

BV-BRC Test Report

V3. Proteome Comparison Viewer

Item to test	Proteome Comparison Viewer
URL	[Insert URL linking to genome browser for test case]
Prerequisites	None
Tester(s)	Rebecca Wattam
References	https://www.bv-brc.org/docs/quick_references/services/proteome_comparison_service.html
Test date	7-Feb -22 (original - passed), 10-May-2022 (follow-up - passed)
Test Result	Passed

Overview

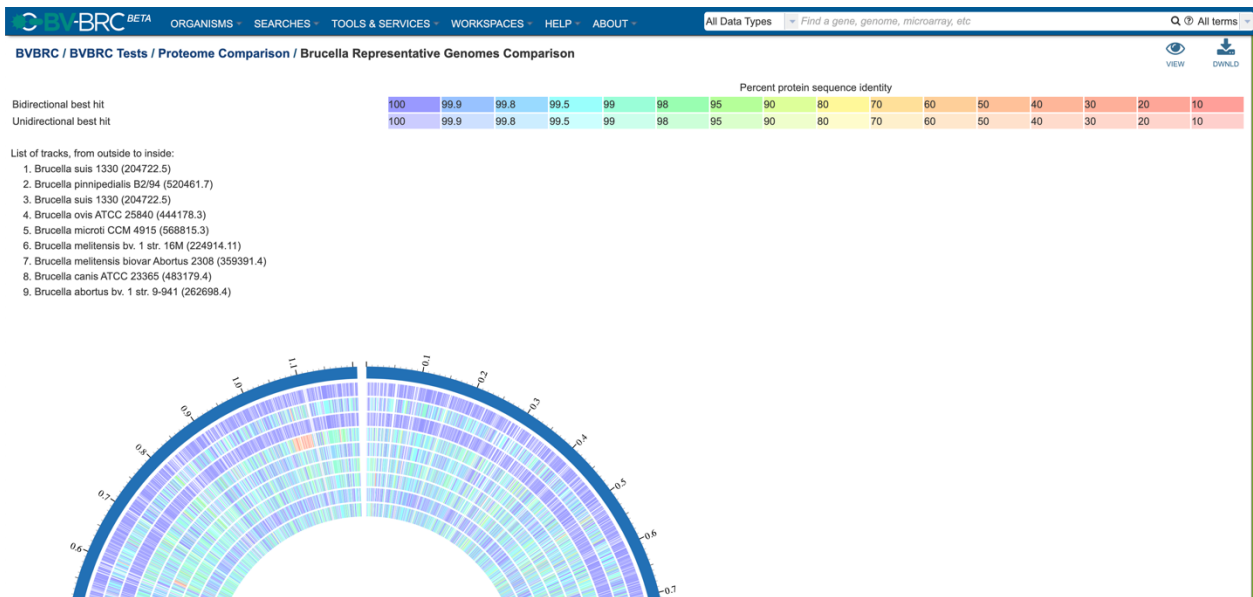
- Test the Proteome Comparison Viewer using an example set of bacterial genomes.
- Test proteome viewer.
- Test sequence identity colors.
- Test links.
- Test download.

Test Results

- Test results were verified by inspection.
- All visualization functions performed as expected.

Genome Set:

Genome ID	Genome Name
204722.5	Brucella suis 1330
224914.11	Brucella melitensis bv. 1 str. 16M
262698.4	Brucella abortus bv. 1 str. 9-941
359391.4	Brucella melitensis biovar Abortus 2308
444178.3	Brucella ovis ATCC 25840
483179.4	Brucella canis ATCC 23365
520461.7	Brucella pinnipedialis B2/94
568815.3	Brucella microti CCM 4915



Sequence Identity Colors:

uni (->)	CP002079	2866	351	fig 520461.7	BPI_II715	ugpC	Glycerol-3-ph	0.327	0.59
uni (->)	CP002079	2733	138	fig 520461.7	BPI_II575		Mobile elem	0.363	0.891
uni (->)	CP002079	2887	226	fig 520461.7	BPI_II738		L-cystine Al	0.396	0.889
uni (->)	CP002079	2887	226	fig 520461.7	BPI_II738		L-cystine Al	0.345	0.695
uni (->)	CP002078	1070	264	fig 520461.7	BPI_II1100		Diguanylate	0.309	0.769
uni (->)	CP002079	2205	523	fig 520461.7.peg.2205			Branched-c	0.441	0.878
uni (->)	CP002079	2391	509	fig 520461.7	BPI_II221		Enoyl-CoA I	0.503	0.974
uni (->)	CP002079	2390	253	fig 520461.7	BPI_II220		Enoyl-CoA I	0.558	0.98

Links:

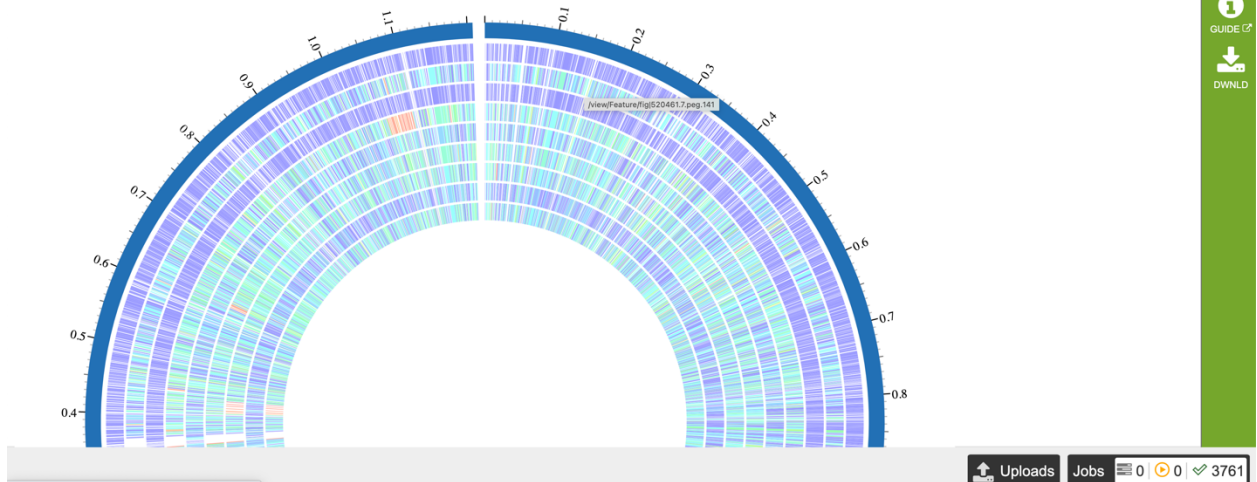
BVBC / BVBRC Tests / Proteome Comparison / Brucella Representative Genomes Comparison

VIEW DWNLD

SHOW

GUIDE

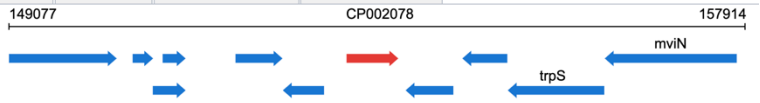
DWNLD



Feature View
 Bacteria » Proteobacteria » Alphaproteobacteria » Hyphomicrobiales » Brucellaceae » Brucella » Brucella pinnipedialis » Brucella pinnipedialis B2/94
 fig|520461.7.peg.141 | BPI_1140 | L,D-transpeptidase

Overview Genome Browser Compare Region Viewer Transcriptomics Interactions Domain and Motifs Protein Structures

fig|520461.7.peg.141



Genome	
Genome ID	520461.7
Genome Name	Brucella pinnipedialis B2/94
Taxon ID	520461
Source	
Annotation	PATRIC
Feature Type	CDS
Identifiers	
BRC ID	fig 520461.7.peg.141
Database Cross References	
RefSeq Locus Tag	BPI_1140
Protein ID	AEK53459.1
Location	
Start	153130
End	153750
Strand	+
Location	153130..153750
Sequences	

Functional Properties

PATRIC Local Family	PLF_234_00001998
PATRIC Global Family	PGF_00930759
FIGfam	FIG00883594
Identical Proteins	View (new tab)
Identical Genes	View (new tab)
GO Terms	-

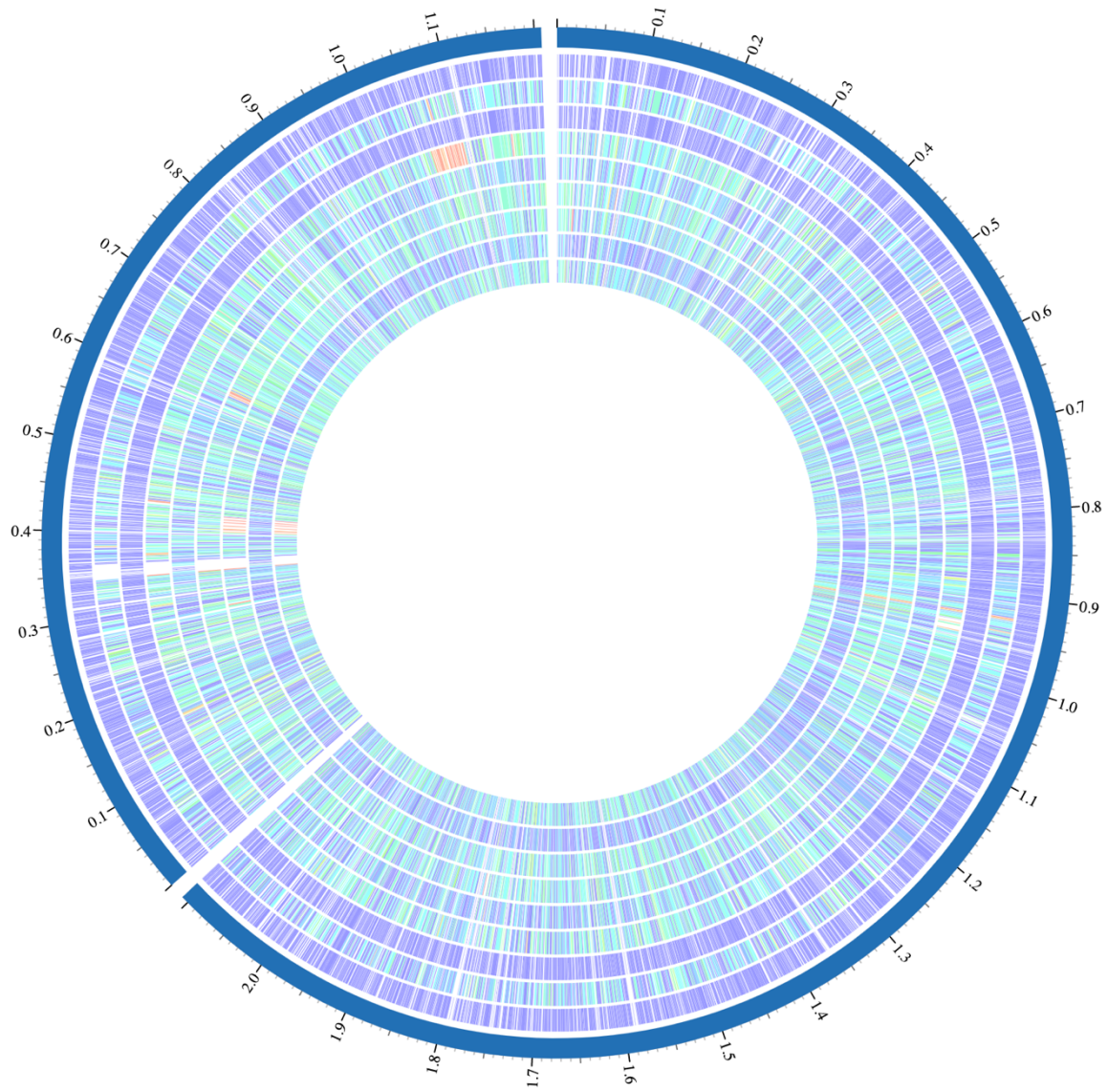
Submit a request for structure determination to SSGCID

Special Properties

Evidence	Property	Source	Source ID	Function	PubMed Subject coverage	Query coverage	Identity	E-value	
BLAT	Virulence Factors	Virulence Factors	17988092		1497932	100	100	99	1e-118

Download:

	A	B	C	D	E	F	G	H	I	J	K	L	M	N	O	P	Q	R	S	T	U
1	Brucella suis 1330										Brucella pinnipedialis B2/94										
2	ref_genom	ref_genom	ref_genom	ref_genom	ref_genom	ref_genom	ref_genom	ref_genom	ref_genom	ref_genom	ref_genom	ref_genom	ref_genom	ref_genom	ref_genom	ref_genom	ref_genom	ref_genom	ref_genom	ref_genom	ref_genom
3	NC_004310	1	38	figl204722.5.psg.1		PLF_234_O_PGF_00345	hypothetical	619	735 -		bi (<->)	CP002078	1	38	figl520461.7.psg.1					hypothetical	1
4	NC_004310	2	527	figl204722.5.BR0001	dnaA	PLF_234_O_PGF_00876	Chromosom	691	2274 +		bi (<->)	CP002078	2	527	figl520461.7.BPI_11	dnaA	Chromosom	0.998			
5	NC_004310	3	376	figl204722.5.BR0002	dnaN	PLF_234_O_PGF_06473	DNA polym	2566	3696 +		bi (<->)	CP002078	3	376	figl520461.7.BPI_12	dnaN	DNA polym	1			
6	NC_004310	4	384	figl204722.5.BR0003	recF	PLF_234_O_PGF_10387	DNA recom	3878	5032 +		bi (<->)	CP002078	4	384	figl520461.7.BPI_13	recF	DNA recom	1			
7	NC_004310	5	260	figl204722.5.BR0004	moeB	PLF_234_O_PGF_05867	Molybdoptei	5070	5852 +		bi (<->)	CP002078	5	260	figl520461.7.BPI_14	moeB	Molybdoptei	0.992			
8	NC_004310	6	318	figl204722.5.BR0005		PLF_234_O_PGF_00012	D-3-phosph	5869	6825 -		bi (<->)	CP002078	6	318	figl520461.7.BPI_15		D-3-phosph	1			
9	NC_004310	7	541	figl204722.5.BR0006		PLF_234_O_PGF_06357	ABC transp	6822	8447 -		bi (<->)	CP002078	7	541	figl520461.7.BPI_16		ABC transp	0.998			
10	NC_004310	8	379	figl204722.5.BR0007		PLF_234_O_PGF_10565	ABC transp	8471	9610 -		bi (<->)	CP002078	8	379	figl520461.7.BPI_17		ABC transp	0.997			
11	NC_004310	9	365	figl204722.5.BR0008		PLF_234_O_PGF_07935	ABC transp	9610	10707 -		bi (<->)	CP002078	9	365	figl520461.7.BPI_18		ABC transp	0.997			
12	NC_004310	10	615	figl204722.5.BR0009		PLF_234_O_PGF_09106	ABC transp	10819	12666 -		bi (<->)	CP002078	10	615	figl520461.7.BPI_19		ABC transp	0.998			
13	NC_004310	11	622	figl204722.5.BR0010		PLF_234_O_PGF_09106	ABC transp	12680	14548 -		bi (<->)	CP002078	11	622	figl520461.7.BPI_10		ABC transp	0.998			
14	NC_004310	12	48	figl204722.5.psg.12		PLF_234_O_PGF_00124	hypothetical	14462	14608 +		bi (<->)	CP002078	12	48	figl520461.7.psg.12		hypothetical	1			
15	NC_004310	13	107	figl204722.5.BR0011		PLF_234_O_PGF_01031	hypothetical	14779	15102 -												
16	NC_004310	14	66	figl204722.5.BR0012		PLF_234_O_PGF_00426	FIG004509'	15148	15348 -		bi (<->)	CP002078	13	66	figl520461.7.BPI_112		FIG004509'	0.985			
17	NC_004310	15	116	figl204722.5.BR0013		PLF_234_O_PGF_01031	hypothetical	15388	15738 -												
18	NC_004310	16	368	figl204722.5.BR0014		PLF_234_O_PGF_00412	ABC transp	16003	17109 -		bi (<->)	CP002078	14	368	figl520461.7.BPI_114		ABC transp	0.995			
19	NC_004310	17	264	figl204722.5.BR0016		PLF_234_O_PGF_00942	Methylglut	17578	18372 -		bi (<->)	CP002078	15	264	figl520461.7.BPI_116		Methylglut	1			
20	NC_004310	18	61	figl204722.5.psg.18		PLF_234_O_PGF_02966	Hydroxyme	16369	16554 -												
21	NC_004310	19	250	figl204722.5.psg.19		PLF_234_O_PGF_02996	Hydroxyme	18479	19231 -		bi (<->)	CP002078	16	287	figl520461.7.BPI_117	mvaB	Hydroxyme	1			
22	NC_004310	20	673	figl204722.5.BR0018		PLF_234_O_PGF_04057	Methylcroto	19224	21245 -		bi (<->)	CP002078	17	673	figl520461.7.BPI_118		Methylcroto	0.999			
23	NC_004310	21	535	figl204722.5.BR0019		PLF_234_O_PGF_05365	Methylcroto	21257	22864 -		bi (<->)	CP002078	18	535	figl520461.7.BPI_119		Methylcroto	0.996			
24	NC_004310	22	382	figl204722.5.BR0020	ivd	PLF_234_O_PGF_00032	Isovaleryl-C	22864	24012 -		bi (<->)	CP002078	19	382	figl520461.7.BPI_120	ivd	Isovaleryl-C	1			
25	NC_004310	23	48	figl204722.5.psg.23		PLF_234_O_PGF_07656	hypothetical	24025	24171 +		bi (<->)	CP002078	20	48	figl520461.7.psg.20		hypothetical	1			
26	NC_004310	24	662	figl204722.5.BR0021		PLF_234_O_PGF_00024	Acetoacetyl	24189	26177 -		bi (<->)	CP002078	21	662	figl520461.7.BPI_121		Acetoacetyl	0.998			
27	NC_004310	25	144	figl204722.5.BR0022		PLF_234_O_PGF_00123	hypothetical	26362	26796 -		bi (<->)	CP002078	22	144	figl520461.7.BPI_122		hypothetical	1			
28	NC_004310	26	373	figl204722.5.BR0023		PLF_234_O_PGF_00034	Acyitransfer	26973	28094 -		bi (<->)	CP002078	23	373	figl520461.7.BPI_123		Acyitransfer	1			
29	NC_004310	27	127	figl204722.5.BR0024		PLF_234_O_PGF_00426	FIG004184;	28617	29000 -		bi (<->)	CP002078	24	127	figl520461.7.BPI_125		FIG004184;	1			
30	NC_004310	28	450	figl204722.5.BR0025	aroA	PLF_234_O_PGF_07844	3-phosphos	29385	30737 +		bi (<->)	CP002078	25	450	figl520461.7.BPI_126	aroA	3-phosphos	0.998			
31	NC_004310	29	219	figl204722.5.BR0026	cmk	PLF_234_O_PGF_02455	Cytidylate k	30734	31393 +		bi (<->)	CP002078	26	219	figl520461.7.BPI_127	cmk	Cytidylate k	0.995			
32	NC_004310	30	49	figl204722.5.psg.30		PLF_234_O_PGF_07466	hypothetical	31426	31575 -		bi (<->)	CP002078	27	49	figl520461.7.psg.27		hypothetical	1			
33	NC_004310	31	566	figl204722.5.BR0027	mpsA	PLF_234_O_PGF_09835	SSU ribosom	31609	33309 +		bi (<->)	CP002078	28	566	figl520461.7.BPI_128	mpsA	SSU ribosom	1			
34	NC_004310	32	336	figl204722.5.BR0028		PLF_234_O_PGF_08102	Putative me	33727	34737 -		bi (<->)	CP002078	29	336	figl520461.7.BPI_129		Putative me	0.997			
35	NC_004310	33	299	figl204722.5.BR0029		PLF_234_O_PGF_07173	Transcriptio	34853	36752 +		bi (<->)	CP002078	30	299	figl520461.7.BPI_130		Transcriptio	1			
36	NC_004310	34	191	figl204722.5.BR0030		PLF_234_O_PGF_01031	hypothetical	35746	36321 -												
37	NC_004310	35	427	figl204722.5.BR0031		PLF_234_O_PGF_03116	Membrane-I	36357	37640 -		bi (<->)	CP002078	31	427	figl520461.7.BPI_132		Membrane-I	1			
38	NC_004310	36	201	figl204722.5.BR0032	recR	PLF_234_O_PGF_02463	Recombinat	37656	38261 -		bi (<->)	CP002078	32	201	figl520461.7.BPI_133	recR	Recombinat	1			





genome_comparison (18).txt

ref_genome_contig	ref_genome_gene	ref_genome_aa_length	ref_genome_patric_id	ref_genome_locus_tag	ref_genome_gene_name	ref_genome_plfam_id	
ref_genome_pgfam_id	ref_genome_function	ref_genome_start	ref_genome_end	ref_genome_strand	comp_genome_1_hit	comp_genome_1_contig	
comp_genome_1_gene	comp_genome_1_aa_length	comp_genome_1_patric_id	comp_genome_1_locus_tag	comp_genome_1_gene_name	comp_genome_1_function		
comp_genome_1_percent_identity	comp_genome_1_seq_coverage	comp_genome_2_hit	comp_genome_2_contig	comp_genome_2_gene	comp_genome_2_aa_length		
comp_genome_2_patric_id	comp_genome_2_locus_tag	comp_genome_2_gene_name	comp_genome_2_function	comp_genome_2_percent_identity	comp_genome_2_seq_coverage		
comp_genome_3_hit	comp_genome_3_contig	comp_genome_3_gene	comp_genome_3_aa_length	comp_genome_3_patric_id	comp_genome_3_locus_tag		
comp_genome_3_gene_name	comp_genome_3_function	comp_genome_3_percent_identity	comp_genome_3_seq_coverage	comp_genome_4_hit	comp_genome_4_contig		
comp_genome_4_gene	comp_genome_4_aa_length	comp_genome_4_patric_id	comp_genome_4_locus_tag	comp_genome_4_gene_name	comp_genome_4_function		
comp_genome_4_percent_identity	comp_genome_4_seq_coverage	comp_genome_5_hit	comp_genome_5_contig	comp_genome_5_gene	comp_genome_5_aa_length		
comp_genome_5_patric_id	comp_genome_5_locus_tag	comp_genome_5_gene_name	comp_genome_5_function	comp_genome_5_percent_identity	comp_genome_5_seq_coverage		
comp_genome_6_hit	comp_genome_6_contig	comp_genome_6_gene	comp_genome_6_aa_length	comp_genome_6_patric_id	comp_genome_6_locus_tag		
comp_genome_6_gene_name	comp_genome_6_function	comp_genome_6_percent_identity	comp_genome_6_seq_coverage	comp_genome_7_hit	comp_genome_7_contig		
comp_genome_7_gene	comp_genome_7_aa_length	comp_genome_7_patric_id	comp_genome_7_locus_tag	comp_genome_7_gene_name	comp_genome_7_function		
comp_genome_7_percent_identity	comp_genome_7_seq_coverage	comp_genome_8_hit	comp_genome_8_contig	comp_genome_8_gene	comp_genome_8_aa_length		
comp_genome_8_patric_id	comp_genome_8_locus_tag	comp_genome_8_gene_name	comp_genome_8_function	comp_genome_8_percent_identity	comp_genome_8_seq_coverage		
NC_004310	38	fig 204722.5.peg.1		PLF_234_00002778	PGF_00345022	hypothetical protein 619_735	bi (<->)
CP002078.1	38	fig 520461.7.peg.1		hypothetical protein 1.000	0.974	bi (<->)	NC_004310 1 38 fig 204722.5.peg.1 1.000 0.974
hypothetical protein	1.000	0.974	bi (<->)	NC_009505	1265	38	fig 444178.3.peg.1265
bi (<->)	NC_013119	1207	43	fig 568815.3.peg.1207			hypothetical protein 1.000 0.860
fig 224914.11.peg.2147				hypothetical protein 1.000	0.974	bi (<->)	NC_007618 1 38 fig 359391.4.peg.1 1.000 0.974
hypothetical protein	1.000	0.974	bi (<->)	NC_010103	1	38	fig 483179.4.peg.1
bi (<->)	NC_006932	1	38	fig 262698.4.peg.1			hypothetical protein 1.000 0.974
NC_004310	2	527	fig 204722.5.peg.2	BR0001	dnaA	PLF_234_00000530	PGF_00076106
hypothetical protein	1.000	0.974	bi (<->)	NC_009505	1265	38	fig 444178.3.peg.1265
bi (<->)	NC_013119	1207	43	fig 568815.3.peg.1207			hypothetical protein 1.000 0.860
fig 224914.11.peg.2147				hypothetical protein 1.000	0.974	bi (<->)	NC_007618 1 38 fig 359391.4.peg.1 1.000 0.974
hypothetical protein	1.000	0.974	bi (<->)	NC_010103	1	38	fig 483179.4.peg.1
bi (<->)	NC_006932	1	38	fig 262698.4.peg.1			hypothetical protein 1.000 0.974
NC_004310	2	527	fig 204722.5.peg.2	BR0001	dnaA	PLF_234_00000530	PGF_00076106
2274	+	bi (<->)	CP002078.2	527	fig 520461.7.peg.2		
NC_004310	2	527	fig 204722.5.peg.2	BR0001	dnaA	Chromosomal replication initiator protein DnaA	1.000 0.998
1266	540	fig 444178.3.peg.1266	BOV_0001	dnaA	Chromosomal replication initiator protein DnaA	0.998 0.974	bi (<->)
fig 568815.3.peg.1208			BMI_I1	dnaA	Chromosomal replication initiator protein DnaA	0.998 0.998	bi (<->)
224914.11.peg.2146			BMEI1943	dnaA	Chromosomal replication initiator protein DnaA	0.998 0.998	bi (<->)
BAB1_0001	dnaA	Chromosomal replication initiator protein DnaA	0.998 0.998	bi (<->)	NC_010103	2	527
dnaA	Chromosomal replication initiator protein DnaA	1.000 0.998	bi (<->)	NC_006932	2	527	fig 483179.4.peg.2
Chromosomal replication initiator protein DnaA	0.998 0.998	bi (<->)	NC_006932	2	527	fig 262698.4.peg.2	BruAb1_0001
NC_004310	3	376	fig 204722.5.peg.3	BR0002	dnaN	PLF_234_00000785	PGF_06473395
3696	+	bi (<->)	CP002078.3	376	fig 520461.7.peg.3		
NC_004310	3	376	fig 204722.5.peg.3	BR0002	dnaN	DNA polymerase III beta subunit (EC 2.7.7.7)	1.000 0.997
1267	376	fig 444178.3.peg.1267	BOV_0002	dnaN	DNA polymerase III beta subunit (EC 2.7.7.7)	0.997 0.997	bi (<->)
fig 568815.3.peg.1209			BMI_I2	dnaN	DNA polymerase III beta subunit (EC 2.7.7.7)	0.997 0.997	bi (<->)
224914.11.peg.2145			BMEI1942	dnaN	DNA polymerase III beta subunit (EC 2.7.7.7)	0.997 0.997	bi (<->)
BAB1_0002	dnaN	DNA polymerase III beta subunit (EC 2.7.7.7)	0.997 0.997	bi (<->)	NC_010103	3	372
dnaN	DNA polymerase III beta subunit (EC 2.7.7.7)	0.997 0.997	bi (<->)	NC_006932	3	376	fig 483179.4.peg.3
DNA polymerase III beta subunit (EC 2.7.7.7)	0.997 0.997	bi (<->)	NC_006932	3	376	fig 262698.4.peg.3	BruAb1_0002
NC_004310	4	382	fig 204722.5.peg.4	BR0003	parF	PLF_234_00000647	PGF_10387100