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).



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.

Brucella melitensis_F3_99_548_contigs 164 Contigs										
Bacteria • Proteobacteria • Alphaproteobacter	ia • Rhizobiales • Bru	cellaceae • Bru	icella • Bruce	lla melite	ensis_F3_99_5	i48_contigs				
Overview Phylogeny Genome Cir Browser Vi	cular Feature ewer Table	Specialty Genes	Pathways	Protein Familie	Literature					
Search Tools	Genome Summ	nary								
GF Genome Finder						Add Genome to Workspace				
FF Feature Finder	Summary			1	.ength: 3281509b	p, Chromosomes: 0, Plasmids: 0, Contigs: 164				
CP Comparative Pathway Tool		Genome ID			29459.27					
PFS Protein Family Sorter	Organism Info	Genome Sta	tus		WGS					
		Antimicrobia	l Resistance							
Recent PubMed Articles	Taalata Tafa	Collection D	ate							
→ 2016 Jan	Isolate Info	Isolation Co	untry							
Serological survey of bovine brucellosis in Fulani nomadic cattle	Host Info	Host Name								
breeds (Bos indicus) of North-central Nigeria: Potential risk factors and	Sequence Info	Sequencing	Status							
zoonotic implications.	Phenotype Info	Disease								
Alhaji NB et al Acta Trop	Artia Trop Project Info Completion Date									
• 2016 Jan	Others									
Isocitrate treatment of acute anemia of inflammation in a mouse model.	Click for more*									
Kim A et al Blood Cells Mol Dis	Genomic Feature Summary									

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.

Overview	Phylogeny	Genome Browser	Circular Viewer	Feature Table	Specialty Genes	Pathways	Protein Families	Literature
A Jiew He	lp 1,000 1,500	2,000 2,500	3,000 3,5	600 4,000	4,500 5,000	•• Link 5,500 6,000	B	
	€	(२ 🕀 👤 2945	59.27.con.0001 - 2945	9.27.con.0001:16168 (6.	17 Kb) Go	<i>A</i>	29459.2	7.con.0001 🝷
) © Reference sequen	1,250	2,500 to see sequence	Zoom in to see sequence	1 Zoom in to :	5,000 see sequence Zo	6 pom in to see sequence	29459 . 29459.	27.con.0001 27.con.0002
PATRIC Annotatio	n fig 29459.27.peg.	→ 1 fig 29459.27.peg.2	fig 29459 →	.27.peg.3 fig 29459.27.peg.4	fig 29459.27.peg →	.5	29459. 29459. 29459.	27.con.0003 27.con.0004 27.con.0005
	·						29459	27.con.0006
							29459. 29459. 29459.	27.con.0008 27.con.0009

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 asterixs below), but these are not seen in private genomes.

Overview	Phylogeny	Genome Browse	e Circular Viewer	Feat Tab	ure s le	Specialty Genes	Path	ways	Protein Families	Literature
					7					
Feature tables contain a	I of the identified features	for all of the genom	es in a particular genus. Tab	es may be refined	to show subsets	of features via v	arious user cont	trols, as descri	ibed in Feature Table User	Guide.
Feature Tures CDS	× Annotal	ion: PATRIC	× Kenword:		Filter Table	1				
226E features found	Annota	ion: mae	. Reyword.							
Workspace	View	Download	Tools		Columns					Help
Add Feature(s)	S FASTA DNA	Table • 🔀	Pathway Summary 🔛 Multiple S	Seq Alignment	Show/Hide	Default				Iter Guides
	🔊 FASTA Protein	FASTA 🝷 🐂	MAP IDs to			berduit				
PATRIC ID	RefSeq Locus	Fag ቾ	Alt Locus Tag 🏋	Gene Symbol	Start	FIGfam ID	Length (AA)	Product Descri	iption 🔺	
fig 29459.27.peg.277	<u>'4</u>				22981	FIG01306569	304	(2E,6E)-farnes	yl diphosphate synthase (EC 2.	5.1.10)
fig 29459.27.peg.988					16349	FIG00044820	107	(AF179595) Vo	:033	
fig 29459.27.peg.200	8				182	FIG00021407	537	(R)-citramalate	e synthase (EC 2.3.1.182)	
fig 29459.27.peg.224	5				45445	FIG01320775	175	(U62541) imm	unoreactive 14 kDa protein BA	14k
fig 29459.27.peg.190	17				15547	FIG01319654	142	(U95165) OrfY		
fig 29459.27.peg.754					2092	FIG00005243	267	1-acyl-sn-glyce	erol-3-phosphate acyltransferas	ie (EC 2.3.1.51)
fig 29459.27.peg.140	9				4601	FIG00005243	260	1-acyl-sn-glyce	erol-3-phosphate acyltransferas	ie (EC 2.3.1.51)
fig 29459.27.peg.125	9				77897	FIG01349528	329	1-carboxy-3-ch	hloro-3,4-dihydroxycyclo hexa-	L,5-diene dehydrogenase (
fig 29459.27.peg.325	8				2081	FIG00000343	643	1-deoxy-D-xylu	ulose 5-phosphate synthase (El	C 2.2.1.7)
fig 29459.27.peg.277	5				23903	FIG00000449	420	1-hydroxy-2-m	nethyl-2-(E)-butenyl 4-diphosph	ate synthase (EC 1.17.7.1)
fig 29459.27.peg.261	7				9324	FIG00133510	320	1-pyrroline-4-h	nydroxy-2-carboxylate deamina	se (EC 3.5.4.22)
fig 29459.27.peg.159	6				39675	FIG00008665	156	16 kDa heat sh	hock protein A	
fig 29459.27.peg.280	9				61078	FIG01304909	465	16S rRNA (cyto	osine(967)-C(5))-methyltransfe	rase (EC 2.1.1.176)
fig129459.27.peg.570					33243	FIG00005547	187	16S rRNA (gua	anine(966)-N(2))-methyltransfe	rase (EC 2.1.1.171)
tigi29459.27.peg.992					18274	FIG00000312	189	165 rKNA proc	cessing protein RimM	

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		 Annotat 	ion: PATRIC	*	Key	/word:		Filter Table
Keyword:	virB				Filter Tal	ole			
ne, norai									
						1			
Feature Type: CDS	× ,	nnotation: PATRIC	Keyword:	VIFB	Plitter	Table			
13 features found	Minus	Deumland		Taola	C				Hole
Add Feature(s)	FASTA DNA	Table •	MAP IDs to	Multiple Seq Alignme	ent Show/	lide -	Default		User Guides
PATRIC ID	RefSeq	Locus Tag	Alt Locus Tag	Gene	Symbol	Start	FIGfam ID	Length (AA)	Product Description *
fig 29459.27.peg.1588						26741	FIG00055840	361	ATPase required for both assembly of type IV secretion complex and se
fig 29459.27.peg.1581						19241	FIG00001460	831	ATPase required for both assembly of type IV secretion complex and se
fig 29459.27.peg.1580						18891	FIG00002012	116	Inner membrane protein forms channel for type IV secretion of T-DNA c
fig 29459.27.peg.1585						24024	FIG01304041	239	Inner membrane protein forms channel for type IV secretion of T-DNA c
fig 29459.27.peg.1587						25606	FIG00001567	383	Inner membrane protein of type IV secretion of T-DNA complex, TonB-li
fig 29459.27.peg.1583						22641	FIG00002241	347	Inner membrane protein of type IV secretion of T-DNA complex, VirB6
fig 29459.27.peg.1584						23848	FIG00002241	57	Lipoprotein of type IV secretion complex that spans outer membrane an
fig 29459.27.peg.2361						13088	FIG00629430	82	Lipoprotein, VirB7-like
fig 29459.27.peg.2755						5481	FIG01288861	94	Lipoprotein, VirB7-like
tig129459.27.peg.1579						18560	FIG00038155	105	Major pilus subunit of type IV secretion complex, VirB2
mg129459.27.peg.1582						21/41	5100001517	238	Minor pillin or type 1V secretion complex, VirB5
E 6a/20450.27.peg.1586						24/40	FIG00003640	289	Outer memorane and perpiasm component of type IV secretion of T-D
igiz2459.27.peg.1578						1/408	F100002640	238	republygycan nyurolase virbi, 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.



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).

Workspace	Add Selected Feature(s) to Workspace
Add Feature(s)	Save as Feature Group Save as Genome Group Add to group: None
PATRIC ID	New group name
✓ fig 29459.27.peg.1588	
✓ fig 29459.27.peg.1581	
✓ fig 29459.27.peg.1580	Save to Workspace Cancel
✓ fig 29459.27.peg.1585	
✓ fig 29459.27.peg.1587	Add Selected Feature(s) to Workspace
✓ fig 29459.27.peg.1583	Save as Feature Group Save 2 Senome Group
✓ fig 29459.27.peg.1584	Add to group: Create New Group
✓ fig 29459.27.peg.2361	F3 virB genes
✓ fig 29459.27.peg.2755	Description 3
✓ fig 29459.27.peg.1579	
✓ fig 29459.27.peg.1582	4
✓ fig 29459.27.peg.1586	Save to Workspace Cancel
✓ fig 29459.27.peg.1578	

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.

Overview	Phylog	jeny		Gen Brov	ome vser	C V	Circular /iewer		Fea Ta	ature able	Sp G	ecialt ienes	y	Pathway	rs	Protein Families		.iterat	ure:
Filter By	~	Spe	cialty Gen	es															
keyword	Clear All	339	records	found															
Property (339) Virulence Factor (255) Human Homolog (80) Drug Target (3)		×.	Morkspace	ture(s)	V S FAST/ N FAST/	iew DNA Protein	Downloa Table FASTA	d	Y Pat	hway Summary IAP IDs to •	Fools E Multipl	e Seq Align	nment	Columns	 Default 			Help	r Guides
Antibiotic Resistance (1)			Evidence	Pro	operty	Source	P	ATRIC I	D	RefSeq	.o Alt Lo	cus Tag		Source ID	Gene	Product	Pubmed	Identity •	E-value
Source (339) Victors (230)			BLASTP	Viruler	nce Factor	Victors	fig12	459.27.	peg.47					1253		CAIB/BAIF family	PubMed	100	0
Human (80)			BLASTP	Viruler	nce Factor	Victors	fig12	459.27.	peg.50					1394		transporter, putati	PubMed	100	0.0
VFDB (23)			BLASTP	Viruler	nce Factor	Victors	fig 2	459.27.	peg.51					1393		Glutaredoxin-like	PubMed	100	0
PATRIC VF (2)			BLASTP	Viruler	nce Factor	Victors	fig 2	H59.27.	peg.52					1392		Ribonucleotide re	PubMed	100	0
ARDB (1)			BLASTP	Viruler	nce Factor	Victors	fig 2	459.27.	peg.81					1023		SSU ribosomal pr	PubMed	100	0
TTD (1)			BLASTP	Viruler	nce Factor	Victors	fig 29	459.27.	<u>eg.121</u>					1215		Phosphoribosylam	PubMed	100	0
Evidence (339)			BLASTP	Viruler	nce Factor	Victors	fig]29	459.27.	eg.158					1232		Carbamoyl-phosp	PubMed	100	0
BLASTP (339)			BLASTP	Viruler	nce Factor	Victors	fig 29	459.27.	beg.175					1224		Dipeptide-binding	PubMed	100	0
			BLASTP	Viruler	nce Factor	Victors	fig 29	459.27.0	beg.177					1223		Transcriptional re	PubMed	100	0
			BLASTP	Viruler	nce Factor	Victors	fig129	459.27.0	0eg.186					1243		Lactoylglutathione	PubMed	100	0
Filter BLAST Hits by:			BLASTP	Viruler	nce Factor	VFDB	fig 29	459.27.0	peg.195					VFG2225		GDP-mannose 4,6		100	0
Source organism			BLASTP	Viruler	nce Factor	Victors	fig129	459.27.	peg.195					1717		GDP-mannose 4,6	PubMed	100	0
Same Genome			BLASTP	Viruler	nce Factor	VFDB	fig 29	459.27.	peg.196					VFG2226		Perosamine synth		100	0
Same Species			BLASTP	Viruler	nce Factor	Victors	fig 29	459.27.	beg.196					1285		Perosamine synth	PubMed	100	0
Same Genus			BLASTP	Viruler	nce Factor	VFDB	fig129	459.27.	peg.199					VFG2229		Perosamine synth		100	0
II I			BLASTP	Viruler	nce Factor	VFDB	fig129	459.27.0	200 200					VFG2230		Formyltransferase		100	0
% Query Coverage >=	0 🗘		BLASTP	Virule	nce Factor	Victors	tig129	159.27.0	20 <u>6</u>					1286		undecaprenyl-gly	PubMed	100	0
% Subject Coverage >=	0 🗘		BLASTP	virulei	toe Factor	Victors	10129	159.27.1	2eg.232					4890		DNA-binding resp	PubMed	100	0
% Identity >=	0 🗘		BLASTP	Viruler	nce Hactor	Victors	tig[29	109.27.	xeg.257					1324		Dreve-binding resp	PubMed	100	0
			BLASTP	virulei	toe Hactor	victors	<u>fig 29</u>	159.27.0	beg.272					1297		repagy-prolyl as	PubMed	100	U
	Filter	14	Page	1 0	f 17 🕨	2				Show 20	per page	Apply	Apply t	o ALL tables			Displaying	records 1 -	20 of 339

10. To see this specific evidence, you can 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.

Specialty	Genes														
230 recor	ds found														
Work	space	Vi	ew	C	Download		т	ools		Column	5			Help	.
Add	Feature(s)	🎖 FASTA	DNA Protein		Table • FASTA •	A Pathway	Summary s to 🝷	EE Multiple Seq Align	ment	Show/Hide	 Default 			User	Guides
Eviden	ce Prop	erty	Source		PATRIC	ID	RefSeq L	.c Alt Locus Tag		Source ID	Gene	Product	Pubmed	Identity 🔻	E-value
BLAST	TP Virulenc	e Factor	Victors		fig 29459.27	.peg.47				1253		CAIB/BAIF family	PubMe	1	0
BLAST	TP Virulenc	e Factor	Victors		fig 29459.27	.peg.50				1394		transporter, putati	PubMer	100	0.0
BLAST	TP Virulenc	e Factor	Victors		fig 29459.27	.peg.51				1393		Glutaredoxin-like	PubMer	100	0
BLAST	TP Virulenc	e Factor	Victors		fig 29459.27	.peg.52				1392		Ribonucleotide re	PubMec	100	0
BLAST	TP Virulenc	e Factor	Victors		fig 29459.27	.peg.81				1023		SSU ribosomal pr	PubMec	100	0
BLAST	TP Virulenc	e Factor	Victors		fig 29459.27	peg.121				1215		Phosphoribosylam	PubMec	100	0
Abstrac	ct 👻													Send 1	to: 🕶
FEMS N	licrobiol Lett.	2004 Fe	eb 9;231(1):1-12.											
Bruce	alla nath	onene	asis n	ones	identifi	ad from r	andon	n large-scale	- er	reens					
Delrue	RM ¹ . Lestra	ate P. Tit	oor A. Let	tesson	JJ. De Boll	e X.	unaon	in lange-seal							
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FINID: 1	HOI BOZZ [PU	Dividu - II	Indexed 10	WEDL	und the	e fun text									

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

01	verview	Phylogeny	Genom Brows	ne er	Circula Viewe	r r	Feature Table	Specialty Genes	Ра	thways	Pi Fa	rotein milies	Literature
Path	way Class:	LL		~	Pathwa	y Name:	ALL		~	EC Number:	ALL	▼ A	nnotation: PATRI
Pat	hways EC N	lumbers Genes											
132	unique pathy	vay(s) found											
	Workspace	View		Download			Tools			Col	umns		Help
8	Add Feature(s) 🙀 FASTA DNA	n 🔊	Table FASTA	Ţ	🖍 Pathway 🛶 MAP I	y Summary 🔡 I Ds to 👻	Multiple Seq Alignn	ient	Show/H	lide 🝷	Default	User Guides
	Pathway ID	Pathway Name		Pathway Cla	ass		Annotation	Unique Genome	Unique Ge	ene Cc Unique	e EC Cour	EC Conservatio	Gene Conservat
	00930	Caprolactam degradation	on	Xenobiotics	Biodegra	dation a	PATRIC	1	11		3	100.00	3.00
	00053	Ascorbate and aldarate	metab	Carbohydra	ate Metabo	olism	PATRIC	1	<u>35</u>		10	100.00	3.00
	00051	Fructose and mannose	metab	Carbohydra	ate Metabo	olism	PATRIC	1	<u>27</u>		14	100.00	1.00
	01056 <u>Biosynthesis of type II polyket</u> Biosynthesis of Polyketides and					etides an	PATRIC	1	<u>13</u>		3	100.00	4.00
	00052 <u>Galactose metabolism</u> Carbohydrate Metabolism					olism	PATRIC	1	<u>14</u>		10	100.00	1.00
	01057	Biosynthesis of type II	polyket	Biosynthesi	is of Polyk	etides an	PATRIC	1	<u>24</u>		<u>6</u>	100.00	4.00

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.

Overview Phylog	geny Ger Bro	nome wser	Circ Viev	ular ver		Feature Table	Specialty Genes	Pathways	Protein Families	I	iterat	ure:
									Ţ			
PATRIC genus-specific families (PLfa	ns) O PATRIC cross	-genus families (PG	ifams)	FIG	Fam							
Alter By «	Table Heatmap											
 genomes (<u>Change Genome Selection</u>) Present in all families 	2623 families found											
Absent from all families	Workspace	View		Downle	oad		Tools	Columns			Hdg	¢.
C C C Genome Name Genom	Add Peature(s)	FASTA DNA		FAST	le ∙ rA •	MAP IDs to	Multiple Seq Alignment	ShowHide • Default			🕜 Use	r Guldes
Brucella melitensis WGS	P1 10	Po	steins G	eromes	Product D	escription			Min AA I	e Nex AA	le Mean	9:4
	E				-	170 handballad ambaia						0.00
	F1300130728		1	1	CASE/COL	225. Ingool eads a process	Rise" Has		207	21	31	0.00
	E 51000050310				51006947	 beneficial contain in 	Mo/2+) transport ATPase due	har.	67	67	67	0.00
	F1600450313		1	1	F1G00450	114: hypothetical protein	THE CONTRACT OF A		114	114	114	0.00
	FIG00450314		1	1	FIG13943	5: lipporotein B			196	195	196	0.00
	F1G00079328		2	1	Nitrous on	ide reductase maturation	periplasmic protein NosX		70	268	169	140.01
	F1G00450317		1	1	F1920450	318: hypothetical protein			54	54	54	0.00
	FIG00450318		1	1	Gene Tran	sfer Agent tail tape mean	are		181	181	181	0.00
	F1G00450315		1	1	E1900450	116: hypothetical protein			117	117	117	0.00
	FIG00450316		1	1	NifU prote	in			190	190	190	0.00
	F1G00136922		1	1	Succinate	dehydrogenase flavoprot	ein subunit (EC 1.3.99.1)		613	613	613	0.00
	F1G00515945		1	1	Methyltran	sferase (EC 2.1.1)			321	321	321	0.00
	FIG00450721		1	1	E1900450	722: hypothetical protein			58	58	58	0.0
	F1G00004244		1	1	Propional-	CoA carboxylase biotin-o	ontaining subunit (EC 6.4.1.3)		667	667	667	0.00
liter by one or more keywords	F1G00120617		1	1	TPR repeat	t containing exported pro	stein; Putative periplasmic prot	ein contains a protein prenylyfzansf	arase d 484	484	484	0.00
	FIG00883567		1	1	DsbA fami	ly, Com1-like subfamily			204	204	204	0.0
	F1G00450725		2	1	F1900450	728: hypothetical protein			37	97	67	42.43
	FIG00450724		1	1	E3930450	725: hypothetical protein			143	143	143	0.00
	F1G00138938		1	1	tRN4(Cyto	sine32)-2-thiocytidine av	othetase		293	293	293	0.00
Derfort Families (One protein per	F1G01377698		1	1	Oligopepti	de-binding protein AppA			527	527	527	0.00
processo)	14 4 Page 1	of 132 🕨 🔰				Show 20	per page Apply Apply I	to ALL tables		Displaying	families 1 - 1	20 of 262

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.

	Table H	eatmap									
Filter by one or more keywords	9 families f	found									
	Works	pace Viev	/	Down	load	Tools	Columns			Help	2
VirB	Add F	Feature(s) FASTA D	NA rotein	Tab	le • TA •	MAP IDs to	Show/Hide - Default			2 User	Guides
	🗂 ID		Proteins	Genomes	Product D	rescription		Min AA Le	Max AA le	Mean	Std
	FIG000	02012	1	1	Inner mer	mbrane protein forms channel for type IV secretion of T	-DNA complex (VirB3)	116	116	116	0.00
	FIG000	01567	1	1	Inner mer	mbrane protein forms channel for type IV secretion of T	-DNA complex (VirB10)	383	383	383	0.00
Perfect Families (One protein per	FIG000	01517	1	1	Forms the	bulk of type IV secretion complex that spans outer me	mbrane and periplasm (VirB9)	289	289	289	0.00
genome)	FIG000	02640	1	1	Bores hole	e in peptidoglycan layer allowing type IV secretion comp	lex assembly to occur (VirB1)	238	238	238	0.00
Non Perfect Families	FIG000	01460	1	1	ATPase pr	rovides energy for both assembly of type IV secretion or	implex and secretion of T-DNA complex (V	<u>ir</u> 831	831	831	0.00
All Families	FIG013	04041	1	1	Inner mer	mbrane protein forms channel for type IV secretion of T	-DNA complex, VirB8	239	239	239	0.00
Number of Proteins per Family	FIG000	02241	2	1	Integral in	aner membrane protein of type IV secretion complex (V	rB6)	57	347	202	205.06
	FIG000	55840	1	1	ATPase pr	rovides energy for both assembly of type IV secretion or	implex and secretion of T-DNA complex (V	<u>r</u> 361	361	361	0.00
to	FIG0003	38155	1	1	Major pilu	is subunit of type IV secretion complex (VirB2)		105	105	105	0.00
Number of Genomes per Family	2										

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	Ph	ylogeny	Genome Browser	Circular Viewer	Feature Table	Specialty Genes	Pathways	Protein Families	Literature
10976 publications f	ouna	Bublications							•
Filter Publications	<u></u>	Publications							
Filter Publications		Publication		la la Falant a succida sat			. Batantial state for stores a		
By Date: Coming Soon Past Week		Alhaji NB, Wung Acta tropica (Fri Abstract Isocitrate trea Kim A, Fung E, diseases (Fri Ja	ak YS, Bertu WJ i Jan 01 2016 00:00:00 GMT atment of acute anemia (Parikh SG, Gabayan V, Nem 0.1 2016 00:00:00 GMT-00	-0500 (EST)), PubMed: 20 of inflammation in a mo eth E, Ganz T i00 (EST)) PubMed: 2660	6464048 Duse model.) or North-Central Nigeri	a: Potentiai risk factors a	no zoonotic impiicatioi	15.
Past Month			101 2010 00.00.00 011 0.	(L31)), Fublica. <u>2000</u> .	<u> </u>				
All		Structural, Fu Pratt AJ, DiDona Journal of bacter Abstract	nctional, and Immunoge ato M, Shin DS, Cabelli DE, eriology (Tue Dec 15 2015 0	nic Insights on Cu,Zn S Bruns CK, Belzer CA, Gorri 0:00:00 GMT-0500 (EST))	Superoxide Dismutase F nge AR, Langford PR, Tab , PubMed: <u>26459556</u>	athogenic Virulence Fact atabai LB, Kroll JS, Tainer JA	t ors from Neisseria menir I, Getzoff ED	ngitidis and Brucella ab	ortus.
By Keyword:		Vaccination se Lacasta D, Ferre Veterinary micro	chedules in small rumina er LM, Ramos JJ, González J obiology (Mon Dec 14 2015	nt farms. M, Ortín A, Fthenakis GC 00:00:00 GMT-0500 (EST))), PubMed: <u>26220514</u>				
Disease Host Transmission		Microbial dise Gouletsou PG a Veterinary micro	ases of the genital syste nd Fthenakis GC obiology (Mon Dec 14 2015	m of rams or bucks. 00:00:00 GMT-0500 (EST))), PubMed: <u>26209019</u>				
Pathogenesis Countermeasures Genome		[Brucella meli Ç?rakl? A, Ç?rak Archivos argent	itensis is an agent in ped kl? S, Göçer H, Deveci M, Er inos de pediatria (Tue Dec I	iatric arthritis: Case se soy SG 01 2015 00:00:00 GMT-05	ries]. 00 (EST)), PubMed: <u>26593</u>	815			
Experiment Data		Identification	of Recombination and P	ositively Selected Gene	es in Brucella.				

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.

234 publications found	
Filter Publications	Publications
	Publication
Filter Publications	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, Gorringe AR, Langford PR, Tabatabai LB, Kroll JS, Tainer JA, Getzoff ED
By Date:	Journal of bacteriology (Tue Dec 15 2015 00:00:00 GMT-0500 (EST)), PubMed: <u>26459556</u> B Abstract
Coming Soon Past Week Past Month	Identification of Recombination and Positively Selected Genes in Brucella. Vishnu US, Sankarsubrananian J, Sirdhar J, Gunaekaran P, Rajendrina J Indian journal of microbiology (Tue Dec 01 2015 00:00:00 GMT-0500 (EST)), PubMed: <u>26543263</u> B Abstract
Past Year All	The microbiological, histological, immunological and molecular determinants of Helicobacter pylori infection in guinea pigs as a convenient animal model to study patt Walencka M, Gondrar W, Minki E, Gajewski A, Stalwerski P, Knajik-Dabrovicz A, Chenileia M Acta biochimica Polonica (Fri Nov 27 2015 00:00:00 GMT-0500 (EST)), PubMed: 26610308
By Keyword:	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: <u>26242322</u>
Reservoir Disease Host Transmission	G, Böttcher D, Melzer F, Shehata AA, Roesler U, Neubauer H, Schoon HA ative immunology, microbiology and infectious diseases (Sat Aug 01 2015 00:00:00 GMT-0400 (EDT)), PubMed: <u>26264524</u> act
Pathogenesis	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