1_genomic.fna'	*Pseudomonas nicosulfuronedens* LAM1902T	12.7	[10.1 - 16.0]	21.3	[19.0 - 23.7]	13.1	[10.8 - 15.9]	17.59
'GCF_001267215.1_ASM126721v1_genomic.fna'	*Thiopseudomonas denitrificans* DSM 28679	13.0	[10.3 - 16.3]	21.2	[19.0 - 23.7]	13.4	[11.0 - 16.2]	11.46
'GCF_001267295.1_ASM126729v1_genomic.fna'	*Pseudomonas pharmacofabricae* 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'	*Azomonas agilis* DSM 375	12.9	[10.2 - 16.2]	21.2	[19.0 - 23.7]	13.3	[11.0 - 16.1]	4.42
'GCF_030328955.1_ASM3032895v1_genomic.fna'	*Pseudomonas tensinigenes* ZA 5.3	12.8	[10.1 - 16.1]	21.2	[19.0 - 23.6]	13.2	[10.8 - 15.9]	11.56
'GCF_001267315.1_ASM126731v1_genomic.fna'	*Pseudomonas campi* 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'	*Atopomonas sediminilitoris* A3.4T	12.9	[10.2 - 16.1]	21.2	[19.0 - 23.6]	13.2	[10.9 - 16.0]	10.26
'GCF_001267295.1_ASM126729v1_genomic.fna'	*Atopomonas sediminilitoris* A3.4T	12.9	[10.2 - 16.2]	21.2	[18.9 - 23.6]	13.3	[10.9 - 16.0]	10.18
'GCF_001267295.1_ASM126729v1_genomic.fna'	*Azomonas agilis* DSM 375	13.0	[10.2 - 16.2]	21.2	[19.0 - 23.6]	13.3	[11.0 - 16.1]	4.33

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'	*Azomonas agilis* DSM 375	13.0	[10.3 - 16.2]	21.2	[19.0 - 23.7]	13.3	[11.0 - 16.1]	4.27
'GCF_001267275.1_ASM126727v1_genomic.fna'	*Halopseudomonas sabulinigri* JCM 14963	12.9	[10.2 - 16.2]	21.2	[19.0 - 23.6]	13.3	[10.9 - 16.0]	12.53
'GCF_001267175.1_ASM126717v1_genomic.fna'	*Pseudomonas pharmacofabricae* ZYSR67-Z	13.1	[10.4 - 16.4]	21.1	[18.9 - 23.6]	13.4	[11.1 - 16.2]	15.26
'GCF_001267275.1_ASM126727v1_genomic.fna'	*Pseudomonas toyotomiensis* JCM 15604	12.8	[10.1 - 16.0]	21.1	[18.9 - 23.6]	13.2	[10.8 - 15.9]	15.22
'GCF_001267315.1_ASM126731v1_genomic.fna'	*Pseudomonas peli* 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'	*Atopomonas sediminilitoris* A3.4T	12.9	[10.2 - 16.2]	21.1	[18.8 - 23.5]	13.3	[10.9 - 16.0]	10.42
'GCF_001267255.1_ASM126725v1_genomic.fna'	*Pseudomonas abyssi* MT5	12.8	[10.1 - 16.0]	21.1	[18.8 - 23.5]	13.1	[10.8 - 15.9]	13.83
'GCF_001267315.1_ASM126731v1_genomic.fna'	*Pseudomonas aestuarii* SA3-5T	12.8	[10.1 - 16.1]	21.1	[18.9 - 23.6]	13.2	[10.9 - 16.0]	15.31
'GCF_001267175.1_ASM126717v1_genomic.fna'	*Pseudomonas campi* DSM 110222	13.0	[10.2 - 16.2]	21.1	[18.8 - 23.5]	13.3	[11.0 - 16.1]	16.09
'GCF_030329025.1_ASM3032902v1_genomic.fna'	*Pseudomonas tensinigenes* ZA 5.3	12.8	[10.1 - 16.1]	21.1	[18.9 - 23.6]	13.2	[10.9 - 16.0]	12.07
'GCF_001267295.1_ASM126729v1_genomic.fna'	*Pseudomonas campi* DSM 110222	13.0	[10.3 - 16.3]	21.1	[18.9 - 23.6]	13.3	[11.0 - 16.1]	16.0
'GCF_001267255.1_ASM126725v1_genomic.fna'	*Pseudomonas toyotomiensis* 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'	*Pseudomonas pharmacofabricae* 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'	*Atopomonas hussainii* 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'	*Thiopseudomonas denitrificans* DSM 28679	12.9	[10.2 - 16.2]	21.0	[18.8 - 23.5]	13.3	[10.9 - 16.1]	11.51
'GCF_001267175.1_ASM126717v1_genomic.fna'	*Pseudomonas peli* DSM 17833	12.9	[10.2 - 16.2]	21.0	[18.8 - 23.4]	13.3	[10.9 - 16.1]	12.36
'GCF_001267315.1_ASM126731v1_genomic.fna'	*Pseudomonas taeanensis* MS-3	12.8	[10.2 - 16.1]	21.0	[18.8 - 23.4]	13.2	[10.9 - 16.0]	13.7
'GCF_001267215.1_ASM126721v1_genomic.fna'	*Atopomonas sediminilitoris* A3.4T	12.9	[10.2 - 16.2]	21.0	[18.8 - 23.5]	13.3	[10.9 - 16.0]	10.12
'GCF_001267195.1_ASM126719v1_genomic.fna'	*Pseudomonas pharmacofabricae* ZYSR67-Z	13.0	[10.3 - 16.3]	21.0	[18.8 - 23.4]	13.4	[11.0 - 16.1]	15.16
'GCF_001267295.1_ASM126729v1_genomic.fna'	*Pseudomonas aestuarii* SA3-5T	12.9	[10.2 - 16.1]	21.0	[18.7 - 23.4]	13.2	[10.9 - 16.0]	15.07
'GCF_001267215.1_ASM126721v1_genomic.fna'	*Pseudomonas peli* DSM 17833	12.9	[10.2 - 16.2]	20.9	[18.7 - 23.3]	13.3	[11.0 - 16.1]	12.22
'GCF_001267195.1_ASM126719v1_genomic.fna'	*Halopseudomonas sabulinigri* JCM 14963	12.8	[10.2 - 16.1]	20.9	[18.7 - 23.3]	13.2	[10.9 - 16.0]	12.46
'GCF_001267255.1_ASM126725v1_genomic.fna'	*Azomonas agilis* DSM 375	12.9	[10.2 - 16.2]	20.9	[18.7 - 23.4]	13.3	[11.0 - 16.1]	4.35
'GCF_001267275.1_ASM126727v1_genomic.fna'	*Azomonas agilis* DSM 375	12.9	[10.2 - 16.2]	20.9	[18.6 - 23.3]	13.3	[10.9 - 16.1]	4.39
'GCF_001267275.1_ASM126727v1_genomic.fna'	*Pseudomonas indica* JCM 21544	12.8	[10.1 - 16.1]	20.9	[18.7 - 23.3]	13.2	[10.8 - 15.9]	16.73

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'	*Pseudomonas sediminis* 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'	*Pseudomonas subflava* YIM B01952	12.8	[10.1 - 16.1]	20.9	[18.7 - 23.4]	13.2	[10.8 - 15.9]	19.08
'GCF_001267255.1_ASM126725v1_genomic.fna'	*Thiopseudomonas denitrificans* DSM 28679	13.0	[10.3 - 16.3]	20.9	[18.7 - 23.3]	13.4	[11.0 - 16.2]	11.54
'GCF_001267295.1_ASM126729v1_genomic.fna'	*Pseudomonas peli* DSM 17833	12.9	[10.2 - 16.2]	20.9	[18.7 - 23.3]	13.3	[11.0 - 16.1]	12.28
'GCF_001267175.1_ASM126717v1_genomic.fna'	*Pseudomonas aestuarii* SA3-5T	12.9	[10.2 - 16.1]	20.9	[18.7 - 23.4]	13.2	[10.9 - 16.0]	15.15
'GCF_001267255.1_ASM126725v1_genomic.fna'	*Pseudomonas subflava* YIM B01952	12.8	[10.1 - 16.1]	20.9	[18.7 - 23.4]	13.2	[10.8 - 15.9]	19.04
'GCF_030328955.1_ASM3032895v1_genomic.fna'	*Denitrificimonas caeni* DSM 24390	14.1	[11.3 - 17.4]	20.8	[18.5 - 23.2]	14.3	[11.9 - 17.2]	0.66
'GCF_001267255.1_ASM126725v1_genomic.fna'	*Pseudomonas pharmacofabricae* ZYSR67-Z	13.1	[10.4 - 16.4]	20.8	[18.5 - 23.2]	13.4	[11.1 - 16.2]	15.2
'GCF_001267275.1_ASM126727v1_genomic.fna'	*Thiopseudomonas denitrificans* DSM 28679	13.0	[10.3 - 16.3]	20.8	[18.6 - 23.2]	13.4	[11.0 - 16.2]	11.59
'GCF_001267275.1_ASM126727v1_genomic.fna'	*Pseudomonas pharmacofabricae* ZYSR67-Z	13.1	[10.4 - 16.4]	20.8	[18.5 - 23.2]	13.4	[11.1 - 16.2]	15.24
'GCF_030328955.1_ASM3032895v1_genomic.fna'	*Thiopseudomonas acetoxidans* CY1220	13.5	[10.7 - 16.8]	20.8	[18.6 - 23.2]	13.8	[11.4 - 16.6]	0.96
'GCF_030328955.1_ASM3032895v1_genomic.fna'	*Thiopseudomonas denitrificans* DSM 28679	13.0	[10.2 - 16.2]	20.8	[18.6 - 23.2]	13.3	[11.0 - 16.1]	11.37
'GCF_001267255.1_ASM126725v1_genomic.fna'	*Pseudomonas indica* JCM 21544	12.8	[10.1 - 16.1]	20.8	[18.6 - 23.2]	13.2	[10.8 - 15.9]	16.69
'GCF_001267295.1_ASM126729v1_genomic.fna'	*Pseudomonas flexibilis* ATCC 29606	12.9	[10.2 - 16.2]	20.8	[18.6 - 23.2]	13.3	[10.9 - 16.0]	18.36
'GCF_001267215.1_ASM126721v1_genomic.fna'	*Pseudomonas campi* DSM 110222	13.0	[10.3 - 16.3]	20.8	[18.6 - 23.2]	13.4	[11.0 - 16.1]	15.94
'GCF_001267315.1_ASM126731v1_genomic.fna'	*Pseudomonas flexibilis* ATCC 29606	12.9	[10.2 - 16.2]	20.8	[18.5 - 23.2]	13.3	[10.9 - 16.0]	18.6
'GCF_001267215.1_ASM126721v1_genomic.fna'	*Pseudomonas flexibilis* 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'	*Pseudomonas campi* DSM 110222	12.9	[10.2 - 16.2]	20.7	[18.5 - 23.1]	13.3	[11.0 - 16.1]	16.06
'GCF_001267195.1_ASM126719v1_genomic.fna'	*Azomonas agilis* DSM 375	12.9	[10.2 - 16.2]	20.7	[18.4 - 23.1]	13.2	[10.9 - 16.0]	4.32
'GCF_001267275.1_ASM126727v1_genomic.fna'	*Atopomonas sediminilitoris* 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'	*Pseudomonas flexibilis* ATCC 29606	12.9	[10.2 - 16.2]	20.7	[18.5 - 23.1]	13.3	[10.9 - 16.0]	18.45
'GCF_030328955.1_ASM3032895v1_genomic.fna'	*Azomonas agilis* DSM 375	12.8	[10.1 - 16.0]	20.7	[18.4 - 23.1]	13.1	[10.8 - 15.9]	4.17
'GCF_030328955.1_ASM3032895v1_genomic.fna'	*Pseudomonas sessilinigenes* CMR12a	12.8	[10.1 - 16.1]	20.7	[18.5 - 23.1]	13.2	[10.8 - 15.9]	15.2
'GCF_001267275.1_ASM126727v1_genomic.fna'	*Pseudomonas peli* DSM 17833	12.9	[10.2 - 16.2]	20.6	[18.4 - 23.1]	13.3	[10.9 - 16.0]	12.34
'GCF_001267215.1_ASM126721v1_genomic.fna'	*Pseudomonas taeanensis* MS-3	12.9	[10.2 - 16.2]	20.6	[18.4 - 23.0]	13.2	[10.9 - 16.0]	13.4

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_001267255.1_ASM126725v1_genomic.fna'	*Pseudomonas peli* DSM 17833	12.9	[10.2 - 16.2]	20.6	[18.3 - 23.0]	13.3	[10.9 - 16.1]	12.29
'GCF_001267295.1_ASM126729v1_genomic.fna'	*Pseudomonas taeanensis* MS-3	12.9	[10.2 - 16.2]	20.6	[18.4 - 23.0]	13.3	[10.9 - 16.0]	13.46
'GCF_001267195.1_ASM126719v1_genomic.fna'	*Pseudomonas indica* JCM 21544	12.8	[10.1 - 16.0]	20.6	[18.4 - 23.0]	13.1	[10.8 - 15.9]	16.65
'GCF_001267315.1_ASM126731v1_genomic.fna'	*Pseudomonas fluvialis* ASS-1	13.0	[10.3 - 16.3]	20.6	[18.4 - 23.0]	13.4	[11.0 - 16.2]	15.46
'GCF_001267315.1_ASM126731v1_genomic.fna'	*Thiopseudomonas denitrificans* DSM 28679	13.0	[10.3 - 16.3]	20.6	[18.3 - 23.0]	13.4	[11.0 - 16.1]	11.77
'GCF_001267195.1_ASM126719v1_genomic.fna'	*Pseudomonas peli* 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'	*Atopomonas hussainii* JCM 19513	12.9	[10.2 - 16.2]	20.6	[18.4 - 23.1]	13.3	[10.9 - 16.0]	11.36
'GCF_001267255.1_ASM126725v1_genomic.fna'	*Pseudomonas campi* DSM 110222	13.0	[10.3 - 16.3]	20.6	[18.4 - 23.1]	13.4	[11.0 - 16.1]	16.02
'GCF_001267255.1_ASM126725v1_genomic.fna'	*Atopomonas sediminilitoris* A3.4T	12.9	[10.2 - 16.2]	20.6	[18.4 - 23.1]	13.2	[10.9 - 16.0]	10.2
'GCF_001267275.1_ASM126727v1_genomic.fna'	*Pseudomonas aestuarii* SA3-5T	12.8	[10.1 - 16.1]	20.5	[18.3 - 22.9]	13.2	[10.9 - 16.0]	15.13
'GCF_001267315.1_ASM126731v1_genomic.fna'	*Pseudomonas fluvialis* CCM 8778	13.0	[10.3 - 16.3]	20.5	[18.2 - 22.9]	13.4	[11.0 - 16.2]	15.45
'GCF_030328995.1_ASM3032899v1_genomic.fna'	*Thiopseudomonas denitrificans* DSM 28679	13.0	[10.3 - 16.3]	20.5	[18.2 - 22.9]	13.3	[11.0 - 16.1]	10.81
'GCF_001267195.1_ASM126719v1_genomic.fna'	*Atopomonas sediminilitoris* A3.4T	12.8	[10.1 - 16.1]	20.5	[18.3 - 22.9]	13.2	[10.9 - 16.0]	10.16
'GCF_001267295.1_ASM126729v1_genomic.fna'	*Pseudomonas fluvialis* ASS-1	13.0	[10.3 - 16.3]	20.5	[18.3 - 22.9]	13.4	[11.0 - 16.2]	15.21
'GCF_001267215.1_ASM126721v1_genomic.fna'	*Pseudomonas aestuarii* SA3-5T	12.9	[10.2 - 16.2]	20.5	[18.3 - 22.9]	13.3	[10.9 - 16.0]	15.01
'GCF_030329025.1_ASM3032902v1_genomic.fna'	*Pseudomonas indoloxydans* JCM 14246	12.8	[10.1 - 16.0]	20.5	[18.3 - 22.9]	13.1	[10.8 - 15.9]	15.14
'GCF_001267255.1_ASM126725v1_genomic.fna'	*Pseudomonas aestuarii* SA3-5T	12.8	[10.2 - 16.1]	20.5	[18.3 - 22.9]	13.2	[10.9 - 16.0]	15.09
'GCF_030329025.1_ASM3032902v1_genomic.fna'	*Chryseomonas asuensis* 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'	*Pseudomonas fluvialis* 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'	*Pseudomonas indoloxydans* JCM 14246	12.7	[10.1 - 16.0]	20.4	[18.2 - 22.8]	13.1	[10.8 - 15.9]	14.64
'GCF_001267175.1_ASM126717v1_genomic.fna'	*Denitrificimonas caeni* DSM 24390	14.0	[11.2 - 17.3]	20.4	[18.2 - 22.8]	14.2	[11.8 - 17.0]	0.9
'GCF_001267175.1_ASM126717v1_genomic.fna'	*Pseudomonas fluvialis* ASS-1	13.0	[10.3 - 16.3]	20.4	[18.2 - 22.9]	13.4	[11.0 - 16.2]	15.3
'GCF_001267295.1_ASM126729v1_genomic.fna'	*Pseudomonas fluvialis* 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'	*Pseudomonas campi* DSM 110222	12.9	[10.2 - 16.2]	20.4	[18.1 - 22.8]	13.3	[10.9 - 16.1]	15.99
'GCF_001267215.1_ASM126721v1_genomic.fna'	*Thiopseudomonas acetoxidans* CY1220	13.6	[10.8 - 16.9]	20.3	[18.1 - 22.7]	13.9	[11.5 - 16.7]	1.06
'GCF_001267215.1_ASM126721v1_genomic.fna'	*Pseudomonas fluvialis* CCM 8778	13.1	[10.3 - 16.4]	20.3	[18.1 - 22.8]	13.4	[11.0 - 16.2]	15.15

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'	*Pseudomonas perfectomarina* CCUG 16156	12.8	[10.1 - 16.0]	20.3	[18.1 - 22.8]	13.1	[10.8 - 15.9]	14.28
'GCF_001267175.1_ASM126717v1_genomic.fna'	*Pseudomonas nicosulfuronedens* LAM1902T	12.8	[10.1 - 16.0]	20.3	[18.1 - 22.8]	13.1	[10.8 - 15.9]	17.43
'GCF_030328995.1_ASM3032899v1_genomic.fna'	*Pseudomonas perfectomarina* CCUG 16156	12.8	[10.1 - 16.0]	20.3	[18.0 - 22.7]	13.1	[10.8 - 15.9]	13.22
'GCF_030328955.1_ASM3032895v1_genomic.fna'	*Halopseudomonas sabulinigri* JCM 14963	12.8	[10.1 - 16.1]	20.3	[18.1 - 22.8]	13.2	[10.8 - 15.9]	12.31
'GCF_001267275.1_ASM126727v1_genomic.fna'	*Pseudomonas flexibilis* ATCC 29606	12.9	[10.2 - 16.2]	20.3	[18.1 - 22.7]	13.3	[10.9 - 16.0]	18.42
'GCF_001267315.1_ASM126731v1_genomic.fna'	*Denitrificimonas caeni* DSM 24390	13.9	[11.1 - 17.3]	20.3	[18.1 - 22.8]	14.2	[11.8 - 17.0]	1.06
'GCF_001267175.1_ASM126717v1_genomic.fna'	*Pseudomonas taeanensis* 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'	*Thiopseudomonas acetoxidans* CY1220	13.5	[10.7 - 16.8]	20.3	[18.1 - 22.7]	13.8	[11.4 - 16.6]	1.46
'GCF_001267175.1_ASM126717v1_genomic.fna'	*Pseudomonas fluvialis* CCM 8778	13.0	[10.3 - 16.3]	20.3	[18.1 - 22.8]	13.4	[11.0 - 16.2]	15.29
'GCF_001267255.1_ASM126725v1_genomic.fna'	*Pseudomonas flexibilis* ATCC 29606	12.9	[10.2 - 16.2]	20.3	[18.1 - 22.7]	13.3	[10.9 - 16.0]	18.38
'GCF_030328995.1_ASM3032899v1_genomic.fna'	*Thiopseudomonas denitrificans* DSM 28679	13.0	[10.3 - 16.3]	20.3	[18.1 - 22.7]	13.3	[11.0 - 16.1]	10.82
'GCF_001267255.1_ASM126725v1_genomic.fna'	*Denitrificimonas caeni* DSM 24390	14.1	[11.3 - 17.4]	20.2	[18.0 - 22.6]	14.3	[11.9 - 17.1]	0.83
'GCF_001267195.1_ASM126719v1_genomic.fna'	*Pseudomonas fluvialis* ASS-1	13.0	[10.3 - 16.2]	20.2	[18.0 - 22.6]	13.3	[11.0 - 16.1]	15.2
'GCF_001267295.1_ASM126729v1_genomic.fna'	*Thiopseudomonas denitrificans* DSM 28679	13.0	[10.3 - 16.3]	20.2	[18.0 - 22.6]	13.3	[11.0 - 16.1]	11.53
'GCF_001267295.1_ASM126729v1_genomic.fna'	*Thiopseudomonas acetoxidans* CY1220	13.5	[10.7 - 16.8]	20.2	[18.0 - 22.6]	13.8	[11.4 - 16.6]	1.12
'GCF_001267215.1_ASM126721v1_genomic.fna'	*Pseudomonas nicosulfuronedens* LAM1902T	12.8	[10.1 - 16.0]	20.2	[17.9 - 22.6]	13.1	[10.8 - 15.9]	17.29
'GCF_001267195.1_ASM126719v1_genomic.fna'	*Thiopseudomonas acetoxidans* CY1220	13.4	[10.6 - 16.7]	20.2	[18.0 - 22.6]	13.7	[11.3 - 16.5]	1.11
'GCF_030328995.1_ASM3032899v1_genomic.fna'	*Pseudomonas indoloxydans* 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'	*Pseudomonas nicosulfuronedens* LAM1902T	12.7	[10.0 - 16.0]	20.2	[18.0 - 22.6]	13.1	[10.8 - 15.9]	17.33
'GCF_001267255.1_ASM126725v1_genomic.fna'	*Thiopseudomonas acetoxidans* CY1220	13.6	[10.9 - 17.0]	20.2	[18.0 - 22.6]	13.9	[11.5 - 16.7]	1.14
'GCF_030329025.1_ASM3032902v1_genomic.fna'	*Pseudomonas indica* NBRC 103045	12.7	[10.0 - 16.0]	20.2	[18.0 - 22.6]	13.1	[10.8 - 15.9]	17.03
'GCF_030328955.1_ASM3032895v1_genomic.fna'	*Pseudomonas perfectomarina* CCUG 16156	12.8	[10.1 - 16.0]	20.2	[18.0 - 22.6]	13.1	[10.8 - 15.9]	13.78
'GCF_001267175.1_ASM126717v1_genomic.fna'	*Thiopseudomonas denitrificans* DSM 28679	13.0	[10.3 - 16.3]	20.1	[17.9 - 22.5]	13.3	[11.0 - 16.1]	11.61
'GCF_001267195.1_ASM126719v1_genomic.fna'	*Thiopseudomonas denitrificans* DSM 28679	12.9	[10.2 - 16.2]	20.1	[17.9 - 22.5]	13.2	[10.9 - 16.0]	11.52

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_ASM 3032899v1_genomic.fna'	*Pseudomonas xionganensis* 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_001267295.1_ASM 126729v1_genomic.fna'	*Denitrificimonas caeni* DSM 24390	13.9	[11.1 - 17.3]	20.1	[17.9 - 22.5]	14.2	[11.7 - 17.0]	0.82
'GCF_030329025.1_ASM 3032902v1_genomic.fna'	*Halopseudomonas sabulinigri* JCM 14963	12.8	[10.1 - 16.1]	20.1	[17.9 - 22.5]	13.2	[10.9 - 16.0]	12.81
'GCF_001267275.1_ASM 126727v1_genomic.fna'	*Denitrificimonas caeni* DSM 24390	13.9	[11.1 - 17.2]	20.1	[17.9 - 22.5]	14.1	[11.7 - 17.0]	0.88
'GCF_001267215.1_ASM 126721v1_genomic.fna'	*Thiopseudomonas denitrificans* 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_ASM 126727v1_genomic.fna'	*Pseudomonas taeanensis* MS-3	12.9	[10.2 - 16.1]	20.1	[17.9 - 22.5]	13.2	[10.9 - 16.0]	13.52
'GCF_030329025.1_ASM 3032902v1_genomic.fna'	*Pseudomonas xionganensis* 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_ASM 3032899v1_genomic.fna'	*Pseudomonas indica* NBRC 103045	12.7	[10.0 - 16.0]	20.1	[17.8 - 22.5]	13.1	[10.8 - 15.9]	15.97
'GCF_030328955.1_ASM 3032895v1_genomic.fna'	*Pseudomonas indica* NBRC 103045	12.7	[10.0 - 16.0]	20.1	[17.9 - 22.6]	13.1	[10.8 - 15.9]	16.53
'GCF_001267255.1_ASM 126725v1_genomic.fna'	*Pseudomonas fluvialis* ASS-1	13.0	[10.3 - 16.3]	20.1	[17.8 - 22.5]	13.4	[11.0 - 16.2]	15.23
'GCF_001267275.1_ASM 126727v1_genomic.fna'	*Thiopseudomonas acetoxidans* CY1220	13.6	[10.8 - 16.9]	20.1	[17.9 - 22.5]	13.9	[11.5 - 16.7]	1.18
'GCF_001267295.1_ASM 126729v1_genomic.fna'	*Pseudomonas nicosulfuronedens* LAM1902T	12.8	[10.1 - 16.1]	20.1	[17.9 - 22.5]	13.2	[10.8 - 15.9]	17.35
'GCF_001267195.1_ASM 126719v1_genomic.fna'	*Pseudomonas fluvialis* CCM 8778	13.0	[10.3 - 16.3]	20.1	[17.9 - 22.5]	13.3	[11.0 - 16.1]	15.19
'GCF_001267195.1_ASM 126719v1_genomic.fna'	*Pseudomonas aestuarii* SA3-5T	12.8	[10.1 - 16.1]	20.1	[17.8 - 22.5]	13.2	[10.9 - 16.0]	15.05
'GCF_030328955.1_ASM 3032895v1_genomic.fna'	*Pseudomonas pseudoalcaligenes* 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_ASM 126725v1_genomic.fna'	*Pseudomonas taeanensis* MS-3	12.9	[10.2 - 16.2]	20.1	[17.9 - 22.5]	13.2	[10.9 - 16.0]	13.47
'GCF_030329025.1_ASM 3032902v1_genomic.fna'	*Denitrificimonas caeni* 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_ASM 3032899v1_genomic.fna'	*Halopseudomonas sabulinigri* JCM 14963	12.8	[10.1 - 16.1]	20.1	[17.9 - 22.5]	13.2	[10.9 - 16.0]	11.76
'GCF_030329025.1_ASM 3032902v1_genomic.fna'	*Pseudomonas matsuisoli* JCM 30078	12.7	[10.0 - 16.0]	20.0	[17.8 - 22.4]	13.1	[10.8 - 15.8]	12.37
'GCF_030329025.1_ASM 3032902v1_genomic.fna'	*Thiopseudomonas denitrificans* DSM 28679	12.9	[10.2 - 16.2]	20.0	[17.8 - 22.5]	13.3	[11.0 - 16.1]	11.87
'GCF_030328955.1_ASM 3032895v1_genomic.fna'	*Pseudomonas pharmacofabricae* ZYSR67-Z	13.0	[10.3 - 16.3]	20.0	[17.8 - 22.4]	13.4	[11.0 - 16.1]	15.02
'GCF_030328955.1_ASM 3032895v1_genomic.fna'	*Thiopseudomonas denitrificans* DSM 28679	12.9	[10.2 - 16.2]	20.0	[17.8 - 22.4]	13.3	[10.9 - 16.1]	11.37
'GCF_001267255.1_ASM 126725v1_genomic.fna'	*Pseudomonas fluvialis* CCM 8778	13.0	[10.3 - 16.3]	20.0	[17.8 - 22.4]	13.4	[11.0 - 16.2]	15.23

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'	*Pseudomonas matsuisoli* JCM 30078	12.7	[10.0 - 16.0]	20.0	[17.8 - 22.4]	13.1	[10.8 - 15.8]	11.87
'GCF_001267175.1_ASM126717v1_genomic.fna'	*Thiopseudomonas acetoxidans* CY1220	13.4	[10.7 - 16.8]	20.0	[17.8 - 22.4]	13.8	[11.4 - 16.5]	1.21
'GCF_001267275.1_ASM126727v1_genomic.fna'	*Pseudomonas fluvialis* ASS-1	13.0	[10.3 - 16.3]	20.0	[17.8 - 22.4]	13.4	[11.0 - 16.2]	15.27
'GCF_001267255.1_ASM126725v1_genomic.fna'	*Thiopseudomonas denitrificans* DSM 28679	13.0	[10.3 - 16.3]	20.0	[17.8 - 22.4]	13.3	[11.0 - 16.1]	11.55
'GCF_001267275.1_ASM126727v1_genomic.fna'	*Pseudomonas fluvialis* CCM 8778	13.0	[10.3 - 16.3]	20.0	[17.8 - 22.4]	13.4	[11.0 - 16.2]	15.27
'GCF_001267195.1_ASM126719v1_genomic.fna'	*Pseudomonas taeanensis* MS-3	12.8	[10.1 - 16.1]	20.0	[17.8 - 22.4]	13.2	[10.9 - 16.0]	13.44
'GCF_030329025.1_ASM3032902v1_genomic.fna'	*Pseudomonas sediminis* PI11	12.8	[10.1 - 16.1]	20.0	[17.8 - 22.4]	13.2	[10.8 - 15.9]	15.38
'GCF_030328995.1_ASM3032899v1_genomic.fna'	*Pseudomonas pharmacofabricae* 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'	*Pseudomonas toyotomiensis* 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'	*Pseudomonas matsuisoli* JCM 30078	12.7	[10.0 - 16.0]	19.8	[17.6 - 22.2]	13.1	[10.8 - 15.9]	11.32
'GCF_030328955.1_ASM3032895v1_genomic.fna'	*Pseudomonas xionganensis* 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_030329025.1_ASM3032902v1_genomic.fna'	*Pseudomonas indica* 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'	*Pseudomonas sediminis* PI11	12.8	[10.1 - 16.1]	19.8	[17.6 - 22.2]	13.2	[10.8 - 15.9]	14.32
'GCF_001267275.1_ASM126727v1_genomic.fna'	*Thiopseudomonas denitrificans* DSM 28679	13.0	[10.3 - 16.3]	19.8	[17.6 - 22.2]	13.3	[11.0 - 16.1]	11.59
'GCF_030329025.1_ASM3032902v1_genomic.fna'	*Pseudomonas pseudoalcaligenes* 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'	*Pseudomonas toyotomiensis* JCM 15604	12.8	[10.1 - 16.0]	19.8	[17.6 - 22.2]	13.1	[10.8 - 15.9]	14.45
'GCF_030329025.1_ASM3032902v1_genomic.fna'	*Pseudomonas pharmacofabricae* ZYSR67-Z	13.0	[10.3 - 16.3]	19.8	[17.6 - 22.2]	13.4	[11.0 - 16.1]	15.52
'GCF_030329025.1_ASM3032902v1_genomic.fna'	*Pseudomonas peli* DSM 17833	12.9	[10.2 - 16.1]	19.7	[17.5 - 22.1]	13.2	[10.9 - 16.0]	12.62
'GCF_001267255.1_ASM126725v1_genomic.fna'	*Pseudomonas nicosulfuronedens* LAM1902T	12.8	[10.1 - 16.1]	19.7	[17.5 - 22.1]	13.2	[10.8 - 15.9]	17.36
'GCF_001267215.1_ASM126721v1_genomic.fna'	*Denitrificimonas caeni* DSM 24390	14.0	[11.2 - 17.3]	19.7	[17.5 - 22.1]	14.2	[11.8 - 17.0]	0.75
'GCF_030328995.1_ASM3032899v1_genomic.fna'	*Pseudomonas pseudoalcaligenes* NBRC 14167	12.8	[10.1 - 16.1]	19.7	[17.5 - 22.1]	13.2	[10.8 - 15.9]	14.09
'GCF_030328995.1_ASM3032899v1_genomic.fna'	*Pseudomonas peli* DSM 17833	12.9	[10.2 - 16.2]	19.7	[17.5 - 22.1]	13.2	[10.9 - 16.0]	11.56

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'	*Azomonas agilis* 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'	*Atopomonas hussainii* JCM 19513	12.8	[10.1 - 16.1]	19.7	[17.5 - 22.1]	13.2	[10.9 - 16.0]	11.72
'GCF_030328955.1_ASM3032895v1_genomic.fna'	*Atopomonas hussainii* 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'	*Pseudomonas campi* DSM 110222	12.9	[10.2 - 16.2]	19.7	[17.5 - 22.1]	13.3	[10.9 - 16.0]	16.34
'GCF_030328955.1_ASM3032895v1_genomic.fna'	*Pseudomonas indica* 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'	*Thiopseudomonas denitrificans* DSM 28679	12.9	[10.2 - 16.2]	19.6	[17.4 - 22.0]	13.3	[10.9 - 16.1]	11.87
'GCF_001267275.1_ASM126727v1_genomic.fna'	*Pseudomonas nicosulfuronedens* LAM1902T	12.8	[10.1 - 16.0]	19.6	[17.4 - 22.0]	13.2	[10.8 - 15.9]	17.41
'GCF_030328995.1_ASM3032899v1_genomic.fna'	*Azomonas agilis* DSM 375	12.9	[10.2 - 16.2]	19.6	[17.4 - 22.0]	13.3	[10.9 - 16.0]	3.62
'GCF_030328995.1_ASM3032899v1_genomic.fna'	*Pseudomonas indica* JCM 21544	12.8	[10.1 - 16.0]	19.6	[17.4 - 22.0]	13.1	[10.8 - 15.9]	15.95
'GCF_030328995.1_ASM3032899v1_genomic.fna'	*Denitrificimonas caeni* DSM 24390	14.0	[11.2 - 17.3]	19.6	[17.4 - 22.0]	14.2	[11.8 - 17.0]	0.1
'GCF_030328955.1_ASM3032895v1_genomic.fna'	*Pseudomonas campi* 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'	*Pseudomonas subflava* YIM B01952	12.7	[10.0 - 16.0]	19.5	[17.3 - 21.9]	13.1	[10.8 - 15.9]	18.31
'GCF_030328955.1_ASM3032895v1_genomic.fna'	*Pseudomonas toyotomiensis* JCM 15604	12.7	[10.1 - 16.0]	19.5	[17.3 - 21.9]	13.1	[10.8 - 15.9]	15.0
'GCF_030328995.1_ASM3032899v1_genomic.fna'	*Pseudomonas campi* DSM 110222	12.9	[10.2 - 16.2]	19.5	[17.3 - 21.9]	13.3	[10.9 - 16.0]	15.29
'GCF_030328995.1_ASM3032899v1_genomic.fna'	*Pseudomonas abyssi* MT5	12.7	[10.0 - 16.0]	19.5	[17.3 - 21.9]	13.1	[10.8 - 15.8]	13.1
'GCF_001267195.1_ASM126719v1_genomic.fna'	*Denitrificimonas caeni* DSM 24390	13.8	[11.0 - 17.2]	19.5	[17.3 - 21.9]	14.1	[11.6 - 16.9]	0.8
'GCF_030328955.1_ASM3032895v1_genomic.fna'	*Pseudomonas peli* DSM 17833	12.9	[10.2 - 16.1]	19.5	[17.3 - 21.9]	13.2	[10.9 - 16.0]	12.12
'GCF_030328955.1_ASM3032895v1_genomic.fna'	*Atopomonas sediminilitoris* A3.4T	12.8	[10.1 - 16.1]	19.5	[17.3 - 21.9]	13.2	[10.8 - 15.9]	10.02
'GCF_030328955.1_ASM3032895v1_genomic.fna'	*Pseudomonas taeanensis* MS-3	12.8	[10.1 - 16.1]	19.4	[17.3 - 21.8]	13.2	[10.8 - 15.9]	13.3
'GCF_030328995.1_ASM3032899v1_genomic.fna'	*Atopomonas hussainii* 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'	*Pseudomonas abyssi* MT5	12.7	[10.0 - 16.0]	19.3	[17.1 - 21.7]	13.1	[10.8 - 15.8]	14.15

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_ASM 3032899v1_genomic.fna'	*Atopomonas sediminilitoris* A3.4T	12.8	[10.1 - 16.1]	19.3	[17.1 - 21.7]	13.2	[10.8 - 15.9]	9.46
'GCF_030329025.1_ASM 3032902v1_genomic.fna'	*Pseudomonas subflava* YIM B01952	12.7	[10.1 - 16.0]	19.2	[17.0 - 21.6]	13.1	[10.8 - 15.9]	19.36
'GCF_030328955.1_ASM 3032895v1_genomic.fna'	*Pseudomonas aestuarii* SA3-5T	12.8	[10.1 - 16.1]	19.2	[17.1 - 21.6]	13.2	[10.8 - 15.9]	14.91
'GCF_030328955.1_ASM 3032895v1_genomic.fna'	*Pseudomonas subflava* YIM B01952	12.7	[10.0 - 16.0]	19.2	[17.0 - 21.6]	13.1	[10.8 - 15.9]	18.86
'GCF_030328955.1_ASM 3032895v1_genomic.fna'	*Pseudomonas abyssi* MT5	12.7	[10.0 - 16.0]	19.2	[17.0 - 21.6]	13.1	[10.7 - 15.8]	13.65
'GCF_030329025.1_ASM 3032902v1_genomic.fna'	*Atopomonas sediminilitoris* 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_ASM 3032899v1_genomic.fna'	*Pseudomonas aestuarii* SA3-5T	12.8	[10.1 - 16.1]	19.0	[16.9 - 21.4]	13.2	[10.8 - 15.9]	14.36
'GCF_030329025.1_ASM 3032902v1_genomic.fna'	*Pseudomonas flexibilis* ATCC 29606	12.8	[10.1 - 16.1]	19.0	[16.8 - 21.4]	13.2	[10.9 - 16.0]	18.7
'GCF_030328995.1_ASM 3032899v1_genomic.fna'	*Pseudomonas fluvialis* ASS-1	13.0	[10.3 - 16.3]	19.0	[16.8 - 21.3]	13.3	[11.0 - 16.1]	14.5
'GCF_030328955.1_ASM 3032895v1_genomic.fna'	*Pseudomonas flexibilis* 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_ASM 3032899v1_genomic.fna'	*Pseudomonas fluvialis* CCM 8778	13.0	[10.3 - 16.3]	18.9	[16.7 - 21.3]	13.3	[11.0 - 16.1]	14.49
'GCF_030328995.1_ASM 3032899v1_genomic.fna'	*Pseudomonas flexibilis* 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_ASM 3032902v1_genomic.fna'	*Pseudomonas fluvialis* ASS-1	13.0	[10.3 - 16.3]	18.9	[16.7 - 21.3]	13.3	[11.0 - 16.1]	15.55
'GCF_030328995.1_ASM 3032899v1_genomic.fna'	*Pseudomonas taeanensis* 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_ASM 3032902v1_genomic.fna'	*Pseudomonas taeanensis* MS-3	12.8	[10.1 - 16.1]	18.8	[16.6 - 21.2]	13.2	[10.9 - 16.0]	13.8
'GCF_030328995.1_ASM 3032899v1_genomic.fna'	*Pseudomonas nicosulfuronedens* LAM1902T	12.7	[10.0 - 16.0]	18.8	[16.6 - 21.2]	13.1	[10.8 - 15.9]	16.63
'GCF_030329025.1_ASM 3032902v1_genomic.fna'	*Pseudomonas fluvialis* 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_ASM 3032902v1_genomic.fna'	*Pseudomonas aestuarii* SA3-5T	12.8	[10.1 - 16.1]	18.8	[16.6 - 21.1]	13.2	[10.8 - 15.9]	15.41
'GCF_030328955.1_ASM 3032895v1_genomic.fna'	*Pseudomonas fluvialis* CCM 8778	13.0	[10.3 - 16.3]	18.6	[16.4 - 21.0]	13.3	[11.0 - 16.1]	15.05
'GCF_030328955.1_ASM 3032895v1_genomic.fna'	*Pseudomonas fluvialis* ASS-1	13.0	[10.3 - 16.3]	18.6	[16.5 - 21.0]	13.3	[11.0 - 16.1]	15.05
'GCF_030329025.1_ASM 3032902v1_genomic.fna'	*Pseudomonas nicosulfuronedens* LAM1902T	12.7	[10.1 - 16.0]	18.4	[16.2 - 20.7]	13.1	[10.8 - 15.9]	17.69

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'	*Pseudomonas nicosulfuronedens* LAM1902T	12.7	[10.0 - 16.0]	18.4	[16.3 - 20.8]	13.1	[10.8 - 15.9]	17.19

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
Thiopseudomonas alkaliphila B4199	(Drobish et al. 2016) Rudra and Gupta 2021	CCUG 67636; DSM 100830	*Oblitimonas alkaliphila*; *Thiopseudomonas alkaliphila*	2494 031	47.4	2365	Gp0132979	PRJNA224116	SAMN03946311	GCF_001267175	
Thiopseudomonas denitrificans DSM 28679	Tan et al. 2015	KCTC 42076; CCTCC M 2013362; X2	*Thiopseudomonas denitrificans*	2840 727	59.0	2579		PRJNA299732	SAMN04214881	GCA_002866065	
Pseudomonas fluvialis ASS-1	Sudan et al. 2018	ASS-1; KCTC 52437; CCM 8778	*Caenipseudomonas fluvialis*; *Pseudomonas fluvialis*	3280 972	62.7	3045	Gp0323573	PRJNA393076	SAMN07314873	GCA_002234375	
Pseudomonas abyssi MT5	Wei et al. 2018	MCCC 1K03351; KCTC 62295	*Neopseudomonas abyssi*; *Pseudomonas abyssi*	4312 941	61.3	3955		PRJNA406957	SAMN07634961	GCA_002307495	
Pseudomonas aestuarii SA3-5T	Kim et al. 2023	KCTC 92395; JCM 35697	*Pseudomonas aestuarii*	5152 070	62.5	4596		PRJNA224116	SAMN32759035	GCF_027988105	
Pseudomonas nicosulfuronedens LAM1902T	Li et al. 2021	KCTC 72830; JCM 33860	*Pseudomonas nicosulfuronedens*	6668 285	64.8	6054		PRJNA533733	SAMN11465145	GCA_005877905	
Acinetobacter seohaensis DSM 16313	Yoon et al. 2007	KCTC 12260; SW-100	*Acinetobacter seohaensis*	2948 101	41.3	2766		PRJDB11573	SAMD00317521	GCA_018403785	
Advenella alkanexedens LAM0050	Wang et al. 2016	ACCC 6485; JCM 30465	*Advenella alkanexedens*	2984 716	49.8	2795		PRJNA224116	SAMN19967794	GCF_019132845	
Citrobacter tructae SNU WT2	Jung et al. 2021	KCTC 72517; JCM 33612	*Citrobacter tructae*	4946 572	52.0	4556		PRJNA224116	SAMN11282944	GCF_004684345	
Pseudomonas xionganensis R-22-3 w-18T	Zhao et al. 2020	CGMCC 1.17250; KCTC 72658	*Pseudomonas xionganensis*	3951 615	63.0	3621		PRJNA589163	SAMN13268013	GCA_009763245	

Strain	Authority	Other deposits	Synonyms	Base pairs	Percent G+C	No. proteins	Goldstamp	Bioproject accession	Biosample accession	Assembly accession	IMG OID
Pseudomonas toyotomiensis JCM 15604	Hirota et al. 2011	NCIMB 14511; DSM 26169; HT-3	*Ectopseudomonas toyotomiensis*; *Pseudomonas toyotomiensis*	5489804	62.6	5160	Gp0127184	PRJEB17410	SAMN05216177	GCA_900115695	
Pseudomonas flexibilis ATCC 29606	(Hespell 1977) Shin et al. 2016	LMG 29034	*Pseudomonas flexibilis*; *Serpens flexibilis*	3757903	65.8	3448	Gp0127303	PRJNA224116	SAMN05421672	GCF_900155995	2681812811
Pseudomonas tensinigenes ZA 5.3	Girard et al. 2022	CFBP 8882; LMG 32032	*Pseudomonas tensinigenes*	6621778	59.2	5788		PRJNA639797	SAMN15248349	GCA_014268445	
Pseudomonas indoloxydans JCM 14246	Manickam et al. 2008	IPL-1; MTCC 8062	*Pseudomonas indoloxydans*	5198577	62.2	4666	Gp0323509	PRJNA449191	SAMN08891239	GCA_003052605	
Denitrificimonas caeni DSM 24390	(Xiao et al. 2009) Saati-Santamaría et al. 2021	KCTC 22292; CECT 7778; CCTCC AB 208156; strain HY-14	*Denitrificimonas caeni*; *Pseudomonas caeni*; *Thiopseudomonas caeni*	3025373	48.3	2803	Gp0013191	PRJNA188884	SAMN02440589	GCA_000421765	2524614874
Pseudomonas pharmacofabricae ZYSR67-Z	Yu et al. 2019	CGMCC 1.15498; JCM 31306	*Caenipseudomonas pharmacofabricae*; *Pseudomonas pharmacofabricae*	3438518	62.6	3212	Gp0369617	PRJNA421062	SAMN08131258	GCA_002835605	
Pseudomonas yangonensis JCM 33396	Tohya et al. 2020	LMG 31602; MY50	*Ectopseudomonas yangonensis*; *Pseudomonas yangonensis*	5040544	62.9	4626		PRJDB8321	SAMD00171901	GCA_009932725	
Acinetobacter towneri DSM 14962	Carr et al. 2003	AB1110; CIP 107472	*Acinetobacter towneri*	2854510	41.2	2749	Gp0013868	PRJNA221010	SAMN02743902	GCA_000688495	2556921621
Thiopseudomonas denitrificans DSM 28679	Tan et al. 2015	KCTC 42076; CCTCC M 2013362; X2	*Thiopseudomonas denitrificans*	2831568	59.0	2581	Gp0290550	PRJNA463350	SAMN09074682	GCA_004363035	2770939502
Nitrosomonas stercoris ATCC BAA-2718	Nakagawa and Takahashi 2017	NBRC 110753; KYUHI-S	*Nitrosomonas stercoris*	2382370	44.8	2274		PRJDB8366	SAMD00173276	GCA_006742785	

Strain	Authority	Other deposits	Synonyms	Base pairs	Percent G+C	No. proteins	Goldstamp	Bioproject accession	Biosample accession	Assembly accession	IMG OID
Azomonas agilis DSM 375	(Beijerinck 1901) Winogradsky 1938	NCIMB 11693; ATCC 7494; JCM 21502; NBRC 102607; NCIB 11693	*Azomonas agilis*; *Azotobacter agilis*	3275 197	51.8	3038	Gp0103623	PRJNA262246	SAMN05660238	GCA_007830255	2596583523
Shigella flexneri ATCC 29903	Castellani and Chalmers 1919	CIP 82.48; DSM 4782	*Shigella flexneri*	4938 295	50.7	5112	Gp0307840	PRJNA218110	SAMN08330274	GCA_002950215	
Pseudomonas pseudoalcaligenes 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	*Ectopseudomonas pseudoalcaligenes*; *Pseudomonas pseudoalcaligenes*; *Pseudomonas pseudoalcaligenes* subsp. *pseudoalcaligenes*	4702 414	62.2	4507	Gp0023768	PRJDB224	SAMD00046936	GCA_002091775	
Acinetobacter defluvii WCHA30	Hu et al. 2017	KCTC 52503; CCTCC AB 2016203; GDMCC 1.1101	*Acinetobacter defluvii*	3737 173	38.0	3562	Gp0189167	PRJNA224116	SAMN05356262	GCF_001704615	
Thiopseudomonas acetoxidans CY1220	An et al. 2024	JCM 35747; GDMCC 1.3503	*Thiopseudomonas acetoxidans*	2534 758	48.6	2371		PRJNA224116	SAMN35795788	GCF_030362935	

Strain	Authority	Other deposits	Synonyms	Base pairs	Percent G+C	No. proteins	Goldstamp	Bioproject accession	Biosample accession	Assembly accession	IMG OID
Pseudomonas taeanensis MS-3	Lee et al. 2010	KCTC 22612; DSM 25633; JCM 16046; KACC 14032; NBRL 105641	*Pseudomonas taeanensis*	5460144	60.9	4594	Gp0049072	PRJNA217843	SAMN02470138	GCA_000498575	
Pseudomonas matsuisoli JCM 30078	Lin et al. 2015	BCRC 80771; CC-MHH0089	*Pseudomonas matsuisoli*	4603598	59.5	4102		PRJDB10510	SAMD00245291	GCA_014647635	
Chryseomonas asuensis JCM 13501	(Reddy and Garcia-Pichel 2015) Saati-Santamaría et al. 2021	LMG 28687; KCTC 32484; ATCC BAA-1264; DSM 17866; CP 155-2	*Chryseomonas asuensis*; *Pseudomonas asuensis*	5328059	53.6	4950		PRJDB10510	SAMD00245237	GCA_014646755	
Pseudomonas fluvialis CCM 8778	Sudan et al. 2018	ASS-1; KCTC 52437; CCM 8778	*Caenipseudomonas fluvialis*; *Pseudomonas fluvialis*	3304463	62.7	3092		PRJDB10511	SAMD00244871	GCA_014635625	
Pseudomonas peli DSM 17833	Vanparys et al. 2006	LMG 23201; R-20805	*Pseudomonas peli*	4486965	59.7	4256	Gp0127168	PRJEB15912	SAMN05216370	GCA_900099645	
Halopseudomonas sabulinigri JCM 14963	(Kim et al. 2009) Rudra and Gupta 2021	KCTC 22137; DSM 23971; J64	*Halopseudomonas sabulinigri*; *Neopseudomonas sabulinigri*; *Pseudomonas sabulinigri*	4030103	59.9	3624	Gp0127171	PRJEB16439	SAMN05216271	GCA_900105255	

Strain	Authority	Other deposits	Synonyms	Base pairs	Percent G+C	No. proteins	Goldstamp	Bioproject accession	Biosample accession	Assembly accession	IMG OID
Enterobacter cloacae 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	*Bacillus cloacae*; *Bacterium cloacae*; *Cloaca cloacae*; *Enterobacter cloacae*; *Enterobacter cloacae* subsp. *cloacae*	5598 795	54.6	5518	Gp0006802	PRJNA45793	SAMN02603901	GCA_000025565	646564529
Pseudomonas perfectomarina CCUG 16156	(ex ZoBell and Upham 1944) Baumann et al. 1983	218; LMG 2243; ATCC 14405; CECT 4899; JCM 20778; Baumann 218; ZoBell 632; ZoBell ATCC 14405	*Pseudomonas perfectomarina*; *Stutzerimonas perfectomarina*	4525 588	61.4	4126	Gp0016674	PRJNA74687	SAMN02471579	GCA_000237885	2529293194
Ignatzschineria cameli UAE-HKU57	Tsang et al. 2018	NBRC 113042; CCOS 1165	*Ignatzschineria cameli*	2485 449	41.7	2034	Gp0377909	PRJNA451073	SAMN08954446	GCA_003121895	
Pseudomonas subflava YIM B01952	Ling et al. 2023	KCTC 92073; CCTCC AB 2021498	*Pseudomonas subflava*	4427 497	66.5	4136		PRJNA849749	SAMN29132573	GCA_023823685	
Acinetobacter rongchengensis WCHAc060115 T	Qin et al. 2021	JCM 33512; GDMCC 1.1625	*Acinetobacter rongchengensis*	4067 804	37.6	3752		PRJNA224116	SAMN09842375	GCF_003611475	
Pseudomonas indica JCM 21544	Pandey et al. 2002	DSM 14015; JCM 21544; NBRC 103045; IMT37; MTCC 3713	*Pseudomonas indica*	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
Pseudomonas sessilinigenes CMR12a	Girard et al. 2022	CFBP 8877; LMG 32173	*Pseudomonas sessilinigenes*	6896 611	62.8	6284		PRJNA433211	SAMN08359212	GCA_003850565	
Atopomonas sediminilitoris A3.4T	Li et al. 2023	MCCC 1K07166; LMG 32563	*Atopomonas sediminilitoris*	3546 461	57.6	3215		PRJNA224116	SAMN26186988	GCF_022601735	
Atopomonas hussainii JCM 19513	(Hameed et al. 2014) Rudra and Gupta 2021	BCRC 80696; CC-AMH-11	*Atopomonas hussainii; Parapseudomonas hussainii; Pseudomonas hussainii*	3680 748	58.8	3429	Gp0127201	PRJEB16845	SAMN05216214	GCA_900109735	
Pseudomonas campi DSM 110222	Timsy et al. 2021	31,521; LMG 31521; S1-A32-2	*Aquipseudomonas campi; Pseudomonas campi*	4436 925	63.5	3980		PRJNA631893	SAMN14896266	GCA_013200955	
Pseudomonas indica NBRC 103045	Pandey et al. 2002	DSM 14015; JCM 21544; NBRC 103045; IMT37; MTCC 3713	*Pseudomonas indica*	5778 617	64.1	5141	Gp0024159	PRJDB211	SAMD00046928	GCA_002091635	
Pseudomonas sediminis PI11	Behera et al. 2018	KCTC 42576; DSM 100245	*Pseudomonas sediminis*	4878 472	62.5	4443	Gp0365654	PRJNA389586	SAMN07203179	GCA_002741105	
GCF_030329025.1_ASM3032902v1_genomic.fna				2440 383	47.1	2368					
GCF_030328995.1_ASM3032899v1_genomic.fna				2475 608	48.2	2344					
GCF_030328955.1_ASM3032895v1_genomic.fna				2572 910	47.6	2431					
GCF_001267315.1_ASM126731v1_genomic.fna				2397 029	47.2	2269					
GCF_001267295.1_ASM126729v1_genomic.fna				2377 259	47.4	2235					

Strain	Authority	Other deposits	Synonyms	Base pairs	Percent G+C	No. proteins	Goldstamp	Bioproject accession	Biosample accession	Assembly accession	IMG OID
GCF_001267275 .1_ASM126727v 1_genomic.fna				2391 994	47.4	2218					
GCF_001267255 .1_ASM126725v 1_genomic.fna				2294 397	47.4	2139					
GCF_001267215 .1_ASM126721v 1_genomic.fna				2312 033	47.5	2158					
GCF_001267195 .1_ASM126719v 1_genomic.fna				2272 143	47.5	2141					
GCF_001267175 .1_ASM126717v 1_genomic.fna				2494 031	47.4	2366					

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 2024-04-01. 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 20806 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 4.0 [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 43 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 39 species clusters and the provided query strains were assigned to 2 of these. Moreover, user strains were located in 3 of 41 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 66.5 %. 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 34.3 %. The tree was rooted at the midpoint [8].

References

[1] Meier-Kolthoff JP, Göker M. TYGS is an automated high-throughput platform for state-of-the-art genome-based taxonomy. Nat. Commun. 2019;10: 2182. DOI: 10.1038/s41467-019-10210-3

[2] Meier-Kolthoff JP, Sardà Carbasse J, Peinado-Olarte RL, Göker M. TYGS and LPSN: a database tandem for fast and reliable genome-based classification and nomenclature of prokaryotes. Nucleic Acid Res. 2022;50: D801−D807. DOI: 10.1093/nar/gkab902

[3] Ondov BD, Treangen TJ, Melsted P, et al. Mash: Fast genome and metagenome distance estimation using MinHash. Genome Biol 2016;17: 1−14. DOI: 10.1186/s13059-016-0997-x

[4] Lagesen K, Hallin P. RNAmmer: consistent and rapid annotation of ribosomal RNA genes. Nucleic Acids Res. Oxford Univ Press; 2007;35: 3100−3108. DOI: 10.1093/nar/gkm160

[5] Camacho C, Coulouris G, Avagyan V, Ma N, Papadopoulos J, Bealer K, et al. BLAST+: architecture and applications. BMC Bioinformatics. 2009;10: 421. DOI: 10.1186/1471-2105-10-421

[6] Meier-Kolthoff JP, Auch AF, Klenk H-P, Göker M. Genome sequence-based species delimitation with confidence intervals and improved distance functions. BMC Bioinformatics. 2013;14: 60. DOI: 10.1186/1471-2105-14-60

[7] Lefort V, Desper R, Gascuel O. FastME 2.0: A comprehensive, accurate, and fast distance-based phylogeny inference program. Mol Biol Evol. 2015;32: 2798−2800. DOI: 10.1093/molbev/msv150

[8] Farris JS. Estimating phylogenetic trees from distance matrices. Am Nat. 1972;106: 645−667.

[9] Kreft L, Botzki A, Coppens F, Vandepoele K, Van Bel M. PhyD3: A phylogenetic tree viewer with extended phyloXML support for functional genomics data visualization. Bioinformatics. 2017;33: 2946−2947. DOI: 10.1093/bioinformatics/btx324

[10] Meier-Kolthoff JP, Hahnke RL, Petersen J, Scheuner C, Michael V, Fiebig A, et al. Complete genome sequence of DSM 30083[T], the type strain (U5/41[T]) of *Escherichia coli*, and a proposal for delineating subspecies in microbial taxonomy. Stand Genomics Sci. 2014;9: 2. DOI: 10.1186/1944-3277-9-2