

# BV-BRC Test Report

## V1. Genome Browser Visualization

<b>Item to test</b>	Genome Browser (JBrowse)
<b>URL</b>	[Insert URL linking to genome browser for test case]
<b>Prerequisites</b>	None
<b>Tester(s)</b>	Rebecca Wattam, Zachary Wallace
<b>References</b>	<a href="https://www.bv-brc.org/docs/quick_references/organisms_genome/genome_browser.html">https://www.bv-brc.org/docs/quick_references/organisms_genome/genome_browser.html</a>
<b>Test date</b>	06-Jan-2022 and 10_feb-22 (original - passed), 10-May-2022 (follow-up - passed)
<b>Test Result</b>	<b>Passed</b>

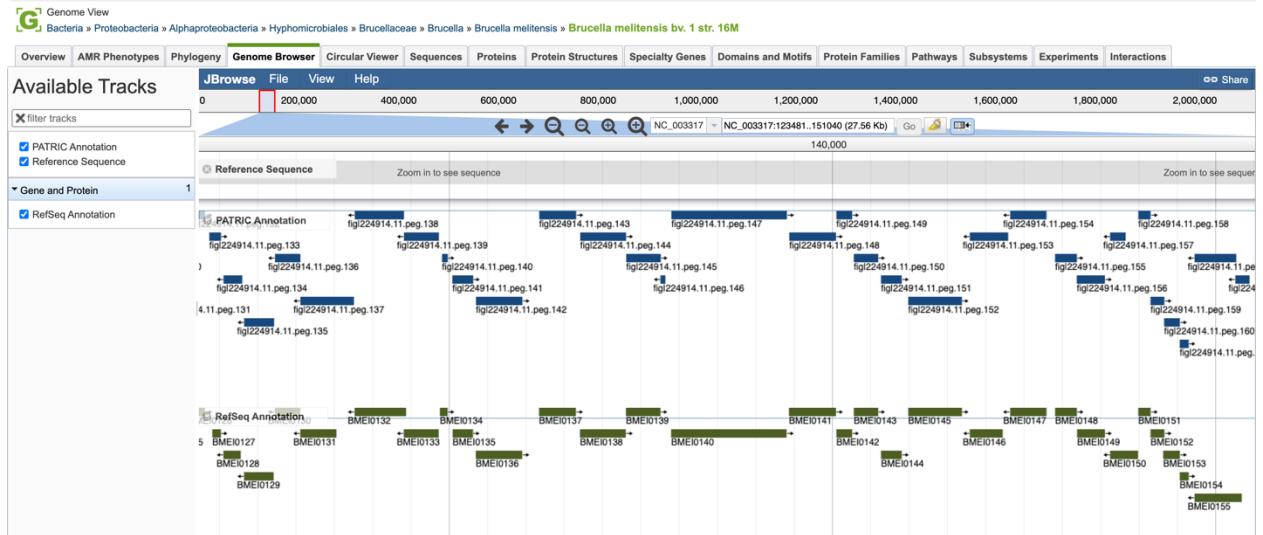
### Overview

- Test the linear Genome Browser using an example bacterial and viral genome.
- Test genome display.
- Test zoom and pan.
- Test feature flyovers/links.
- Show track show/hide.

### Test Results

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

# Genome: [Brucella melitensis bv. 1 str. 16M/224914.11]



## Zoom:

Genome View  
Bacteria » Proteobacteria » Alphaproteobacteria » Hyphomicrobiales » Brucellales » Brucella » *Brucella mellitensis* » *Brucella mellitensis* bv. 1 str. 16M

Overview AMR Phenotypes Phylogeny **Genome Browser** Circular Viewer Sequences Proteins Protein Structures Specialty Genes Domains and Motifs Protein Families Pathways Subsystems Experiments Interactions

Available Tracks  
filter tracks  
 PATRIC Annotation  
 Reference Sequence  
**Gene and Protein**  
 RefSeq Annotation

JBrowse File View Help  
0 200,000 400,000 600,000 800,000 1,000,000 1,200,000 1,400,000 1,600,000 1,800,000 2,000,000

135,800  
NC\_003317:135798..135867 (70 b)  
Reference Sequence  
W Q S A K R T S P R I S G A P Q N D V F A P L Y T L S I F L Y N G  
G A T C  
I H A C F L A C L S F C L A G W S I R P A G L V S V T K R A G R K V G E N E R E I P A

PATRIC Annotation  
RefSeq Annotation

## Pan:

Genome View  
Bacteria » Proteobacteria » Alphaproteobacteria » Hyphomicrobiales » Brucellales » Brucella » *Brucella mellitensis* » *Brucella mellitensis* bv. 1 str. 16M

Overview AMR Phenotypes Phylogeny **Genome Browser** Circular Viewer Sequences Proteins Protein Structures Specialty Genes Domains and Motifs Protein Families Pathways Subsystems Experiments Interactions

Available Tracks  
filter tracks  
 PATRIC Annotation  
 Reference Sequence  
**Gene and Protein**  
 RefSeq Annotation

JBrowse File View Help  
0 200,000 400,000 600,000 800,000 1,000,000 1,200,000 1,400,000 1,600,000 1,800,000 2,000,000

NC\_003317:206801..462400 (275.6 Kb)  
Reference Sequence  
Zoom in to see sequence  
400,000  
PATRIC Annotation  
Gene and Protein  
RefSeq Annotation

## Feature flyovers and links:

Genome View  
Bacteria » Proteobacteria » Alphaproteobacteria » Hyphomicrobiales » Brucellaceae » Brucella » Brucella melitensis » Brucella melitensis bv. 1 str. 16M

Overview AMR Phenotypes Phylogeny **Genome Browser** Circular Viewer Sequences Proteins Protein Structures Specialty Genes Domains and Motifs Protein Families Pathways Subsystems Experiments Interactions

Available Tracks  
filter tracks  
 PATRIC Annotation  
 Reference Sequence  
 Gene and Protein 1  
 RefSeq Annotation

JBrowse File View Help  
0 200,000 400,000 600,000 800,000 1,000,000 1,200,000 1,400,000 1,600,000 1,800,000 2,000,000

NC\_003317:343223..345978 (2.76 Kb) Go

344,000 344,722

Reference Sequence  
Zoom in to see sequence

PATRIC Annotation  
figl224914.11.peg.368 figl224914.11.peg.369 figl224914.11.peg.370 figl224914.11.peg.371

RefSeq Annotation  
BMEI0335 BMEI0336 BMEI0337

figl224914.11.peg.369 | BMEI0336 | 1  
Tol-Pal system protein TolQ  
CDS: 344432..345143 (1)  
Click for detailed information

BV-BRC BETA ORGANISMS SEARCHES TOOLS & SERVICES WORKSPACES HELP ABOUT All Data Types Find a gene, genome, microarray, ...

Genome View  
Bacteria » Proteobacteria » Alphaproteobacteria » Hyphomicrobiales » Brucellaceae » Brucella » Brucella melitensis » Brucella melitensis bv. 1 str. 16M

Overview AMR Phenotypes Phylogeny **Genome Browser** Circular Viewer Sequences

Available Tracks  
filter tracks  
 PATRIC Annotation  
 Reference Sequence  
 Gene and Protein 1  
 RefSeq Annotation

JBrowse File View Help  
0 200,000 400,000

9...346054 (2.76 Kb) Go

Reference Sequence  
Zoom in to see sequence

PATRIC Annotation  
figl224914.11.peg.368

RefSeq Annotation  
BMEI0335

**Feature Summary**

figl224914.11.peg.369

Genome	
Genome ID	224914.11
Genome Name	Brucella melitensis bv. 1 str. 16M
Source	
Annotation	PATRIC
Feature Type	CDS
Identifiers	
BRC ID	figl224914.11.peg.369
Database Cross References	
RefSeq Locus Tag	BMEI0336
Protein ID	NP_539253.1
Gene ID	1196047
Location	
Start	344432
End	345143
Strand	1
Sequences	
NA Length	711
AA Length	236
Annotation	
Product	Tol-Pal system protein TolQ
Families	
None available	
Misc	
None available	

Feature View  
 Bacteria » Proteobacteria » Alphaproteobacteria » Hyphomicrobiales » Brucellaceae » Brucella » Brucella melitensis » Brucella melitensis bv. 1 str. 16M  
 fig|224914.11.peg.369 | BMEI0336 | Tol-Pal system protein TolQ

Overview	Genome Browser	Compare Region Viewer	Transcriptomics	Interactions	Domain and Motifs	Protein Structures														
<p><b>fig 224914.11.peg.369</b></p>																				
<p>Genome</p> <p><b>Genome ID</b> 224914.11  <b>Genome Name</b> Brucella melitensis bv. 1 str. 16M  <b>Taxon ID</b> 224914</p>																				
<p>Source</p> <p><b>Annotation</b> PATRIC  <b>Feature Type</b> CDS</p>																				
<p>Identifiers</p> <p><b>BRC ID</b> fig 224914.11.peg.369</p>																				
<p>Database Cross References</p> <p><b>RefSeq Locus Tag</b> BMEI0336  <b>Protein ID</b> NP_539253.1  <b>Gene ID</b> 1196047</p>																				
<p>Location</p> <p><b>Start</b> 344433  <b>End</b> 345143  <b>Strand</b> +  <b>Location</b> 344433..345143</p>																				
<p>Sequences</p> <p><b>NA Length</b> 711  <b>AA Length</b> 236  <b>NA Sequence</b> <a href="#">view</a>  <b>AA Sequence</b> <a href="#">view</a></p>																				
<p>Functional Properties</p> <table border="1"> <tr> <td>PATRIC Local Family</td> <td>PLF_234_00002701</td> </tr> <tr> <td>PATRIC Global Family</td> <td>PGF_00648054</td> </tr> <tr> <td>FIGfam</td> <td>FIG00002161</td> </tr> <tr> <td>Identical Proteins</td> <td><a href="#">View (new tab)</a></td> </tr> <tr> <td>Identical Genes</td> <td><a href="#">View (new tab)</a></td> </tr> <tr> <td>GO Terms</td> <td>-</td> </tr> <tr> <td>Subsystems</td> <td>Tol-Pal Cell Envelope Complex Tol-Pal system protein TolQ</td> </tr> </table> <p><a href="#">Submit a request for structure determination to SSGCID</a></p>							PATRIC Local Family	PLF_234_00002701	PATRIC Global Family	PGF_00648054	FIGfam	FIG00002161	Identical Proteins	<a href="#">View (new tab)</a>	Identical Genes	<a href="#">View (new tab)</a>	GO Terms	-	Subsystems	Tol-Pal Cell Envelope Complex Tol-Pal system protein TolQ
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Track show/hide:

Genome Browser interface for Severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2). The interface includes a navigation bar with 'All Data Types' and a search bar. The main content area shows a genomic track for NC\_045512 (27.78 Kb). The track displays various annotations including RefSeq annotations, protein structures, and structural features. Key features include the Nucleocapsid protein (N), RNA-dependent RNA polymerase (RdRp), and Surface glycoprotein (S). The track also shows primer and probe locations, such as the VIR-7831 Ab Escape (Starr 2021) primer. The interface includes a 'Mutation Impact' section on the left with various antibody escape options, and a 'Variants' section at the bottom. The track is divided into several sections: Overview, Mutation Impact, Primers and Probes, Structural Features, and Variants. The main track area shows a scale from 0 to 28,000 bp, with a zoomed-in view of the 1,982 bp region. The track includes a 'RefSeq Annotation' track, a 'Protein Structures' track, and a 'Structural Features' track. The 'RefSeq Annotation' track shows the following proteins: Nucleocapsid protein, RNA-dependent RNA polymerase, Nucleocapsid protein, and Surface glycoprotein. The 'Protein Structures' track shows the following domains: 3C-like proteinase, nsp10, helicase, endoRNase, surface glycoprotein, envelope protein, ORF3a protein, ORF7b protein, membrane glycoprotein, ORF6 protein, ORF7a protein, ORF8 protein, and nucleocapsid protein. The 'Structural Features' track shows the following features: Beta Strand, Coiled Coil, Helix, and Turn. The 'Variants' track shows the following variants: Centers for Disease Control, Sanger; Pasteur Institute, COVID-19 Target 1, IP2; Centers for Disease Control, China, novel coronavirus Target 1; and World Health Organization.