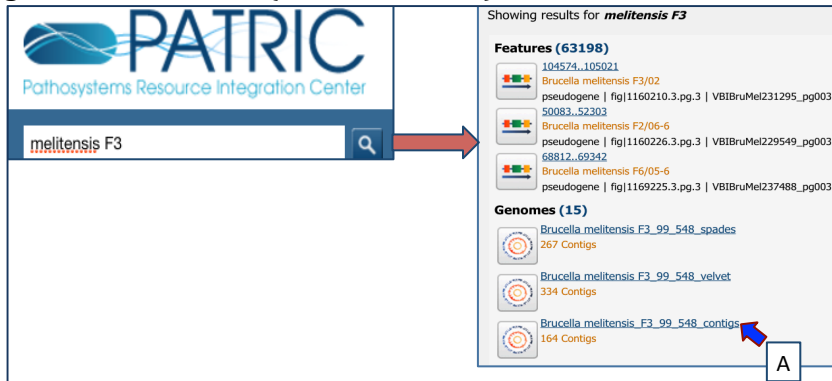


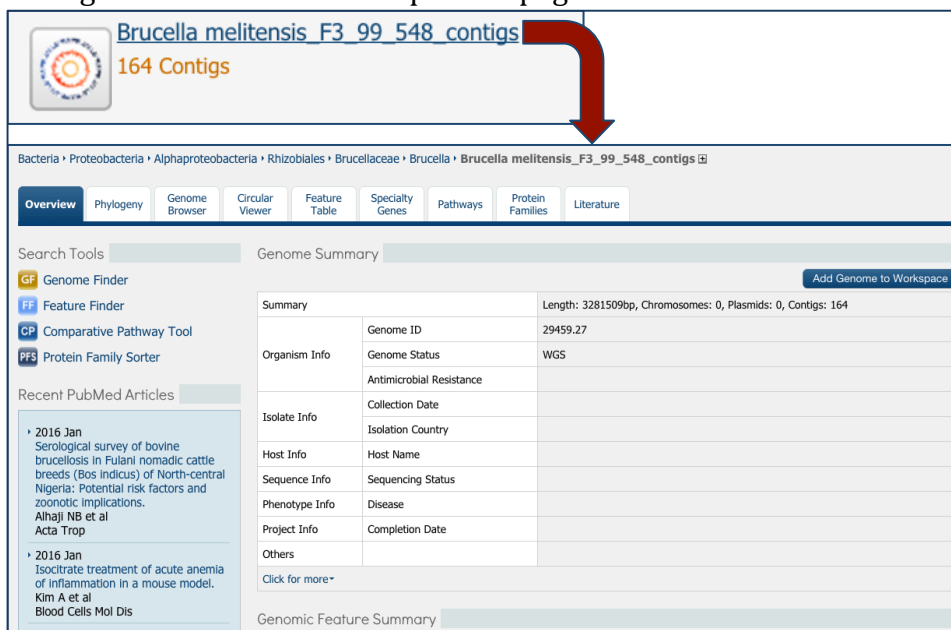
Exploring your annotated genome in PATRIC

1. The first thing you will need to do is to find the genome that you annotated in PATRIC. The search function allows you to submit some key text terms to narrow the search for your genome. In the example below, to find a genome named *Brucella melitensis* F3 99 548, I enter “melitensis” and “F3” as seen in the screenshot below and hit return. This will open up the Search Results page that is divided into Features, Genomes, Taxonomy and Experiments. Under Genomes is the particular genome of interest (Arrow A below).



The screenshot shows the PATRIC search interface. The search bar contains "melitensis F3". The results are categorized into Features (63198) and Genomes (15). Under the Genomes section, the entry "Brucella melitensis F3_99_548_contigs" is highlighted with a blue arrow labeled 'A'. The entry shows it has 164 contigs.

2. Click on the name that you're interested in. This will take you to the landing page for that genome. This page has the information for your genome, like the size and number of genes. We will explore more information about this genome by clicking through the tabs across the top of the page.



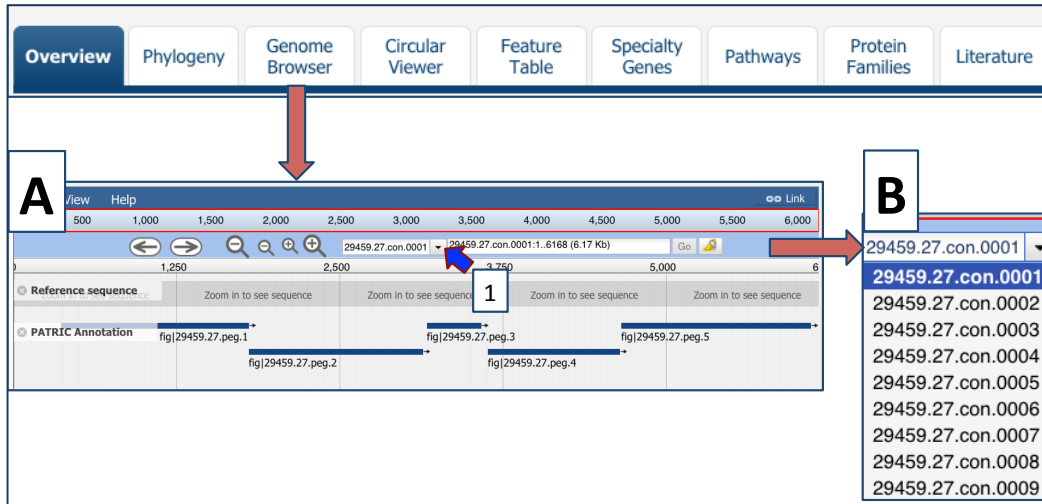
The screenshot shows the landing page for the genome "Brucella melitensis F3_99_548_contigs" with 164 contigs. The page has a navigation bar with tabs: Overview, Phylogeny, Genome Browser, Circular Viewer, Feature Table, Specialty Genes, Pathways, Protein Families, and Literature. The "Genome Browser" tab is selected. Below the navigation bar, there is a "Search Tools" section with links to Genome Finder, Feature Finder, Comparative Pathway Tool, and Protein Family Sorter. The main content area displays a "Genome Summary" table with the following information:

Summary		Length: 3281509bp, Chromosomes: 0, Plasmids: 0, Contigs: 164
Organism Info	Genome ID	29459.27
	Genome Status	WGS
Isolate Info	Antimicrobial Resistance	
	Collection Date	
Host Info	Isolation Country	
	Host Name	
Sequence Info	Sequencing Status	
Phenotype Info	Disease	
Project Info	Completion Date	
Others		

Below the table is a "Click for more-" link and a "Genomic Feature Summary" section.

3. **Genome Browser.** Clicking on the Genome Browser tab will open up the genome browser (A below). As this is a private genome, you will only see the PATRIC annotations. If the genome is in multiple contigs (as this one is), the browser will

load the first contig. If you want to explore a different contig, you will need to click on the down arrow (1 in the screenshot below) that will open up a list of the available contigs (B below). You can scroll down that list to choose the contig you are interested in viewing.



4. Circular Viewer. The circular viewer opens showing you the contigs. The closer a genome is to being closed, the better this image will look. The image below is from a WGS with over 100 contigs, and looks fractured as all the contigs are represented. The image includes the coding sequences (CDS) on the forward and reverse strand, the RNA genes, GC content and GC skew. You can upload custom tracks or your own data, resize the image, and download it as an scaled vector graphic (svg).



5. Feature Table. The tab for Feature Table contains information about all the features annotated on a genome, from CDS to RNAs, pseudogenes and miscellaneous features. Most of the public genomes include RefSeq or alternate locus tags (indicated by the red asterix below), but these are not seen in private genomes.

The screenshot shows the 'Feature Table' tab selected in a navigation bar. Below the navigation bar, a red arrow points to the 'Feature Table' section. This section includes a filter area with 'Feature Type' set to 'CDS', 'Annotation' set to 'PATRIC', and a 'Filter Table' button. Below the filters, it states '3365 features found'. A toolbar contains options for 'Add Feature(s)', 'FASTA DNA', 'FASTA Protein', 'Table', 'FASTA', 'Pathway Summary', 'MAP IDs to...', 'Multiple Seq Alignment', and 'Columns'. The main table displays columns for 'PATRIC ID', 'RefSeq Locus Tag', 'Alt Locus Tag', 'Gene Symbol', 'Start', 'FIGfam ID', 'Length (AA)', and 'Product Description'. Red asterisks are placed above the 'RefSeq Locus Tag' and 'Alt Locus Tag' columns. The table lists various genes such as '22981 FIG01306569' and '16349 FIG00044820'.

PATRIC ID	RefSeq Locus Tag	Alt Locus Tag	Gene Symbol	Start	FIGfam ID	Length (AA)	Product Description
<input type="checkbox"/> fig 29459.27.peg.2274				22981	FIG01306569	304	(2E,6E)-farnesyl diphosphate synthase (EC 2.5.1.10)
<input type="checkbox"/> fig 29459.27.peg.988				16349	FIG00044820	107	(AF179595) Vco33
<input type="checkbox"/> fig 29459.27.peg.2008				182	FIG00021407	537	(R)-citramalate synthase (EC 2.3.1.182)
<input type="checkbox"/> fig 29459.27.peg.2245				45445	FIG01320775	175	(U62541) immunoreactive 14 kDa protein BA14k
<input type="checkbox"/> fig 29459.27.peg.1907				15547	FIG01319654	142	(U95165) OrfY
<input type="checkbox"/> fig 29459.27.peg.754				2092	FIG00005243	267	1-acyl-sn-glycerol-3-phosphate acyltransferase (EC 2.3.1.51)
<input type="checkbox"/> fig 29459.27.peg.1409				4601	FIG00005243	260	1-acyl-sn-glycerol-3-phosphate acyltransferase (EC 2.3.1.51)
<input type="checkbox"/> fig 29459.27.peg.1259				77897	FIG01349528	329	1-carboxy-3-chloro-3,4-dihydroxycyclo hexa-1,5-diene dehydrogenase (...)
<input type="checkbox"/> fig 29459.27.peg.3258				2081	FIG00000343	643	1-deoxy-D-xylose 5-phosphate synthase (EC 2.2.1.7)
<input type="checkbox"/> fig 29459.27.peg.2275				23903	FIG00000449	420	1-hydroxy-2-methyl-2-(E)-butenyl 4-diphosphate synthase (EC 1.17.7.1)
<input type="checkbox"/> fig 29459.27.peg.2617				9324	FIG00133510	320	1-pyrroline-4-hydroxy-2-carboxylate deaminase (EC 3.5.4.22)
<input type="checkbox"/> fig 29459.27.peg.1596				39675	FIG00008665	156	16 kDa heat shock protein A
<input type="checkbox"/> fig 29459.27.peg.2809				61078	FIG01304909	465	16S rRNA (cytosine(967)-C(5))-methyltransferase (EC 2.1.1.176)
<input type="checkbox"/> fig 29459.27.peg.570				33243	FIG00005547	187	16S rRNA (guanine(966)-N(2))-methyltransferase (EC 2.1.1.171)
<input type="checkbox"/> fig 29459.27.peg.992				18274	FIG00000312	189	16S rRNA processing protein RimM
<input type="checkbox"/> fig 29459.27.peg.1284				106107	FIG00853778	364	16S ribosomal RNA m(5)C 967 methyltransferase

6. You can use the filters on top of the table to narrow down to specific annotations, Clicking on the box that follows Feature Type will allow you to filter on specific annotations like tRNAs, CDS or pseudogenes. If the genome was submitted to RefSeq previously, you could use the box that follows Annotation to see only the PATRIC, the RefSeq, or All annotations. The Keyword search is particularly useful. You can look for specific names by enter them in the search box and clicking on the Filter Table button. This will allow you too see all the genes that contain that word somewhere in their annotation. You can also use it to search for locus tags.

Feature Type: CDS Annotation: PATRIC Keyword: **Filter Table**

Keyword: **Filter Table**

Feature Type: CDS Annotation: PATRIC Keyword: virB **Filter Table**

13 features found

PATRIC ID	RefSeq Locus Tag	Alt Locus Tag	Gene Symbol	Start	FIGfam ID	Length (AA)	Product Description
<input type="checkbox"/>	figI29459.27.peg.1588			26741	FIG00055840	361	ATPase required for both assembly of type IV secretion complex and se...
<input type="checkbox"/>	figI29459.27.peg.1581			19241	FIG00001460	831	ATPase required for both assembly of type IV secretion complex and se...
<input type="checkbox"/>	figI29459.27.peg.1580			18891	FIG00002012	116	Inner membrane protein forms channel for type IV secretion of T-DNA c...
<input type="checkbox"/>	figI29459.27.peg.1585			24024	FIG01304041	239	Inner membrane protein forms channel for type IV secretion of T-DNA c...
<input type="checkbox"/>	figI29459.27.peg.1587			25606	FIG00001567	383	Inner membrane protein of type IV secretion of T-DNA complex, TonB-li...
<input type="checkbox"/>	figI29459.27.peg.1583			22641	FIG00002241	347	Inner membrane protein of type IV secretion of T-DNA complex, VirB6
<input type="checkbox"/>	figI29459.27.peg.1584			23848	FIG00002241	57	Lipoprotein of type IV secretion complex that spans outer membrane an...
<input type="checkbox"/>	figI29459.27.peg.2361			13088	FIG00629430	82	Lipoprotein, VirB7-like
<input type="checkbox"/>	figI29459.27.peg.2755			5481	FIG01288861	94	Lipoprotein, VirB7-like
<input type="checkbox"/>	figI29459.27.peg.1579			18560	FIG00038155	105	Major plus subunit of type IV secretion complex, VirB2
<input type="checkbox"/>	figI29459.27.peg.1582			21741		238	Minor pilin of type IV secretion complex, VirB5
<input type="checkbox"/>	figI29459.27.peg.1586			24740	FIG00001517	289	Outer membrane and periplasm component of type IV secretion of T-D...
<input type="checkbox"/>	figI29459.27.peg.1578			17408	FIG00002640	238	Peptidoglycan hydrolase VirB1, involved in T-DNA transfer

7. You can also use this table to save the results of your search. If you click in the box in front of the PATRIC ID (first column, blue arrow 1 below), this will autoselect all the genes in the table. You could also select individual genes.

13 features found

Workspace View Download Tools Columns

PATRIC ID RefSeq Locus Tag Alt Locus Tag Gene Symbol Start FIGfam ID

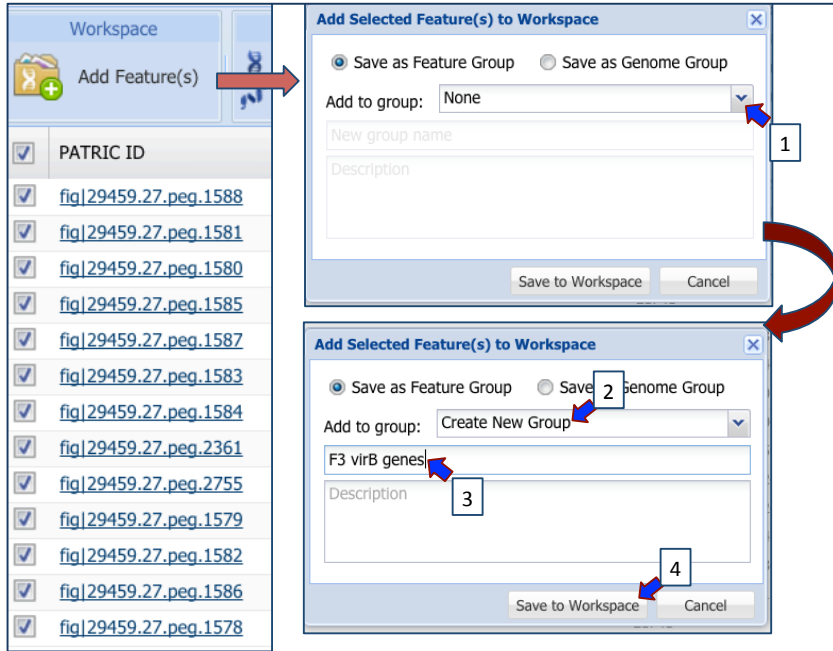
[figI29459.27.peg.1588](#) 26741 FIG00055840

PATRIC ID

1

- PATRIC ID
- [figI29459.27.peg.1588](#)
- [figI29459.27.peg.1581](#)
- [figI29459.27.peg.1580](#)
- [figI29459.27.peg.1585](#)
- [figI29459.27.peg.1587](#)
- [figI29459.27.peg.1583](#)
- [figI29459.27.peg.1584](#)
- [figI29459.27.peg.2361](#)
- [figI29459.27.peg.2755](#)
- [figI29459.27.peg.1579](#)
- [figI29459.27.peg.1582](#)
- [figI29459.27.peg.1586](#)
- [figI29459.27.peg.1578](#)

8. To save that group, click on the folder icon in front of Add Feature(s). This will open up a pop-up window. To create a group, you will need to click on the down arrow that follows the word "None" that you can see in the text box. This will open up a drop down box that allows you to create a new group (Blue arrow 1 below). To create a new group, click on the line that says "Create New Group" (Arrow 2 in the screenshot below). Then you must type in the name that you want to identify the group in the text box (Arrow 3). To save that group, click on the Save to Workshop button at the bottom of the pop-up box (Arrow 4).

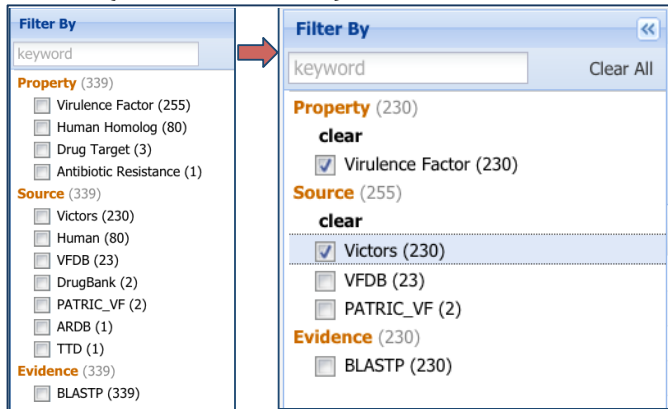


9. Specialty Genes. The Specialty Genes tab shows you all the genes in your genome that have homology to genes that have been identified as having specific properties. PATRIC BLASTs all the genes in the annotated genome against specific databases that contain genes identified as virulence factors, involved in antibiotic resistance, have been used as drug targets, or are human homologs. The left side of this page contains a filter to narrow the results, and a table listing the results on the right.

Evidence	Property	Source	PATRIC ID	RefSeq Locus	Alt Locus Tag	Source ID	Gene	Product	PubMed	Identity	E-value
BLASTP	Virulence Factor	Victors	fig 29459.27.pep.47			1253	CAIB/BAIF family ...	PubMed	100	0	
BLASTP	Virulence Factor	Victors	fig 29459.27.pep.50			1394	transporter, putati...	PubMed	100	0.0	
BLASTP	Virulence Factor	Victors	fig 29459.27.pep.51			1393	Glutaredoxin-like ...	PubMed	100	0	
BLASTP	Virulence Factor	Victors	fig 29459.27.pep.52			1392	Ribonucleotide re...	PubMed	100	0	
BLASTP	Virulence Factor	Victors	fig 29459.27.pep.81			1023	SSU ribosomal pr...	PubMed	100	0	
BLASTP	Virulence Factor	Victors	fig 29459.27.pep.121			1215	Phosphoribosylam...	PubMed	100	0	
BLASTP	Virulence Factor	Victors	fig 29459.27.pep.158			1232	Carbamoyl-phosp...	PubMed	100	0	
BLASTP	Virulence Factor	Victors	fig 29459.27.pep.125			1224	Dipeptide-binding ...	PubMed	100	0	
BLASTP	Virulence Factor	Victors	fig 29459.27.pep.127			1223	Transcriptional re...	PubMed	100	0	
BLASTP	Virulence Factor	Victors	fig 29459.27.pep.186			1243	Lactoylglutathione...	PubMed	100	0	
BLASTP	Virulence Factor	VFDB	fig 29459.27.pep.195			VFG2225	GDP-mannose 4.6...	PubMed	100	0	
BLASTP	Virulence Factor	Victors	fig 29459.27.pep.195			1217	GDP-mannose 4.6...	PubMed	100	0	
BLASTP	Virulence Factor	VFDB	fig 29459.27.pep.196			VFG2226	Perosamine synth...	PubMed	100	0	
BLASTP	Virulence Factor	Victors	fig 29459.27.pep.196			1285	Perosamine synth...	PubMed	100	0	
BLASTP	Virulence Factor	VFDB	fig 29459.27.pep.199			VFG2229	Perosamine synth...	PubMed	100	0	
BLASTP	Virulence Factor	VFDB	fig 29459.27.pep.200			VFG2230	Formyltransferase...	PubMed	100	0	
BLASTP	Virulence Factor	Victors	fig 29459.27.pep.206			1286	Undecaprenyl-gly...	PubMed	100	0	
BLASTP	Virulence Factor	Victors	fig 29459.27.pep.232			4890	DNA-binding resp...	PubMed	100	0	
BLASTP	Virulence Factor	Victors	fig 29459.27.pep.257			1324	DNA-binding resp...	PubMed	100	0	
BLASTP	Virulence Factor	Victors	fig 29459.27.pep.272			1247	Peptidyl-prolyl co...	PubMed	100	0	

10. To see this specific evidence, you can use the filter. As an example, let's filter on the Virulence Factor property. There are three databases to choose from (Victors,

PATRIC_VF and the Virulence Factor Database [VFDB]). Both PATRIC and Victors provide PubMed Ids that show direct links to the evidence. Click on Victors under Source (as shown below).



11. This will resort the table to show all the genes in your genome that have homology to genes in the Victors database. You can see more information about those individual genes by clicking on the Pubmed link (shown below). This will open up a new page that shows you the paper(s) that are the base of that evidence.

The image shows a 'Specialty Genes' interface with 230 records found. The table has columns for Evidence, Property, Source, PATRIC ID, RefSeq Lo, Alt Locus Tag, Source ID, Gene, Product, Pubmed, Identity, and E-value. A red arrow points from the 'PubMed' link in the first row to a detailed abstract page. The abstract page includes the title 'Brucella pathogenesis, genes identified from random large-scale screens.', authors 'Delrue RM¹, Lestrade P, Tibor A, Letesson JJ, De Bolle X', and a full text link. The abstract text discusses pathogenicity islands, secretion systems, and virulence plasmids in Brucella.

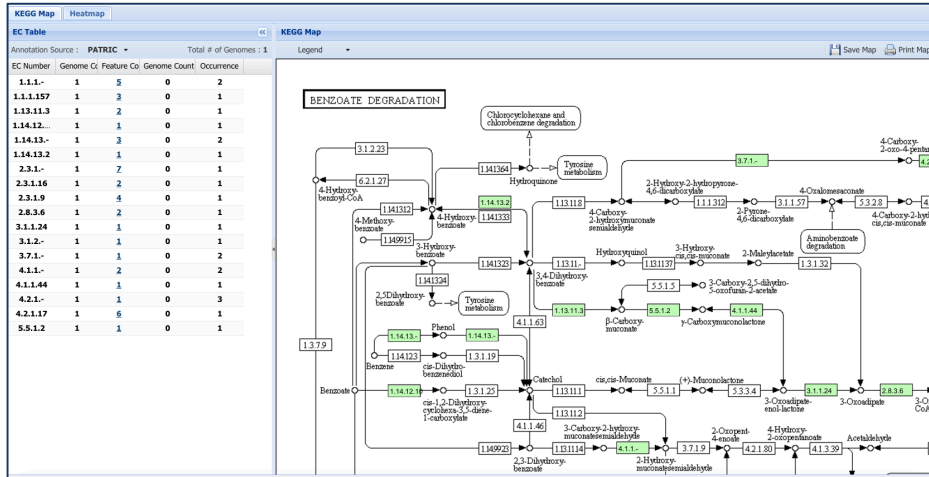
Evidence	Property	Source	PATRIC ID	RefSeq Lo	Alt Locus Tag	Source ID	Gene	Product	Pubmed	Identity	E-value
BLASTP	Virulence Factor	Victors	fig 29459.27.pep.47			1253		CAIB/BAIF family ...	PubMed	100	0
BLASTP	Virulence Factor	Victors	fig 29459.27.pep.50			1394		transporter, putati...	PubMed	100	0.0
BLASTP	Virulence Factor	Victors	fig 29459.27.pep.51			1393		Glutaredoxin-like ...	PubMed	100	0
BLASTP	Virulence Factor	Victors	fig 29459.27.pep.52			1392		Ribonucleotide re...	PubMed	100	0
BLASTP	Virulence Factor	Victors	fig 29459.27.pep.81			1023		SSU ribosomal pr...	PubMed	100	0
BLASTP	Virulence Factor	Victors	fig 29459.27.pep.121			1215		Phosphoribosylam...	PubMed	100	0

Abstract
 FEMS Microbiol Lett, 2004 Feb 9;231(1):1-12.
Brucella pathogenesis, genes identified from random large-scale screens.
 Delrue RM¹, Lestrade P, Tibor A, Letesson JJ, De Bolle X.
 Author information
Abstract
 Pathogenicity islands, specialized secretion systems, virulence plasmids, fimbriae, pili, adhesins, and toxins are all classical bacterial virulence factors. However, many of these factors, though widespread among bacterial pathogens, are not necessarily found among bacteria that colonize eukaryotic cells in a pathogenic/symbiotic relationship. Bacteria that form these relationships have developed other strategies to infect and grow in their hosts. This is particularly true for Brucella and other members of the class Proteobacteria. Thus far the identification of virulence factors for Brucella has been largely dependent on large-scale screens and testing in model systems. The genomes of the facultative intracellular pathogens Brucella melitensis and Brucella suis were sequenced recently. This has identified several more potential virulence factors for Brucella that were not found in large screens. Here, we present an overall view of Brucella virulence by compiling virulence data from the study of 184 attenuated mutants.
 PMID: 14979322 [PubMed - indexed for MEDLINE] [Free full text](#)

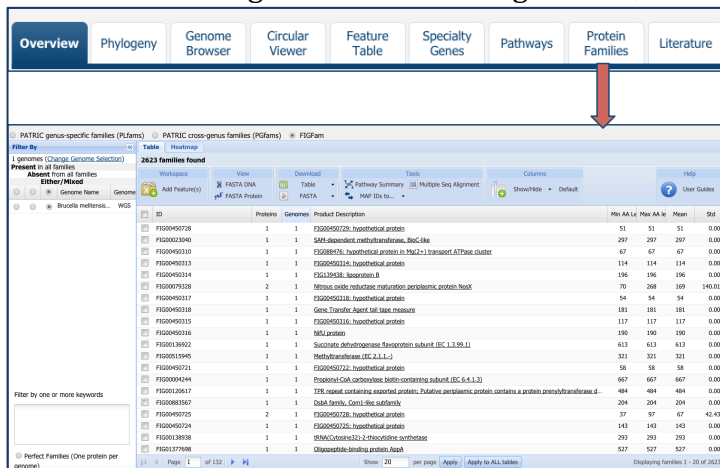
12. **Pathways.** You find all the KEGG pathways that your genome has genes annotated in by clicking on the Pathways tab.

13. At the top of the Pathways table is a filter that allows you to filter the table on the Pathway Class, the Pathway Name, Enzyme Commission (EC) Number or Annotation type (you can see PATRIC or RefSeq annotation). Let's look for a specific pathway. Click on the down arrow in the box that follows the "Pathway Name" and this will open up a list of pathway names. Scroll down until you see the name "Benzoate degradation via hydroxylation). Click on that, and the table will show that single pathway. To see the pathway map, click on the name in the table (Blue arrow 1 below).

14. This will open up a page that shows a list of the EC Numbers on the left side, and the KEGG pathway map on the right. Green boxes correspond to the EC numbers on the left side of the page. White boxes indicate EC numbers that are not present in this genome.



15. Protein Families. PATRIC has three types of protein families. The oldest, called FIGFams, contain isofunctional homologs. We have two new sets of protein families that are assembled from the function-based groups into families by use of k-mers and a Markov Cluster algorithm (MCL). At this time, FIGFams are the only protein family available for private genomes. When you click on the Protein Families tab, you will see a filter on the left and a table that lists the protein families, their IDs, Product Description, and statistics on the amino acids contained across your selection on the right. For individual genomes, these statistics will be limited.



16. As with the Feature Table mentioned above, you can use the filter to search for specific protein families. This will filter on the name of the family, not necessarily on the product description of the individual genes, so the results from the Feature Table and the Protein Family table will not necessarily match. To find specific genes, you can enter a name (NOT a locus tag) in the filter box on the left (Blue arrow 1) and then click the filter button (Blue arrow 2). This will filter the results to show the protein families that match the search.

Filter by one or more keywords

virB 1

Perfect Families (One protein per genome)
 Non Perfect Families
 All Families

Number of Proteins per Family
 to

Number of Genomes per Family
 to

2 Filter

ID	Proteins	Genomes	Product Description	Min AA Le	Max AA le	Mean	Std
FIG00002012	1	1	Inner membrane protein forms channel for type IV secretion of T-DNA complex (VirB3)	116	116	116	0.00
FIG00001567	1	1	Inner membrane protein forms channel for type IV secretion of T-DNA complex (VirB10)	383	383	383	0.00
FIG00001517	1	1	Forms the bulk of type IV secretion complex that spans outer membrane and periplasm (VirB9)	289	289	289	0.00
FIG00002640	1	1	Pores hole in peptidoglycan layer allowing type IV secretion complex assembly to occur (VirB1)	238	238	238	0.00
FIG00001460	1	1	ATPase provides energy for both assembly of type IV secretion complex and secretion of T-DNA complex (VirB11)	831	831	831	0.00
FIG01304041	1	1	Inner membrane protein forms channel for type IV secretion of T-DNA complex (VirB8)	239	239	239	0.00
FIG00002241	2	1	Integral inner membrane protein of type IV secretion complex (VirB6)	57	347	202	205.06
FIG00055840	1	1	ATPase provides energy for both assembly of type IV secretion complex and secretion of T-DNA complex (VirB11)	361	361	361	0.00
FIG00038155	1	1	Major pilus subunit of type IV secretion complex (VirB2)	105	105	105	0.00

17. Literature. The literature tab opens up a page that shows a filter on the right, and on the left, a list of publications relevant to the taxonomic level. For privately annotated genomes, it assemble recent publications at the genus level.

Overview | Phylogeny | Genome Browser | Circular Viewer | Feature Table | Specialty Genes | Pathways | Protein Families | Literature

10976 publications found

Filter Publications

Filter Publications

By Date:

Coming Soon
Past Week
Past Month
Past Year
All

By Keyword:

Reservoir
Disease
Host
Transmission
Pathogenesis
Countermeasures
Genome
Gene expression
Experiment Data

Publications

Publication

Serological survey of bovine brucellosis in Fulani nomadic cattle breeds (*Bos indicus*) of North-central Nigeria: Potential risk factors and zoonotic implications.
 Ahaji NB, Wungak YS, Bertu WJ
 Acta tropica (Fri Jan 01 2016 00:00:00 GMT-0500 (EST)), PubMed: 26464048
 Abstract

Isocitrate treatment of acute anemia of inflammation in a mouse model.
 Kim A, Fung E, Parikh SC, Gabayan V, Nemeth E, Ganz T
 diseases (Fri Jan 01 2016 00:00:00 GMT-0500 (EST)), PubMed: 26603720
 Abstract

Structural, Functional, and Immunogenic Insights on Cu,Zn Superoxide Dismutase Pathogenic Virulence Factors from *Neisseria meningitidis* and *Brucella abortus*.
 Pratt AJ, DiDonato M, Shin DS, Cabelli DE, Bruns CK, Belzer CA, Gorringer AR, Langford PR, Tabatabai LB, Kroll JS, Tainer JA, Getzoff ED
 Journal of bacteriology (Tue Dec 15 2015 00:00:00 GMT-0500 (EST)), PubMed: 26459556
 Abstract

Vaccination schedules in small ruminant farms.
 Lacasta D, Ferrer LM, Ramos J, González JM, Ortín A, Fthenakis GC
 Veterinary microbiology (Mon Dec 14 2015 00:00:00 GMT-0500 (EST)), PubMed: 26220514
 Abstract

Microbial diseases of the genital system of rams or bucks.
 Gouletsou PG and Fthenakis GC
 Veterinary microbiology (Mon Dec 14 2015 00:00:00 GMT-0500 (EST)), PubMed: 26209019
 Abstract

[*Brucella melitensis* is an agent in pediatric arthritis: Case series].
 Ç7raklı? S, Göger H, Deveci M, Ensöy SG
 Archivos argentinos de pediatria (Tue Dec 01 2015 00:00:00 GMT-0500 (EST)), PubMed: 26593815
 Abstract

Identification of Recombination and Positively Selected Genes in *Brucella*.
 Velbou JGC, Ceballos-Hernandez T, Sedláček J, Gurevskaya D, Pálfi-Bucur L

18. You can use the filters on the right side to refine the search by clicking on specific keywords (Arrow 1 below). This will filter the publications to a list that matches your selection.

134 publications found

Filter Publications

Filter Publications

By Date:

Coming Soon
Past Week
Past Month
Past Year
All

By Keyword:

Reservoir
Disease
Host
Transmission
Pathogenesis

Publications

Publication

Structural, Functional, and Immunogenic Insights on Cu,Zn Superoxide Dismutase Pathogenic Virulence Factors from *Neisseria meningitidis* and *Brucella abortus*.
 Pratt AJ, DiDonato M, Shin DS, Cabelli DE, Bruns CK, Belzer CA, Gorringer AR, Langford PR, Tabatabai LB, Kroll JS, Tainer JA, Getzoff ED
 Journal of bacteriology (Tue Dec 15 2015 00:00:00 GMT-0500 (EST)), PubMed: 26459556
 Abstract

Identification of Recombination and Positively Selected Genes in *Brucella*.
 Vishnu US, Sankarasubramanian J, Sridhar J, Gunasekaran P, Rajendhran J
 Indian journal of microbiology (Tue Dec 01 2015 00:00:00 GMT-0500 (EST)), PubMed: 26543263
 Abstract

The microbiological, histological, immunological and molecular determinants of *Helicobacter pylori* infection in guinea pigs as a convenient animal model to study pathogenesis.
 Walencka M, Gonciarz W, Mnich E, Gajewski A, Stawarski P, Knapik-Dabrowicz A, Chmiela M
 Acta biochimica Polonica (Fri Nov 27 2015 00:00:00 GMT-0500 (EST)), PubMed: 26610308
 Abstract

RNA-seq reveals the critical role of OtpR in regulating *Brucella melitensis* metabolism and virulence under acidic stress.
 Liu W, Dong H, Li J, Ou Q, Lv Y, Wang X, Xiang Z, He Y, Wu Q
 Scientific reports (Wed Aug 05 2015 00:00:00 GMT-0400 (EDT)), PubMed: 26242322
 Abstract

Experimental infection of chicken embryos with recently described *Brucella microti*: Pathogenicity and pathological findings.
 G, Böttcher D, Melzer F, Shehata AA, Roesler U, Neubauer H, Schoon HA
 active immunology, microbiology and infectious diseases (Sat Aug 01 2015 00:00:00 GMT-0400 (EDT)), PubMed: 26264524
 Abstract

Screening Household Members of Acute Brucellosis Cases in Endemic Areas and Risk Factors for Brucellosis.
 Deniz S, Ba, ykam N, Celikbas A, Yilmaz SM, Guzel TC, Dokuzoguz B, Ergonul O