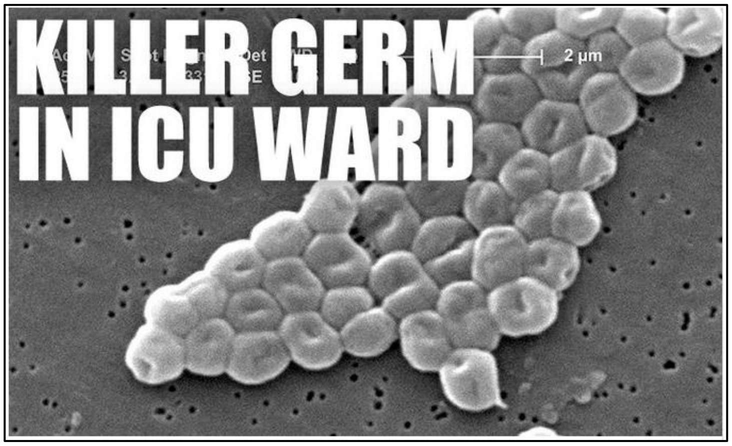
Exploring antibiotic resistance in *Acinetobacter baumannii*

Antibiotic resistance of bacterial pathogens is becoming an area of increasing concern, and this is especially true of *Acinetobacter baumannii.* This organism has emerged as one of the most troublesome bacteria for health institutions globally[1-3]. A recent study examined *A. baumannii*[4] and found that horizontal transfer plays an important part in the development of antibiotic resistance in this pathogen.



We will use a variety of the PATRIC tools to explore genomic islands and the genes associated with resistance and gene neighborhoods. This exercise has five parts.

I. Creating genome groups

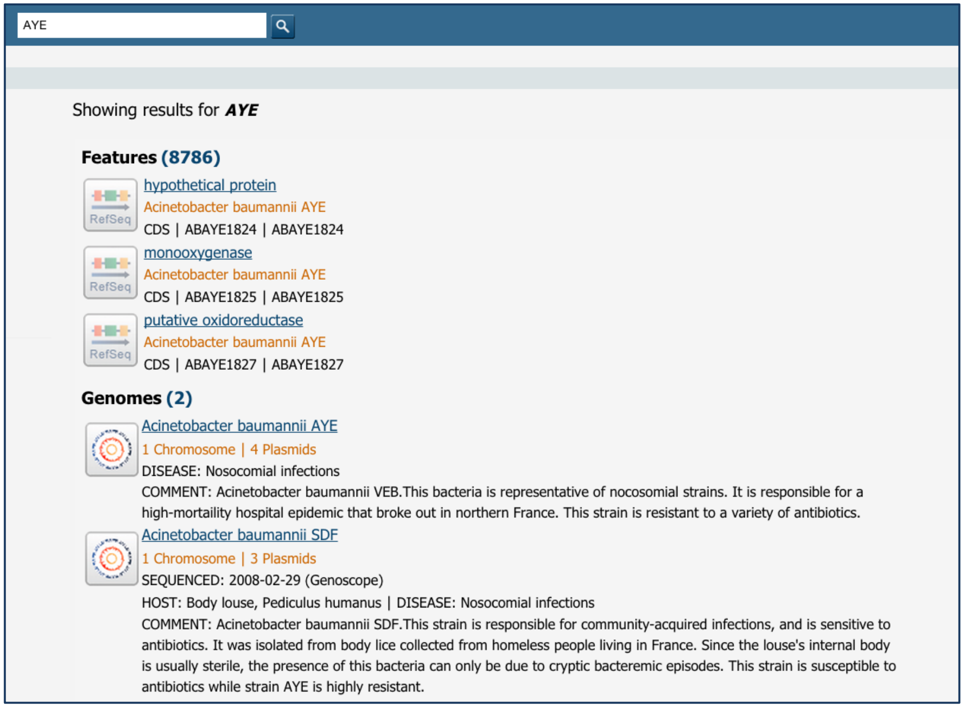
In this part of the exercise, we will examine two particular strains of *A. baumannii* that are known to have benefited from horizontal transfer[4], and compare these two strains to other *A. baumannii* genomes to see how widely spread these genomic islands are.

1. Login to the PATRIC website (patricbrc.org) so that you can use your workspace in the downstream analysis.

2. Two *A. baumannii* genomes (strain AYE and SDF) were used to examine horizontal transfer and antibiotic resistance. In the global search box, enter the word AYE and hit return.

3. This will take you to the Search Results page that is divided into Features, Genomes, Taxonomy and Experiments. Fortuitously enough, under Genomes you

will see both the AYE and SDF genomes. You see SDF because AYE is mentioned in the comment field for the genome.



Showing results for ***AYE***

Features (8786)

hypothetical protein
Acinetobacter baumannii AYE
CDS | ABAYE1824 | ABAYE1824

monooxygenase
Acinetobacter baumannii AYE
CDS | ABAYE1825 | ABAYE1825

putative oxidoreductase
Acinetobacter baumannii AYE
CDS | ABAYE1827 | ABAYE1827

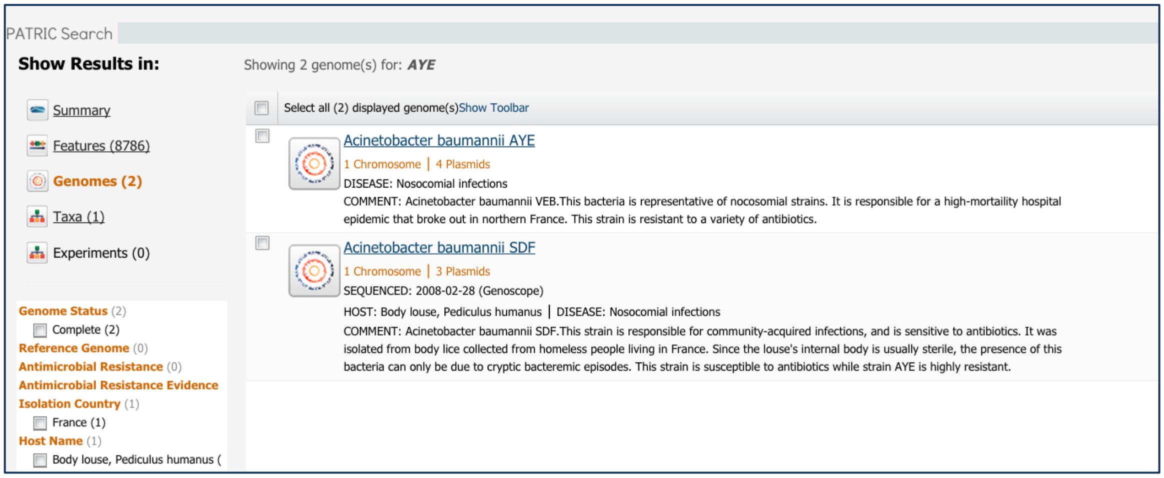
Genomes (2)

Acinetobacter baumannii AYE
1 Chromosome | 4 Plasmids
DISEASE: Nosocomial infections
COMMENT: Acinetobacter baumannii VEB.This bacteria is representative of nocosomial strains. It is responsible for a high-mortaility hospital epidemic that broke out in northern France. This strain is resistant to a variety of antibiotics.

Acinetobacter baumannii SDF
1 Chromosome | 3 Plasmids
SEQUENCED: 2008-02-29 (Genoscope)
HOST: Body louse, Pediculus humanus | DISEASE: Nosocomial infections
COMMENT: Acinetobacter baumannii SDF.This strain is responsible for community-acquired infections, and is sensitive to antibiotics. It was isolated from body lice collected from homeless people living in France. Since the louse's internal body is usually sterile, the presence of this bacteria can only be due to cryptic bacteremic episodes. This strain is susceptible to antibiotics while strain AYE is highly resistant.

4. Click on the number 2 that follows the word Genomes.

5. This opens up a page where you can filter results, or save selections to your workspace. The filter on the left side allows you to narrow down the results based on the metadata that is linked to them. You will need this later on in this exercise.



Show Results in:

- Summary
- Features (8786)
- **Genomes (2)**
- Taxa (1)
- Experiments (0)

Genome Status (2)
☐ Complete (2)
Reference Genome (0)
Antimicrobial Resistance (0)
Antimicrobial Resistance Evidence
Isolation Country (1)
☐ France (1)
Host Name (1)
☐ Body louse, Pediculus humanus (

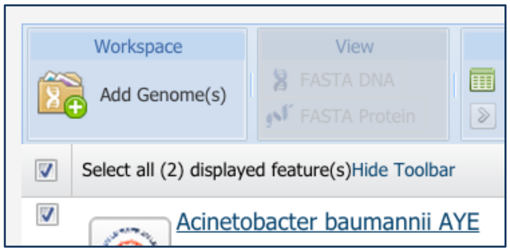
Showing 2 genome(s) for: ***AYE***

☐ Select all (2) displayed genome(s)Show Toolbar

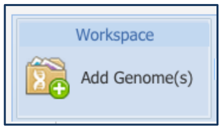
☐ Acinetobacter baumannii AYE
1 Chromosome | 4 Plasmids
DISEASE: Nosocomial infections
COMMENT: Acinetobacter baumannii VEB.This bacteria is representative of nocosomial strains. It is responsible for a high-mortaility hospital epidemic that broke out in northern France. This strain is resistant to a variety of antibiotics.

☐ Acinetobacter baumannii SDF
1 Chromosome | 3 Plasmids
SEQUENCED: 2008-02-28 (Genoscope)
HOST: Body louse, Pediculus humanus | DISEASE: Nosocomial infections
COMMENT: Acinetobacter baumannii SDF.This strain is responsible for community-acquired infections, and is sensitive to antibiotics. It was isolated from body lice collected from homeless people living in France. Since the louse's internal body is usually sterile, the presence of this bacteria can only be due to cryptic bacteremic episodes. This strain is susceptible to antibiotics while strain AYE is highly resistant.

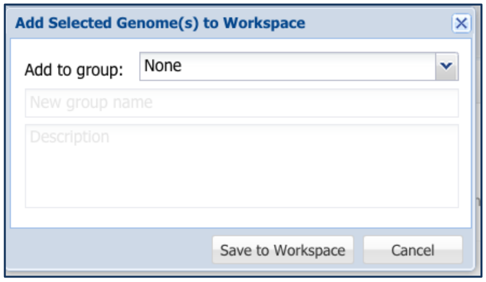
6. Click the check box in front of the words “Select all (2) displayed feature(s).” Doing this will click both of the genomes, and also open up specific tools above the genome list.



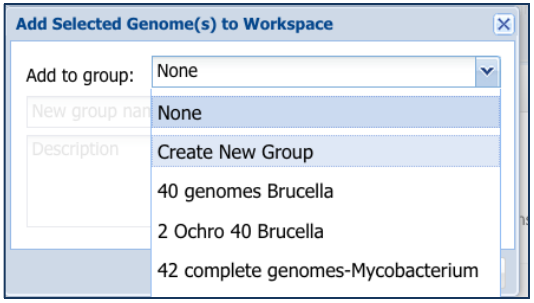
7. Click on the "Add Genomes" next to the folder icon in the Workspace header.



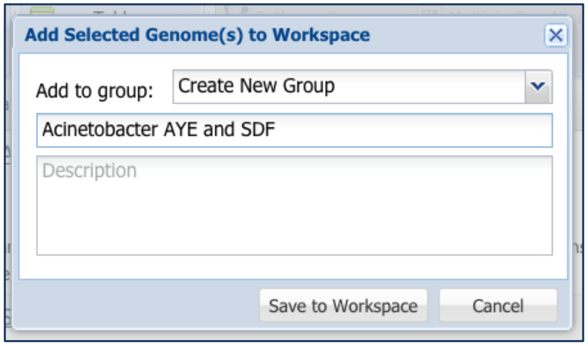
8. This will open up a pop-up window that allows you to save the group.



9. Select the "Create New Group" option.



10. Name the group and click "Save to Workspace". Now that data is saved and you can use a number of tools to explore it.



Add to group: Create New Group

Acinetobacter AYE and SDF

Assignment

Create genome groups for the three categories below. Use the global search text box and the dynamic filter on the Search Results page. When you complete your assignment, you will have four different groups that include the one we just created.

- Create a genome group that contains all the complete *A. baumannii* genomes.
- Create a genome group that contains all the *A. baumannii* genomes that were isolated in China.
- Create a genome group that contains all the *A. baumannii* genomes that were isolated from hospitals (nosocomial).

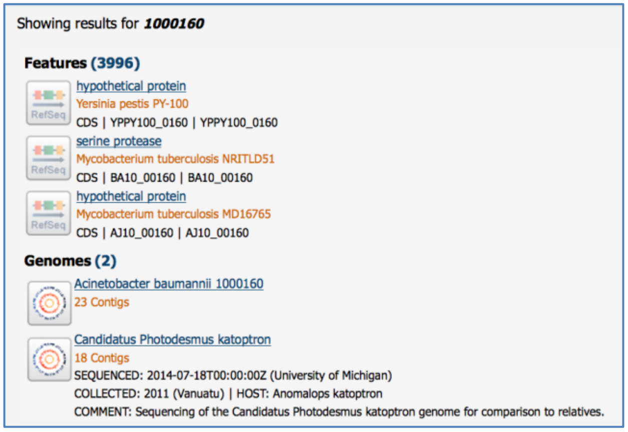
Hint-To complete some of these tasks, you will need to resize the results table (its set to show 20 genomes) to match the number of genomes that are the result of the filtering parameters. You'll need to scroll to the bottom of the table to resize it before selecting all the genomes.

II. Getting a freshly annotated genome ready for comparison in PATRIC

1. We have assembled and annotated two new *A. baumannii* genomes from NCBI's Short Reads Archive (SRA) that have not previously been assembled or annotated. You should have already started the process to annotate these genomes. Once they are annotated, you will first need to make them into their own individual genome group (Note: You can also add them to an existing group, but we'll start with this. Also note that this is MY workspace. You have your own unique workspace and names, and should use those in the following steps. You can find these genomes by using the global search box. Enter the strain number for the *Acinetobacter* genome you annotated into the search box (1000160) and hit return.

1000160

2. This will take you to the Search Results page.



Showing results for ***1000160***

Features (3996)

hypothetical protein
Yersinia pestis PY-100
CDS | YPPY100_0160 | YPPY100_0160

serine protease
Mycobacterium tuberculosis NRITLD51
CDS | BA10_00160 | BA10_00160

hypothetical protein
Mycobacterium tuberculosis MD16765
CDS | AJ10_00160 | AJ10_00160

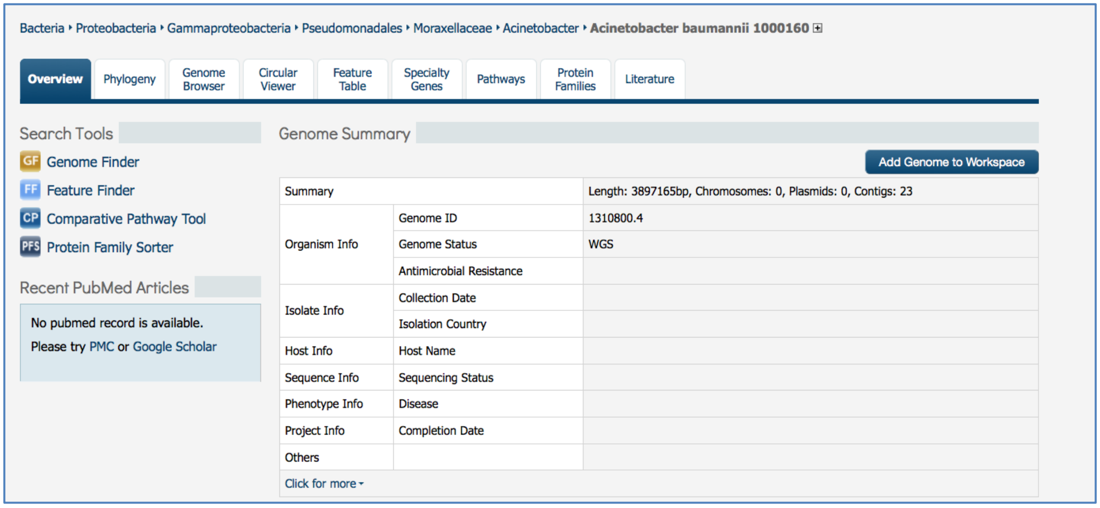
Genomes (2)

Acinetobacter baumannii 1000160
23 Contigs

Candidatus Photodesmus katoptron
18 Contigs
SEQUENCED: 2014-07-18T00:00:00Z (University of Michigan)
COLLECTED: 2011 (Vanuatu) | HOST: Anomalops katoptron
COMMENT: Sequencing of the Candidatus Photodesmus katoptron genome for comparison to relatives.

3. Under the "Genome" division click on the name of the genome you annotated (Acinetobacter baumannii 1000160).

4. This will take you to the landing page for your private genome (the 1000160 genome).

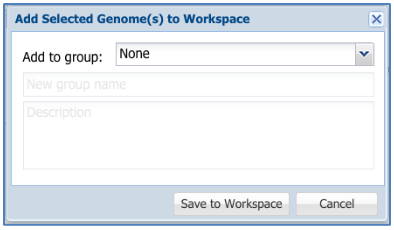


No pubmed record is available.
Please try PMC or Google Scholar

Summary		Length: 3897165bp, Chromosomes: 0, Plasmids: 0, Contigs: 23
Organism Info	Genome ID	1310800.4
	Genome Status	WGS
	Antimicrobial Resistance	
Isolate Info	Collection Date	
	Isolation Country	
Host Info	Host Name	
Sequence Info	Sequencing Status	
Phenotype Info	Disease	
Project Info	Completion Date	
Others		

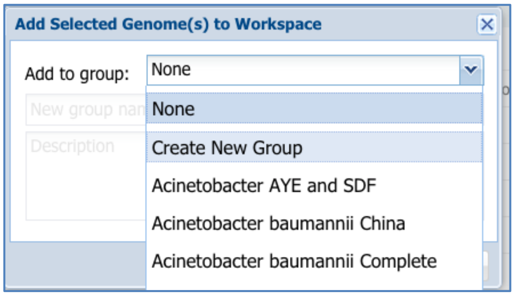
5. To make a genome group using this genome, you will need to click the blue button that says "Add Genome to Workspace."

6. This will pop-up a window that allows you to save a group.



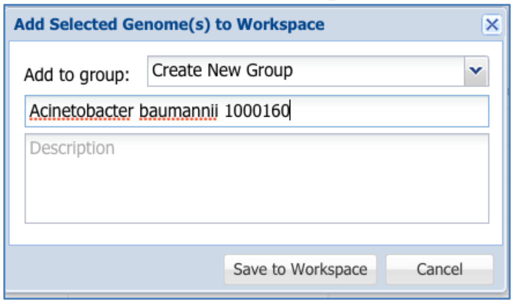
Add to group: None

7. Click on the down arrow next to "None" and then click on "Create New Group."



Add to group: None

8. In the text box below “Add to group” put in a unique name for the genome. Then click the “Save to Workspace” button at the bottom of the window.



Add to group: Create New Group

Acinetobacter baumannii 1000160

Assignment: Create a new genome group for the second Acinetobacter genome that you have annotated (strain 1592857).

III. Comparing genome groups in PATRIC using the Protein Family Sorter tool

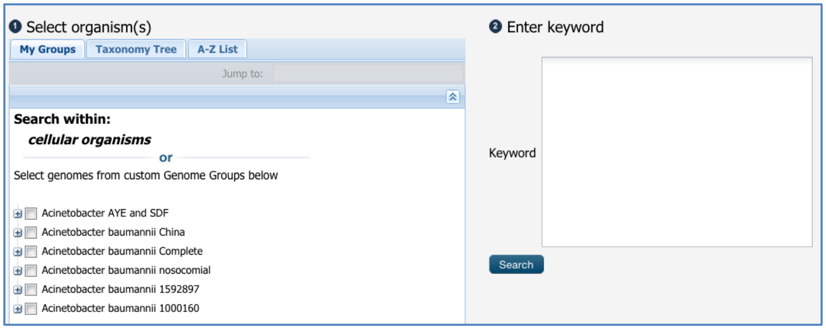
1. To look for presence or absence of the protein families within a genome group that you have created, click on the Tools tab and under Comparative Genomics, select the Protein Family Sorter tool

SPECIALTY GENES
FOR INFECTIOUS DISEASE RESEARCH

PATRIC now offers analysis of Specialty Genes, i.e. genes that possess properties that are of particular interest to infectious disease researchers. Classes of Specialty Genes currently supported include:

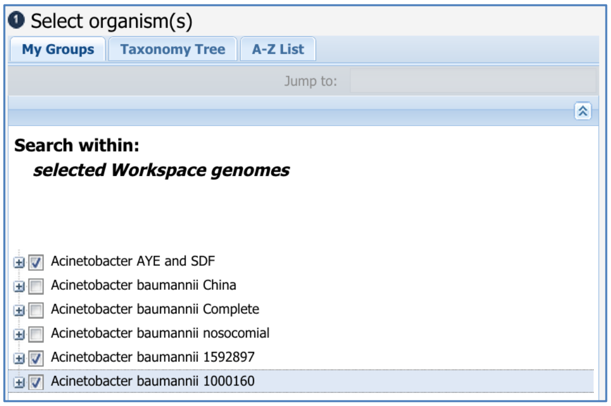
- Antibiotic Resistance Genes
- Drug Targets
- Human Homologs
- Virulence Factors

2. This will take you to the landing page for that tool.



3. Scroll down in the Select Organism box until you see the genome groups you created. Select the boxes in front of the three following *Acinetobacter* groups you created:

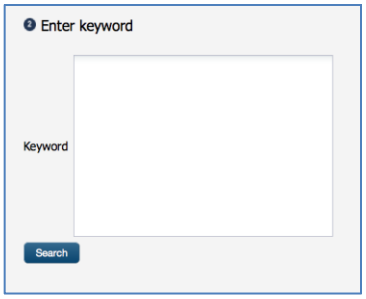
- Acinetobacter AYE and SDF
- Acinetobacter baumannii 1592897
- Acinetobacter baumannii 1000160



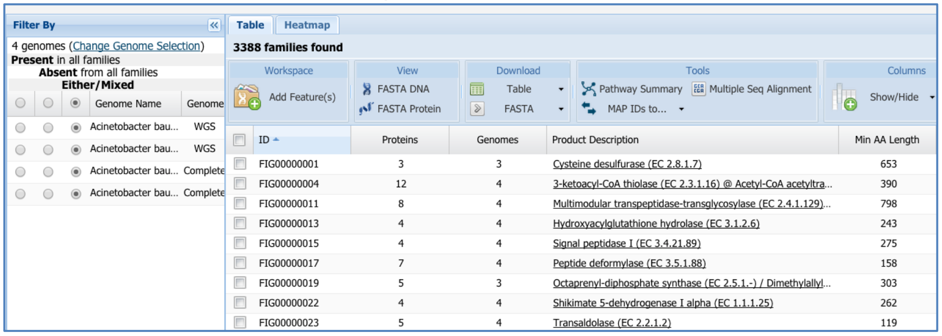
Search within:
selected Workspace genomes

☑ Acinetobacter AYE and SDF
☐ Acinetobacter baumannii China
☐ Acinetobacter baumannii Complete
☐ Acinetobacter baumannii nosocomial
☑ Acinetobacter baumannii 1592897
☑ Acinetobacter baumannii 1000160

4. Hit the Search button under the keyword search box.



5. This takes you to the Protein Family Sorter landing page. On the left you will see a dynamic filter, and on the right a table that lists all the protein families.



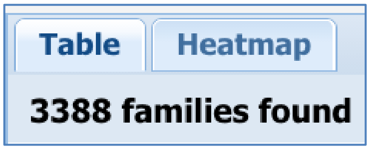
4 genomes (Change Genome Selection)
Present in all families
Absent from all families
Either/Mixed

○	○	●	Genome Name	Genome
○	○	●	Acinetobacter bau...	WGS
○	○	●	Acinetobacter bau...	WGS
○	○	●	Acinetobacter bau...	Complete
○	○	●	Acinetobacter bau...	Complete

3388 families found

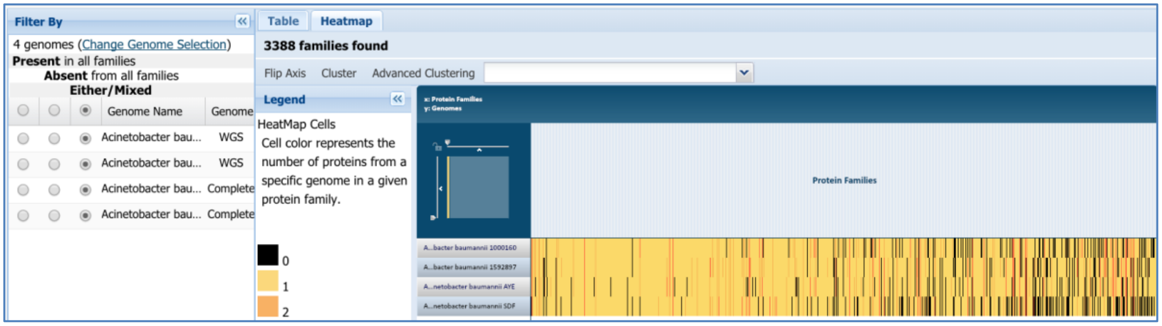
☐	ID	Proteins	Genomes	Product Description	Min AA Length
☐	FIG00000001	3	3	Cysteine desulfurase (EC 2.8.1.7)	653
☐	FIG00000004	12	4	3-ketoacyl-CoA thiolase (EC 2.3.1.16) @ Acetyl-CoA acetyltra...	390
☐	FIG00000011	8	4	Multimodular transpeptidase-transglycosylase (EC 2.4.1.129)...	798
☐	FIG00000013	4	4	Hydroxyacylglutathione hydrolase (EC 3.1.2.6)	243
☐	FIG00000015	4	4	Signal peptidase I (EC 3.4.21.89)	275
☐	FIG00000017	7	4	Peptide deformylase (EC 3.5.1.88)	158
☐	FIG00000019	5	3	Octaprenyl-diphosphate synthase (EC 2.5.1.-) / Dimethylallyl...	303
☐	FIG00000022	4	4	Shikimate 5-dehydrogenase I alpha (EC 1.1.1.25)	262
☐	FIG00000023	5	4	Transaldolase (EC 2.2.1.2)	119

6. One way you can examine differences in your genome groups is to visualize the data. To do this, click on the Heatmap at the top of the table (next to the Table tab).



3388 families found

7. This will take you the heatmap view, where absence (black cells) and presence (yellow, mustard and orange cells) can be seen across all genomes. The genomes are on the y-axis, and the protein families on the x-axis.



4 genomes (Change Genome Selection)
Present in all families
Absent from all families
Either/Mixed

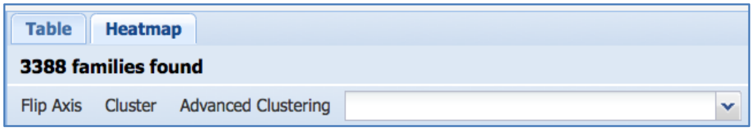
○	○	●	Genome Name	Genome
○	○	●	Acinetobacter bau...	WGS
○	○	●	Acinetobacter bau...	WGS
○	○	●	Acinetobacter bau...	Complete
○	○	●	Acinetobacter bau...	Complete

3388 families found

HeatMap Cells
Cell color represents the number of proteins from a specific genome in a given protein family.

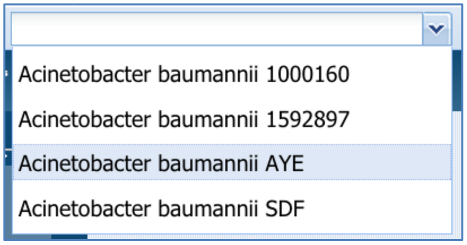
■ 0
■ 1
■ 2

11. You can order the protein families by the way the genes occur in a given genome. This is a good way to check for something called genomic islands, which are parts of a genome that were not directly inherited, but are obtained from different bacteria in what is described as horizontal transfer. To do this using the Protein Family Sorter, click on the down arrow in the text box next to the words "Advanced Clustering."

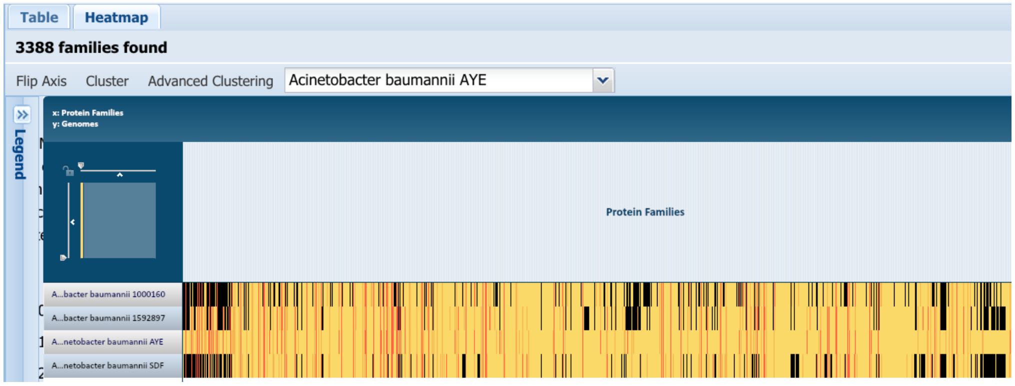


3388 families found

12. This will open up a list of genomes that are included in the groups. Scroll down until you find AYE strain of Acinetobacter baumannii. Click on that name.

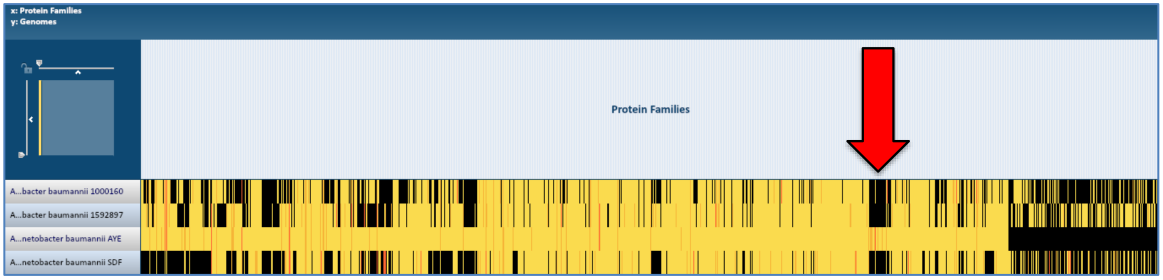


13. This will order all the protein families along the order that the genes occur in the AYE strain. You'll notice that the SDF, 1000160 and 1592897 genomes appear to have long black boxes associated with them. This indicates that these genomes are missing a long section of the genome that is present in the AYE strain. This is an indication of a genomic island.

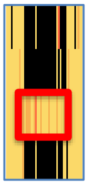


14. Fournier[4] identified a genomic island associated with resistance to antibiotics at the end of the AYE genome. Later on in this exercise, we will find the genes at each end of the island, but for now we will look for the resistance island at the end of the AYE genome. To do this, we'll need to scroll down the heatmap view by moving the slider at the bottom of the heatmap all the way to the right.

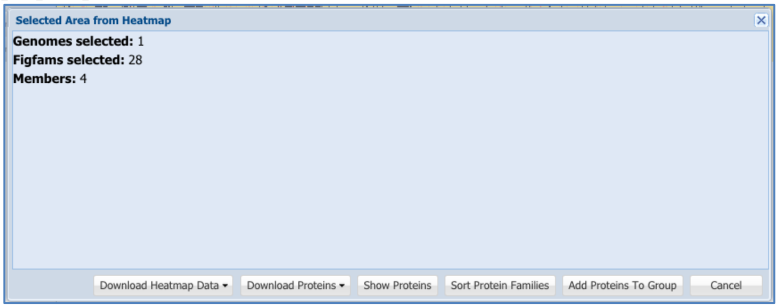
15. The island described by Fournier is found at the far right end. You can see that the other genomes do not have this island.



16. To see the genes that are in this area, you should use your mouse to draw a box around the area of the genome that is next to a black box.



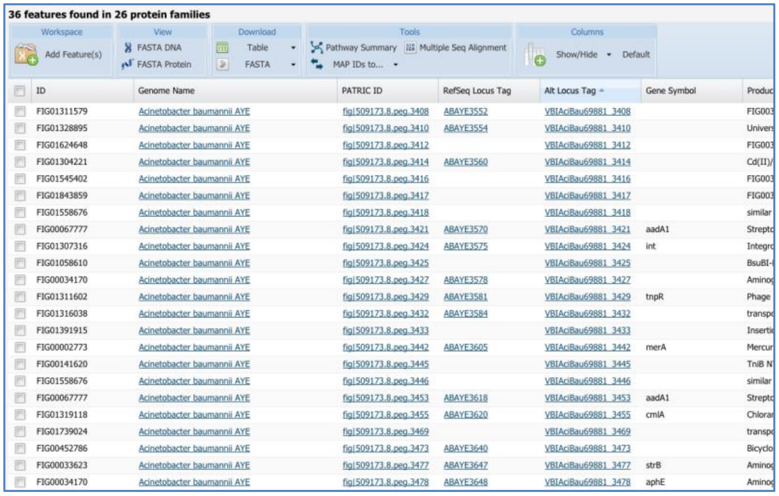
17. This generates a pop-up window that gives the user choices on what they want to do with the selected data. Click the Show Proteins button at the bottom of the pop-up window.



Selected Area from Heatmap

Genomes selected: 1
Figfams selected: 28
Members: 4

18. This will open a new window that shows the genes found in that section of the heatmap view that you selected.



36 features found in 26 protein families

☐	ID	Genome Name	PATRIC ID	RefSeq Locus Tag	Alt Locus Tag	Gene Symbol	Produc
☐	FIG01311579	Acinetobacter baumannii AYE	fig|509173.8.peg.3408	ABAYE3552	VBIAciBau69881_3408		FIG003
☐	FIG01328895	Acinetobacter baumannii AYE	fig|509173.8.peg.3410	ABAYE3554	VBIAciBau69881_3410		Univers
☐	FIG01624648	Acinetobacter baumannii AYE	fig|509173.8.peg.3412		VBIAciBau69881_3412		FIG003
☐	FIG01304221	Acinetobacter baumannii AYE	fig|509173.8.peg.3414	ABAYE3560	VBIAciBau69881_3414		Cd(II)/
☐	FIG01545402	Acinetobacter baumannii AYE	fig|509173.8.peg.3416		VBIAciBau69881_3416		FIG003
☐	FIG01843859	Acinetobacter baumannii AYE	fig|509173.8.peg.3417		VBIAciBau69881_3417		FIG003
☐	FIG01558676	Acinetobacter baumannii AYE	fig|509173.8.peg.3418		VBIAciBau69881_3418		similar
☐	FIG00067777	Acinetobacter baumannii AYE	fig|509173.8.peg.3421	ABAYE3570	VBIAciBau69881_3421	aadA1	Strepto
☐	FIG01307316	Acinetobacter baumannii AYE	fig|509173.8.peg.3424	ABAYE3575	VBIAciBau69881_3424	int	Integro
☐	FIG01058610	Acinetobacter baumannii AYE	fig|509173.8.peg.3425		VBIAciBau69881_3425		BsuBI-
☐	FIG00034170	Acinetobacter baumannii AYE	fig|509173.8.peg.3427	ABAYE3578	VBIAciBau69881_3427		Amino
☐	FIG01311602	Acinetobacter baumannii AYE	fig|509173.8.peg.3429	ABAYE3581	VBIAciBau69881_3429	tnpR	Phage
☐	FIG01316038	Acinetobacter baumannii AYE	fig|509173.8.peg.3432	ABAYE3584	VBIAciBau69881_3432		transp
☐	FIG01391915	Acinetobacter baumannii AYE	fig|509173.8.peg.3433		VBIAciBau69881_3433		Inserti
☐	FIG00002773	Acinetobacter baumannii AYE	fig|509173.8.peg.3442	ABAYE3605	VBIAciBau69881_3442	merA	Mercur
☐	FIG00141620	Acinetobacter baumannii AYE	fig|509173.8.peg.3445		VBIAciBau69881_3445		TniB N
☐	FIG01558676	Acinetobacter baumannii AYE	fig|509173.8.peg.3446		VBIAciBau69881_3446		similar
☐	FIG00067777	Acinetobacter baumannii AYE	fig|509173.8.peg.3453	ABAYE3618	VBIAciBau69881_3453	aadA1	Strepto
☐	FIG01319118	Acinetobacter baumannii AYE	fig|509173.8.peg.3455	ABAYE3620	VBIAciBau69881_3455	cmlA	Chlora
☐	FIG01739024	Acinetobacter baumannii AYE	fig|509173.8.peg.3469		VBIAciBau69881_3469		transp
☐	FIG00452786	Acinetobacter baumannii AYE	fig|509173.8.peg.3473	ABAYE3640	VBIAciBau69881_3473		Bicyclo
☐	FIG00033623	Acinetobacter baumannii AYE	fig|509173.8.peg.3477	ABAYE3647	VBIAciBau69881_3477	strB	Amino
☐	FIG00034170	Acinetobacter baumannii AYE	fig|509173.8.peg.3478	ABAYE3648	VBIAciBau69881_3478	aphE	Amino

19. To see the order the genes occur in, first resize the table by changing the number at the bottom of it to include all the genes and hit return.

Show 36 per page

20. A close examination of all the results shows that I have captured data genes that appear to be ordered sequentially (ABAYE3552 to ABAYE3667), and then two distally located genes (ABAYE3739 and ABAYE3853).

Assignment

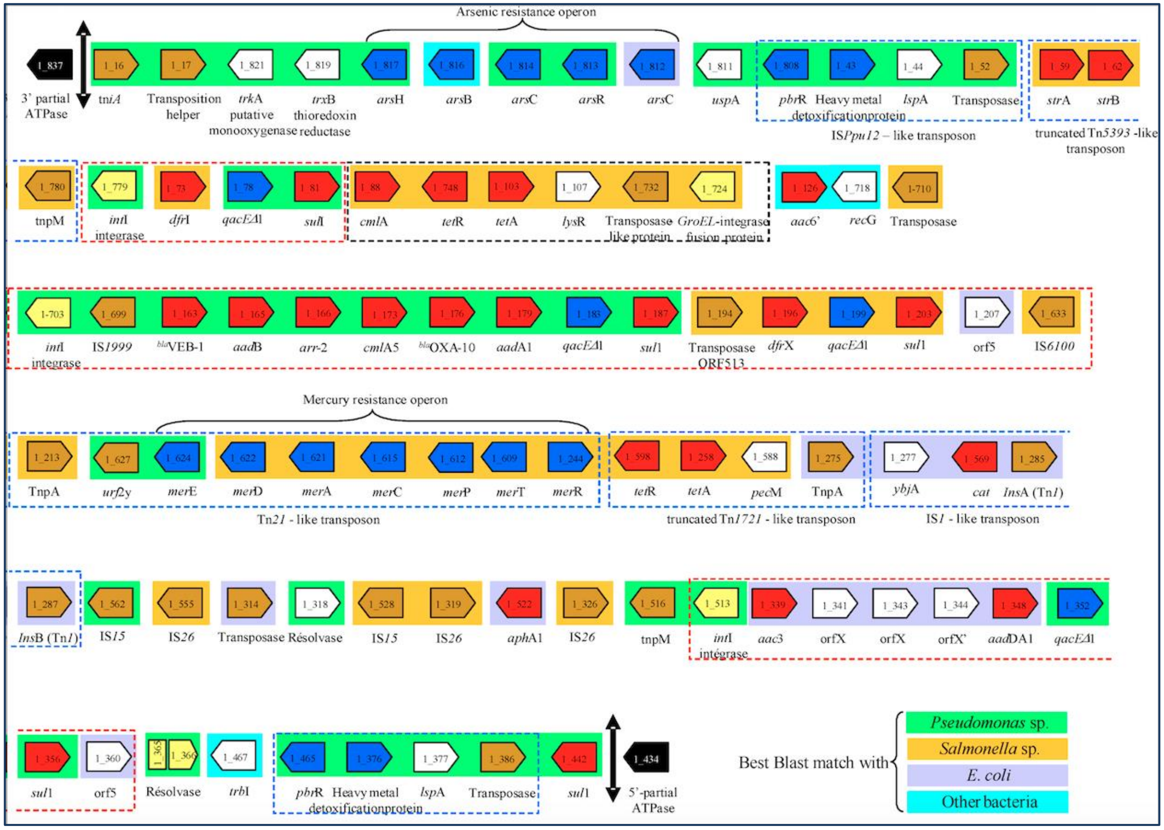
You have created other genome groups in Part I (Creating genome groups) of this exercise. Using the Protein Family Sorter tool as you have learned in this exercise, answer the following questions:

- Do you see any islands in the SDF genome that are not shared with AYE?
- How many of the genomes in each of the groups you created have the resistance island that is specific to the AYE genome?

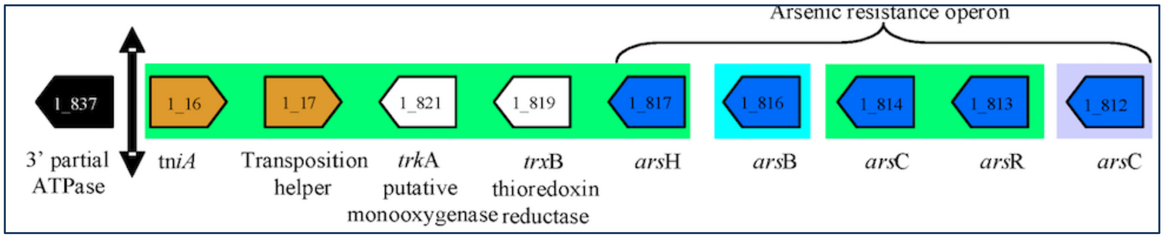
- How many of the genomes in each of the three groups you created share some of the islands that you can see that are specific to the SDF genome?

IV. Finding genes of interest from a published article

Scientists often have a difficult time taking published information and finding it in the public data repositories. The article published by Fournier and others[4] on the two *A. baumannii* genomes is a good example of this difficulty. In their article they show a detailed map of the genes available on an 86-kb resistance island that they identify in the AYE strain, providing the gene names and functional descriptions for some as well as some other information including best BLAST hits (see figure below). In this exercise, we will try to find some of those particular genes in PATRIC. At times this will be a bit frustrating, but it is supposed to demonstrate how individual researchers would need to do to find this. The end goal of this exercise is to find the genes at the beginning and end of the resistance island so that we can figure out the approximate 5' and 3' ends.



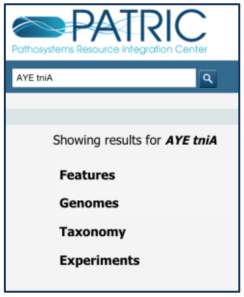
1. Fournier et al. show that the resistance island begins with a number of transposable elements and some other genes of interest, but does not show the exact chromosomal location. These genes include an arsenic resistance operon.



You may want to start by choosing the first gene that from the figure. Enter the genome strain and the gene name in the search box (AYE tniA)

AYE tniA

2. Unfortunately, this does not return a result.



AYE tniA

Showing results for ***AYE tniA***

Features

Genomes

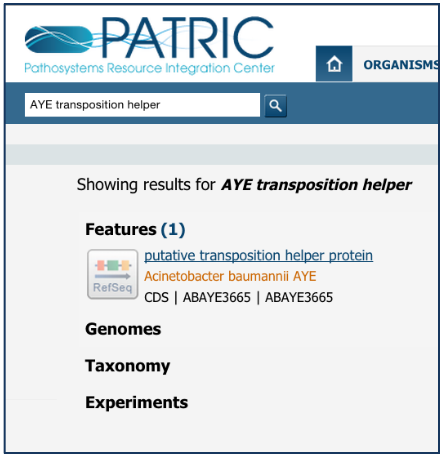
Taxonomy

Experiments

3. Take the next gene, which is called Transposition helper, and use that to search for a corresponding gene in the AYE genome

AYE transposition helper

4. This returns one gene.



AYE transposition helper

Showing results for ***AYE transposition helper***

Features (1)

putative transposition helper protein
Acinetobacter baumannii AYE
CDS | ABAYE3665 | ABAYE3665

Genomes

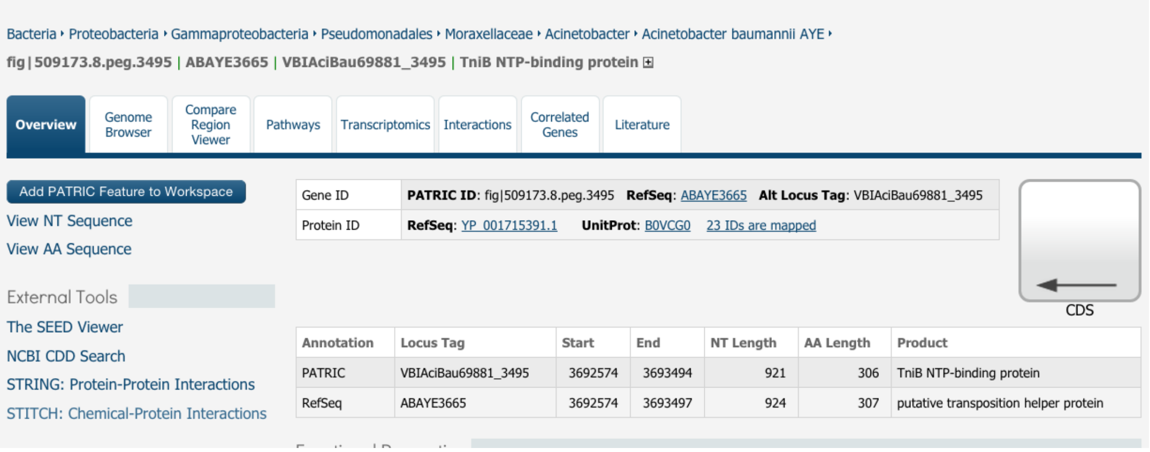
Taxonomy

Experiments

5. We need to make sure that this is the right gene. To do this, you will need to click on the blue text that gives the functional description of the gene.


putative transposition helper protein

6. This takes you to the landing page for that gene. You can see the PATRIC locus tag (fig|509173.8.peg.3495), the RefSeq locus tag (ABAYE3665) and location of the start site (3692574) and the end of the gene (3693497).


Bacteria › Proteobacteria › Gammaproteobacteria › Pseudomonadales › Moraxellaceae › Acinetobacter › Acinetobacter baumannii AYE ›

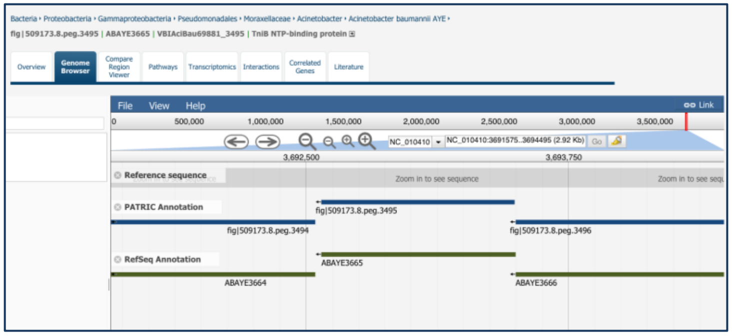
fig|509173.8.peg.3495 | ABAYE3665 | VBIAciBau69881_3495 | TniB NTP-binding protein ⊞

Gene ID	**PATRIC ID:** fig|509173.8.peg.3495 **RefSeq:** ABAYE3665 **Alt Locus Tag:** VBIAciBau69881_3495
Protein ID	**RefSeq:** YP_001715391.1 **UnitProt:** B0VCG0 23 IDs are mapped

Annotation	Locus Tag	Start	End	NT Length	AA Length	Product
PATRIC	VBIAciBau69881_3495	3692574	3693494	921	306	TniB NTP-binding protein
RefSeq	ABAYE3665	3692574	3693497	924	307	putative transposition helper protein

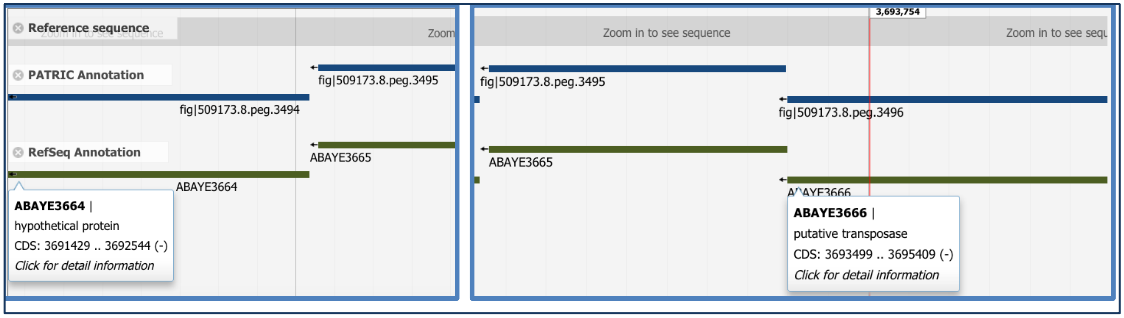
7. In order to see if we have the right gene, we will need to look at the genes that surround it to see if they match the genes described in the large figure at the top of page 12. To do this, you need to click on the second tab (Genome Browser) at the top of the page.

8. This will load the genome browser that shows two different annotations in the same view. The top (blue arrows) is the PATRIC annotation. The bottom (green arrows) is the RefSeq annotation.


Bacteria › Proteobacteria › Gammaproteobacteria › Pseudomonadales › Moraxellaceae › Acinetobacter › Acinetobacter baumannii AYE ›

fig|509173.8.peg.3495 | ABAYE3665 | VBIAciBau69881_3495 | TniB NTP-binding protein ⊞

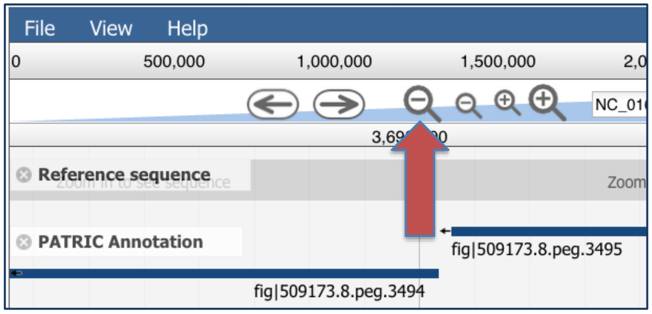
9. Mousing over the genes on either side will show their names. Although the transposase at the 3’ end makes sense, the hypothetical protein at the 3’ end still does not tell us that we are looking at the right gene.



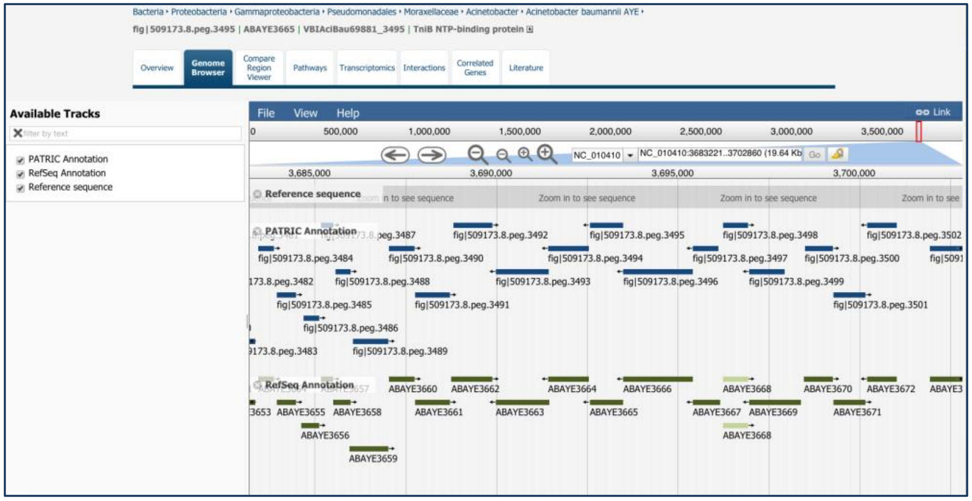
ABAYE3664 |
hypothetical protein
CDS: 3691429 .. 3692544 (-)
Click for detail information

ABAYE3666 |
putative transposase
CDS: 3693499 .. 3695409 (-)
Click for detail information

10. We need to expand the view of the browser. To do this, click on the magnifying glass with the large minus sign in it.

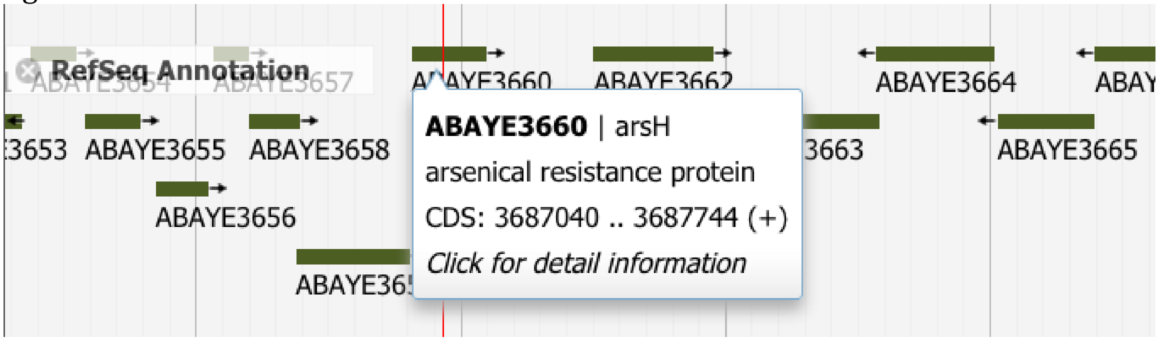


11. This greatly expands the number of genes you see.



12. Mousing over the genes shows the names. ABAYE3660 corresponds to the arsenic resistance protein (*arsH*) that is mentioned in the figure on page 12 of this workflow. We have identified that this corresponds to the same *arsH* gene that Fournier et al shows in the diagram, and now we know that one end of the resistance island is right around the gene identified by the locus tag fig|509173.8.peg.3495 (PATRIC) and ABAYE3665 (RefSeq). You’ll notice that the

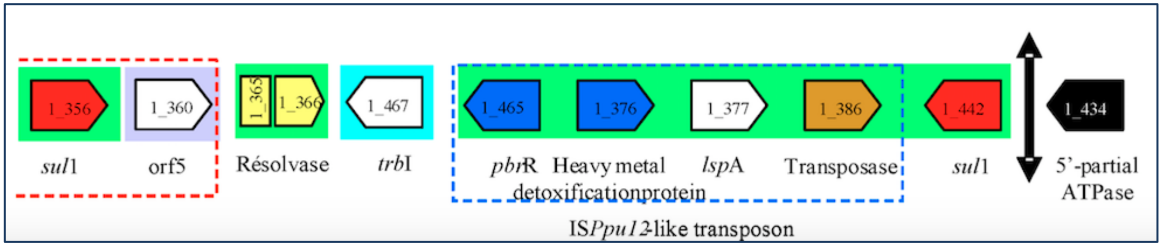
genome browser show the genes in the reverse orientation that you see in the figure.



ABAYE3660 | arsH
arsenical resistance protein
CDS: 3687040 .. 3687744 (+)
Click for detail information

Assignment

- Find the other end of the resistance island in the AYE strain based on the part of the diagram shown below (Hint! You can use the information we found in III.20 above. I also recommend using the work "detoxification" as part of your search).



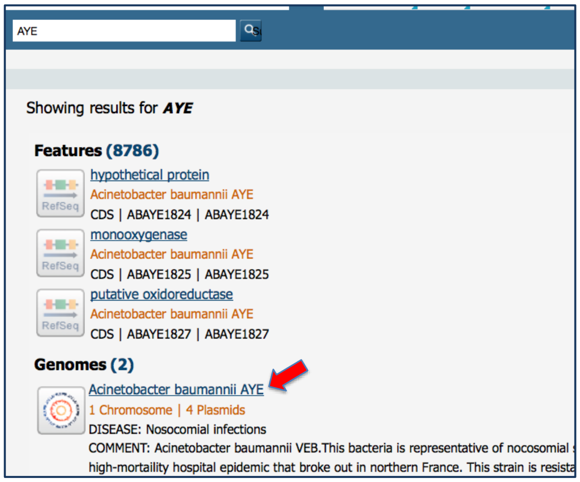
IV. Examining gene neighborhoods

The Fournier paper detailed a careful BLAST analysis that they performed to determine where the genes in the resistance islands came from. PATRIC provides a tool called the Compare Region View that can help to determine if a region has been laterally transferred. You can find any gene of interest using the global search, but I also want to introduce you to a powerful function that PATRIC has in allowing you to filter the feature table. Keep in mind that the global search is a more direct approach, but try to learn how to use the feature table to get specific information you are interested in.

1. In the global search box, enter the word AYE and hit return.

AYE

2. In the Search results page, click on the genome name Acinetobacter baumannii AYE



Showing results for ***AYE***

Features (8786)

hypothetical protein
Acinetobacter baumannii AYE
CDS | ABAYE1824 | ABAYE1824

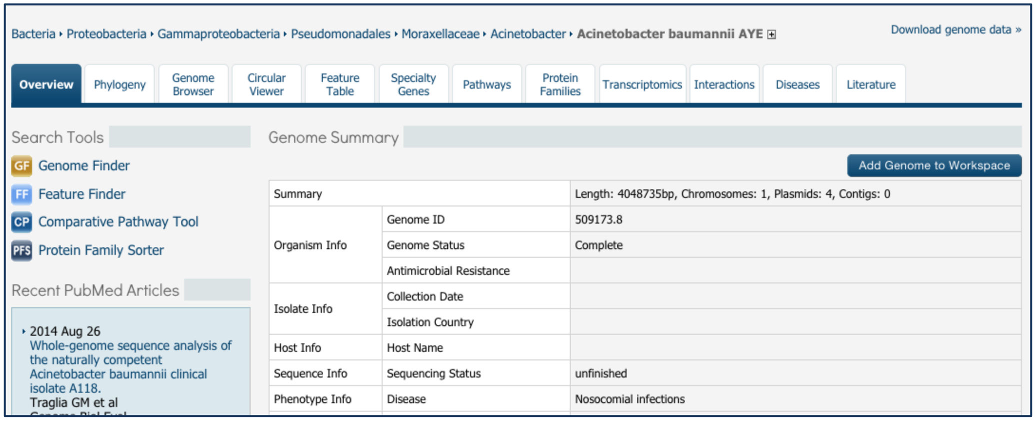
monooxygenase
Acinetobacter baumannii AYE
CDS | ABAYE1825 | ABAYE1825

putative oxidoreductase
Acinetobacter baumannii AYE
CDS | ABAYE1827 | ABAYE1827

Genomes (2)

Acinetobacter baumannii AYE
1 Chromosome | 4 Plasmids
DISEASE: Nosocomial infections
COMMENT: Acinetobacter baumannii VEB.This bacteria is representative of nocosomial
high-mortaility hospital epidemic that broke out in northern France. This strain is resista

3. This will take you to the landing page for the AYE genome.

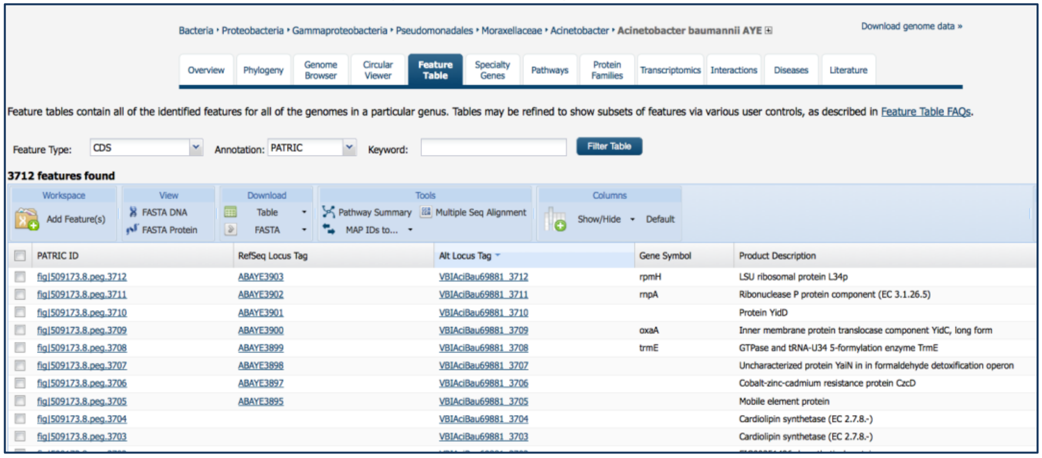


› 2014 Aug 26
Whole-genome sequence analysis of the naturally competent Acinetobacter baumannii clinical isolate A118.
Traglia GM et al

Summary		Length: 4048735bp, Chromosomes: 1, Plasmids: 4, Contigs: 0
Organism Info	Genome ID	509173.8
	Genome Status	Complete
	Antimicrobial Resistance	
Isolate Info	Collection Date	
	Isolation Country	
Host Info	Host Name	
Sequence Info	Sequencing Status	unfinished
Phenotype Info	Disease	Nosocomial infections

4. Click on the 5th tab over, the Features Tab.

5. This will show you all the genes in the genome.



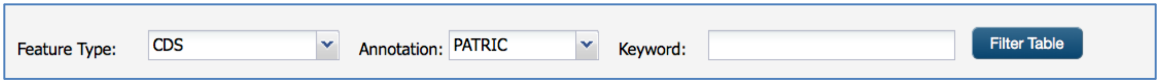
Feature tables contain all of the identified features for all of the genomes in a particular genus. Tables may be refined to show subsets of features via various user controls, as described in Feature Table FAQs.

Feature Type: CDS
Annotation: PATRIC
Keyword:

3712 features found

☐	PATRIC ID	RefSeq Locus Tag	Alt Locus Tag	Gene Symbol	Product Description
☐	fig|509173.8.peg.3712	ABAYE3903	VBIAciBau69881_3712	rpmH	LSU ribosomal protein L34p
☐	fig|509173.8.peg.3711	ABAYE3902	VBIAciBau69881_3711	rnpA	Ribonuclease P protein component (EC 3.1.26.5)
☐	fig|509173.8.peg.3710	ABAYE3901	VBIAciBau69881_3710		Protein YidD
☐	fig|509173.8.peg.3709	ABAYE3900	VBIAciBau69881_3709	oxaA	Inner membrane protein translocase component YidC, long form
☐	fig|509173.8.peg.3708	ABAYE3899	VBIAciBau69881_3708	trmE	GTPase and tRNA-U34 5-formylation enzyme TrmE
☐	fig|509173.8.peg.3707	ABAYE3898	VBIAciBau69881_3707		Uncharacterized protein YaiN in in formaldehyde detoxification operon
☐	fig|509173.8.peg.3706	ABAYE3897	VBIAciBau69881_3706		Cobalt-zinc-cadmium resistance protein CzcD
☐	fig|509173.8.peg.3705	ABAYE3895	VBIAciBau69881_3705		Mobile element protein
☐	fig|509173.8.peg.3704		VBIAciBau69881_3704		Cardiolipin synthetase (EC 2.7.8.-)
☐	fig|509173.8.peg.3703		VBIAciBau69881_3703		Cardiolipin synthetase (EC 2.7.8.-)

6. Look at the filter mechanism across the top of this table.

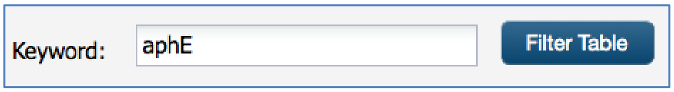


Feature Type: CDS

Annotation: PATRIC

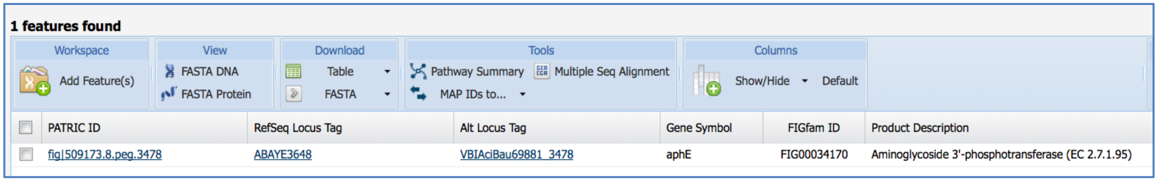
Keyword:

7. Enter your gene of interest into the keyword search (I used "aphE") and click on the Filter Table button



Keyword: aphE

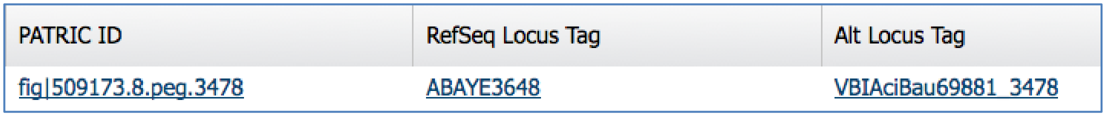
8. This will filter the table to show the locus tags and information associated with aphE for this genome.



1 features found

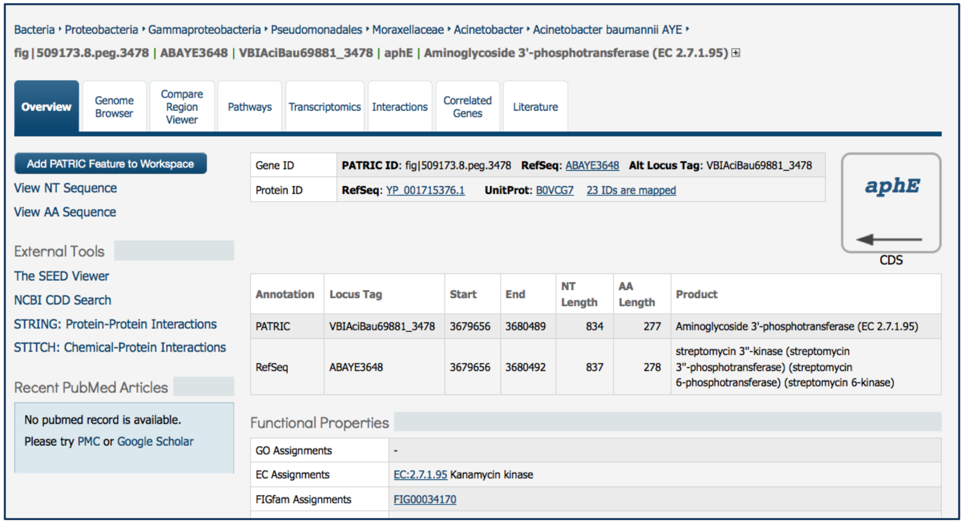
☐	PATRIC ID	RefSeq Locus Tag	Alt Locus Tag	Gene Symbol	FIGfam ID	Product Description
☐	fig|509173.8.peg.3478	ABAYE3648	VBIAciBau69881_3478	aphE	FIG00034170	Aminoglycoside 3'-phosphotransferase (EC 2.7.1.95)

9. Any of the three locus tags can be clicked to take you to the information on that gene. Click on any one of these (they are blue and underlined).



PATRIC ID	RefSeq Locus Tag	Alt Locus Tag
fig|509173.8.peg.3478	ABAYE3648	VBIAciBau69881_3478

10. This will open up the gene-landing page for the aphE gene.



Bacteria ‣ Proteobacteria ‣ Gammaproteobacteria ‣ Pseudomonadales ‣ Moraxellaceae ‣ Acinetobacter ‣ Acinetobacter baumannii AYE ‣

fig|509173.8.peg.3478 | ABAYE3648 | VBIAciBau69881_3478 | aphE | Aminoglycoside 3'-phosphotransferase (EC 2.7.1.95)

Gene ID	**PATRIC ID**: fig|509173.8.peg.3478 **RefSeq**: ABAYE3648 **Alt Locus Tag**: VBIAciBau69881_3478
Protein ID	**RefSeq**: YP_001715376.1 **UnitProt**: B0VCG7 23 IDs are mapped

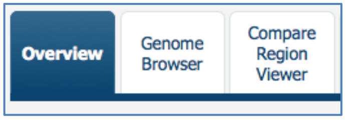
Annotation	Locus Tag	Start	End	NT Length	AA Length	Product
PATRIC	VBIAciBau69881_3478	3679656	3680489	834	277	Aminoglycoside 3'-phosphotransferase (EC 2.7.1.95)
RefSeq	ABAYE3648	3679656	3680492	837	278	streptomycin 3"-kinase (streptomycin 3"-phosphotransferase) (streptomycin 6-phosphotransferase) (streptomycin 6-kinase)

No pubmed record is available.
Please try PMC or Google Scholar

Functional Properties

GO Assignments	-
EC Assignments	EC:2.7.1.95 Kanamycin kinase
FIGfam Assignments	FIG00034170

11. To examine the gene neighborhood, click on the 3rd tab at the top of the page (Compare Region Viewer).



12. This will show you the gene neighborhood around your gene of interest, and also show you the genomes that have similar neighborhoods. Look at the screenshot below. The two top hits are for *Acinetobacter baumannii* genomes, but the next three are for Salmonella genomes. As there are currently 1025 *A. baumanni*i genomes in PATRIC, you would expect that if this were common to this species, the image would contain only genomes from this species. AYE3648 corresponds to the gene identified as *strA* in the Fournier paper. That gene is one that they identified as having the best BLAST match with *Salmonella sp.*

Assignment

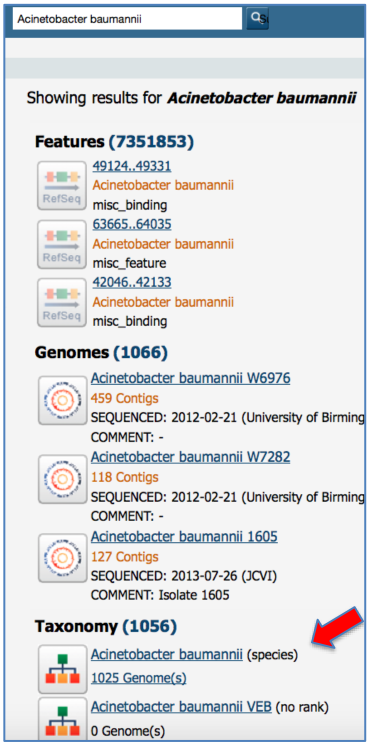
- Open up the feature tables for both the AYE and SDF genomes.
- Identify the genes that correspond to the two islands described by Fournier et al. (see the figures above in the description).
- Using Command Click, go to the gene-landing page for each of the genes and look at the Compare Region View. Which genes appear to match the best BLAST hits that Fournier et al described?

V. Discovering antibiotic resistance genes from other genomes using homology

1. Enter the name Acinetobacter baumannii into the global search box and hit return.

Acinetobacter baumannii

2. This will take you to the search results page. Scroll down until you see the Taxonomy section. Click on Acinetobacter baumannii (species).


Acinetobacter baumannii

Showing results for ***Acinetobacter baumannii***

Features (7351853)

49124..49331
Acinetobacter baumannii
misc_binding

63665..64035
Acinetobacter baumannii
misc_feature

42046..42133
Acinetobacter baumannii
misc_binding

Genomes (1066)

Acinetobacter baumannii W6976
459 Contigs
SEQUENCED: 2012-02-21 (University of Birming
COMMENT: -

Acinetobacter baumannii W7282
118 Contigs
SEQUENCED: 2012-02-21 (University of Birming
COMMENT: -

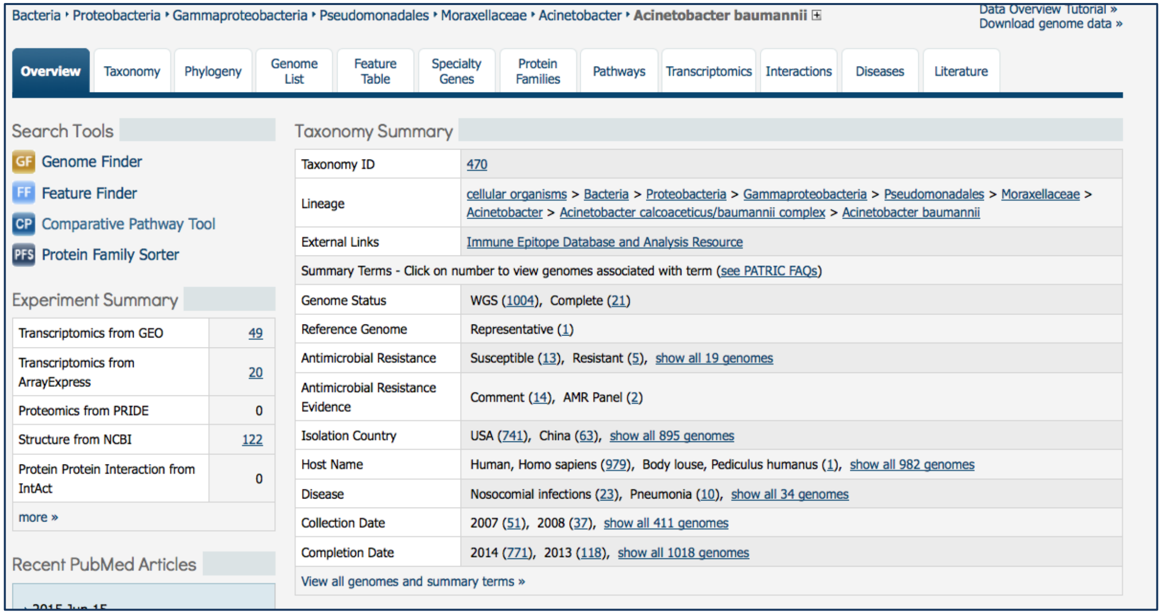
Acinetobacter baumannii 1605
127 Contigs
SEQUENCED: 2013-07-26 (JCVI)
COMMENT: Isolate 1605

Taxonomy (1056)

Acinetobacter baumannii (species)
1025 Genome(s)

Acinetobacter baumannii VEB (no rank)
0 Genome(s)

3. This will take you to the landing page for the *A. baumannii* species.



Bacteria ‣ Proteobacteria ‣ Gammaproteobacteria ‣ Pseudomonadales ‣ Moraxellaceae ‣ Acinetobacter ‣ **Acinetobacter baumannii**

Data Overview Tutorial »
Download genome data »

Search Tools

Genome Finder
Feature Finder
Comparative Pathway Tool
Protein Family Sorter

Experiment Summary

Transcriptomics from GEO	49
Transcriptomics from ArrayExpress	20
Proteomics from PRIDE	0
Structure from NCBI	122
Protein Protein Interaction from IntAct	0

more »

Recent PubMed Articles

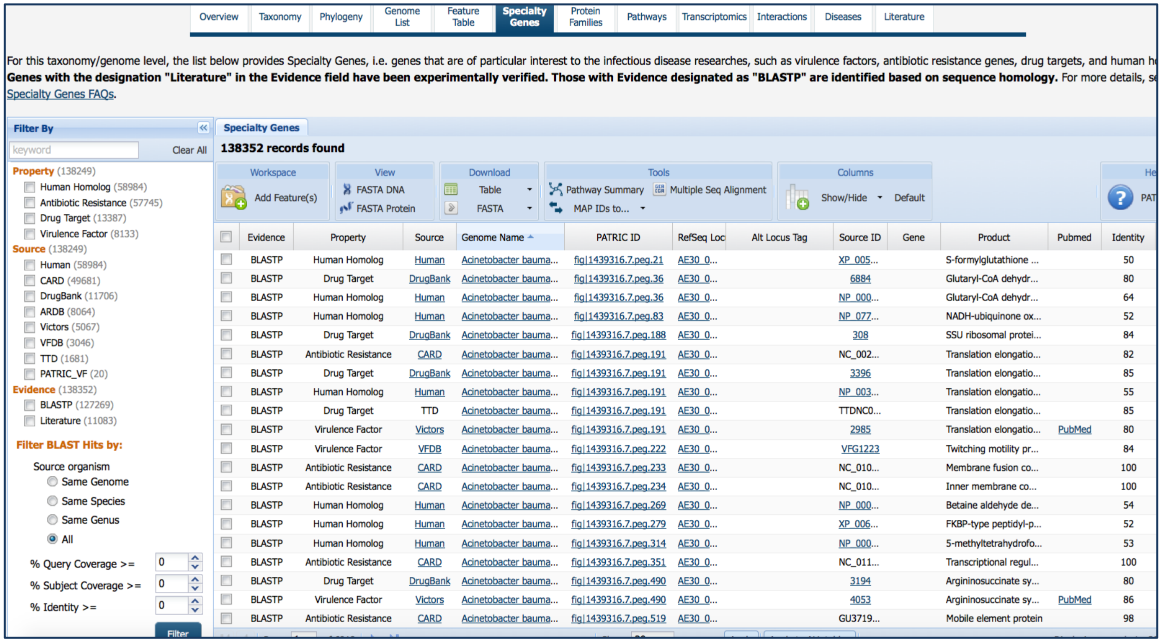
Taxonomy Summary

Taxonomy ID	470
Lineage	cellular organisms > Bacteria > Proteobacteria > Gammaproteobacteria > Pseudomonadales > Moraxellaceae > Acinetobacter > Acinetobacter calcoaceticus/baumannii complex > Acinetobacter baumannii
External Links	Immune Epitope Database and Analysis Resource
Summary Terms - Click on number to view genomes associated with term (see PATRIC FAQs)	
Genome Status	WGS (1004), Complete (21)
Reference Genome	Representative (1)
Antimicrobial Resistance	Susceptible (13), Resistant (5), show all 19 genomes
Antimicrobial Resistance Evidence	Comment (14), AMR Panel (2)
Isolation Country	USA (741), China (63), show all 895 genomes
Host Name	Human, Homo sapiens (979), Body louse, Pediculus humanus (1), show all 982 genomes
Disease	Nosocomial infections (23), Pneumonia (10), show all 34 genomes
Collection Date	2007 (51), 2008 (37), show all 411 genomes
Completion Date	2014 (771), 2013 (118), show all 1018 genomes

View all genomes and summary terms »

4. Click on the 6th tab at the top of the page, Specialty Genes.

5. This will take you to the Specialty Gene landing page for that species. There is a filter on the left-hand side, and a table showing the results on the right.



For this taxonomy/genome level, the list below provides Specialty Genes, i.e. genes that are of particular interest to the infectious disease researches, such as virulence factors, antibiotic resistance genes, drug targets, and human h
Genes with the designation "Literature" in the Evidence field have been experimentally verified. Those with Evidence designated as "BLASTP" are identified based on sequence homology. For more details, s
Specialty Genes FAQs.

Filter By

keyword Clear All

Property (138249)
- ☐ Human Homolog (58984)
- ☐ Antibiotic Resistance (57745)
- ☐ Drug Target (13387)
- ☐ Virulence Factor (8133)

Source (138249)
- ☐ Human (58984)
- ☐ CARD (49681)
- ☐ DrugBank (11706)
- ☐ ARDB (8064)
- ☐ Victors (5067)
- ☐ VFDB (3046)
- ☐ TTD (1681)
- ☐ PATRIC_VF (20)

Evidence (138352)
- ☐ BLASTP (127269)
- ☐ Literature (11083)

Filter BLAST Hits by:

Source organism
- ○ Same Genome
- ○ Same Species
- ○ Same Genus
- ● All

% Query Coverage >= 0
% Subject Coverage >= 0
% Identity >= 0

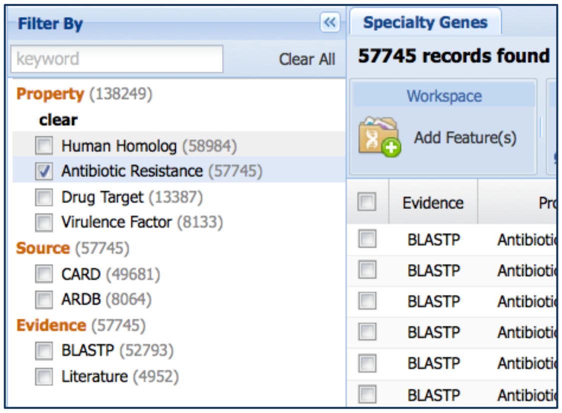
Filter

Specialty Genes

138352 records found

☐	Evidence	Property	Source	Genome Name	PATRIC ID	RefSeq Loc	Alt Locus Tag	Source ID	Gene	Product	Pubmed	Identity
☐	BLASTP	Human Homolog	Human	Acinetobacter bauma...	fig|1439316.7.peg.21	AE30_0...		XP_005...		S-formylglutathione ...		50
☐	BLASTP	Drug Target	DrugBank	Acinetobacter bauma...	fig|1439316.7.peg.36	AE30_0...		6884		Glutaryl-CoA dehydr...		80
☐	BLASTP	Human Homolog	Human	Acinetobacter bauma...	fig|1439316.7.peg.36	AE30_0...		NP_000...		Glutaryl-CoA dehydr...		64
☐	BLASTP	Human Homolog	Human	Acinetobacter bauma...	fig|1439316.7.peg.83	AE30_0...		NP_077...		NADH-ubiquinone ox...		52
☐	BLASTP	Drug Target	DrugBank	Acinetobacter bauma...	fig|1439316.7.peg.188	AE30_0...		308		SSU ribosomal protei...		84
☐	BLASTP	Antibiotic Resistance	CARD	Acinetobacter bauma...	fig|1439316.7.peg.191	AE30_0...		NC_002...		Translation elongatio...		82
☐	BLASTP	Drug Target	DrugBank	Acinetobacter bauma...	fig|1439316.7.peg.191	AE30_0...		3396		Translation elongatio...		85
☐	BLASTP	Human Homolog	Human	Acinetobacter bauma...	fig|1439316.7.peg.191	AE30_0...		NP_003...		Translation elongatio...		55
☐	BLASTP	Drug Target	TTD	Acinetobacter bauma...	fig|1439316.7.peg.191	AE30_0...		TTDNC0...		Translation elongatio...		85
☐	BLASTP	Virulence Factor	Victors	Acinetobacter bauma...	fig|1439316.7.peg.191	AE30_0...		2985		Translation elongatio...	PubMed	80
☐	BLASTP	Virulence Factor	VFDB	Acinetobacter bauma...	fig|1439316.7.peg.222	AE30_0...		VFG1223		Twitching motility pr...		84
☐	BLASTP	Antibiotic Resistance	CARD	Acinetobacter bauma...	fig|1439316.7.peg.233	AE30_0...		NC_010...		Membrane fusion co...		100
☐	BLASTP	Antibiotic Resistance	CARD	Acinetobacter bauma...	fig|1439316.7.peg.234	AE30_0...		NC_010...		Inner membrane co...		100
☐	BLASTP	Human Homolog	Human	Acinetobacter bauma...	fig|1439316.7.peg.269	AE30_0...		NP_000...		Betaine aldehyde de...		54
☐	BLASTP	Human Homolog	Human	Acinetobacter bauma...	fig|1439316.7.peg.279	AE30_0...		XP_006...		FKBP-type peptidyl-p...		52
☐	BLASTP	Human Homolog	Human	Acinetobacter bauma...	fig|1439316.7.peg.314	AE30_0...		NP_000...		5-methyltetrahydrofo...		53
☐	BLASTP	Antibiotic Resistance	CARD	Acinetobacter bauma...	fig|1439316.7.peg.351	AE30_0...		NC_011...		Transcriptional regul...		100
☐	BLASTP	Drug Target	DrugBank	Acinetobacter bauma...	fig|1439316.7.peg.490	AE30_0...		3194		Argininosuccinate sy...		80
☐	BLASTP	Virulence Factor	Victors	Acinetobacter bauma...	fig|1439316.7.peg.490	AE30_0...		4053		Argininosuccinate sy...	PubMed	86
☐	BLASTP	Antibiotic Resistance	CARD	Acinetobacter bauma...	fig|1439316.7.peg.519	AE30_0...		GU3719...		Mobile element protein		98

6. To find the genes that have homology to antibiotic resistance genes that have been identified, click on the text box in the filter that is in front of "Antibiotic Resistance."



Filter By

keyword Clear All

Property (138249)

clear
- ☐ Human Homolog (58984)
- ☑ Antibiotic Resistance (57745)
- ☐ Drug Target (13387)
- ☐ Virulence Factor (8133)

Source (57745)
- ☐ CARD (49681)
- ☐ ARDB (8064)

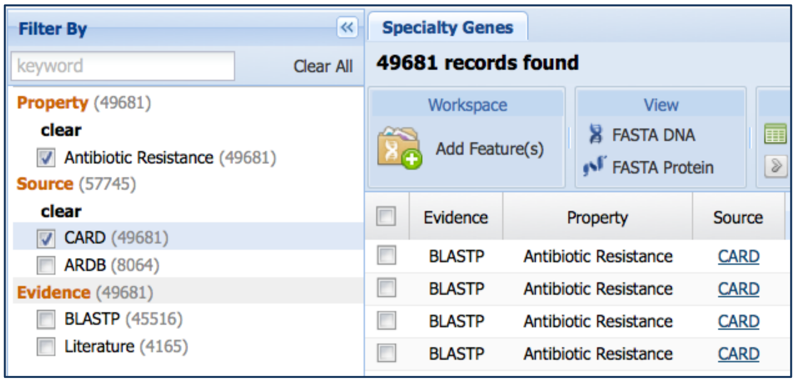
Evidence (57745)
- ☐ BLASTP (52793)
- ☐ Literature (4952)

Specialty Genes

57745 records found

☐	Evidence	Pr
☐	BLASTP	Antibioti
☐	BLASTP	Antibioti
☐	BLASTP	Antibioti
☐	BLASTP	Antibioti
☐	BLASTP	Antibioti
☐	BLASTP	Antibioti

7. PATRIC has several sources of data for specialty genes. For antibiotic resistance genes we include genes from the Comprehensive Antibiotic Resistance Database (CARD)[5] and from the Antibiotic Resistance Database (ARDB)[6]. Click on the text box in the filter that is in front of word "CARD."



Filter By

keyword Clear All

Property (49681)

clear

☑ Antibiotic Resistance (49681)

Source (57745)

clear

☑ CARD (49681)

☐ ARDB (8064)

Evidence (49681)

☐ BLASTP (45516)

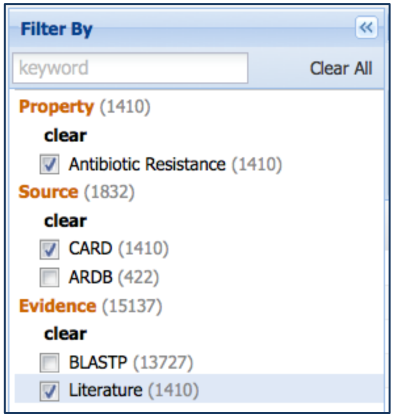
☐ Literature (4165)

Specialty Genes

49681 records found

☐	Evidence	Property	Source
☐	BLASTP	Antibiotic Resistance	CARD
☐	BLASTP	Antibiotic Resistance	CARD
☐	BLASTP	Antibiotic Resistance	CARD
☐	BLASTP	Antibiotic Resistance	CARD

8. You can also filter on genes that have experimental evidence that has been published, as opposed to BLAST-only homology. Click on the text box in front of the word "Literature" to see genes that have experimental evidence.



Filter By

keyword Clear All

Property (1410)

clear

☑ Antibiotic Resistance (1410)

Source (1832)

clear

☑ CARD (1410)

☐ ARDB (422)

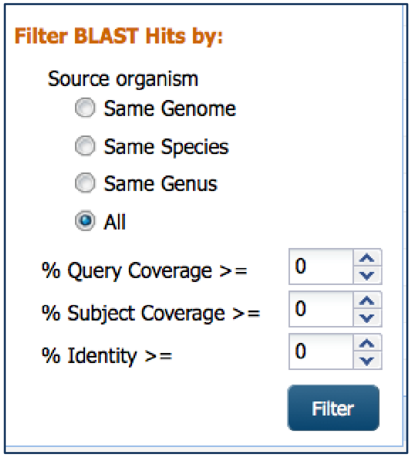
Evidence (15137)

clear

☐ BLASTP (13727)

☑ Literature (1410)

8. You can also filter genes by the BLAST scores. Scroll down to the bottom of the filter box where you will see additional filters



Filter BLAST Hits by:

Source organism

○ Same Genome

○ Same Species

○ Same Genus

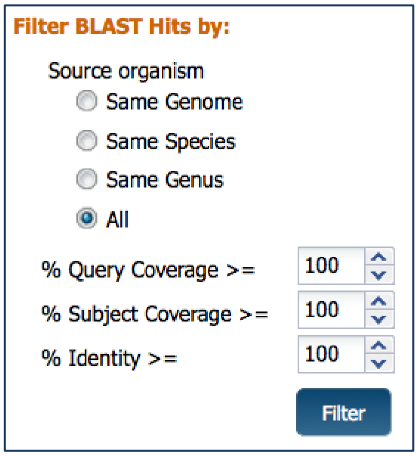
● All

% Query Coverage >= 0

% Subject Coverage >= 0

% Identity >= 0

9. Using the arrows behind the numbers, change the values for % Query, % Subject and % Identity to 100%.



Filter BLAST Hits by:

Source organism

○ Same Genome

○ Same Species

○ Same Genus

● All

% Query Coverage >= 100

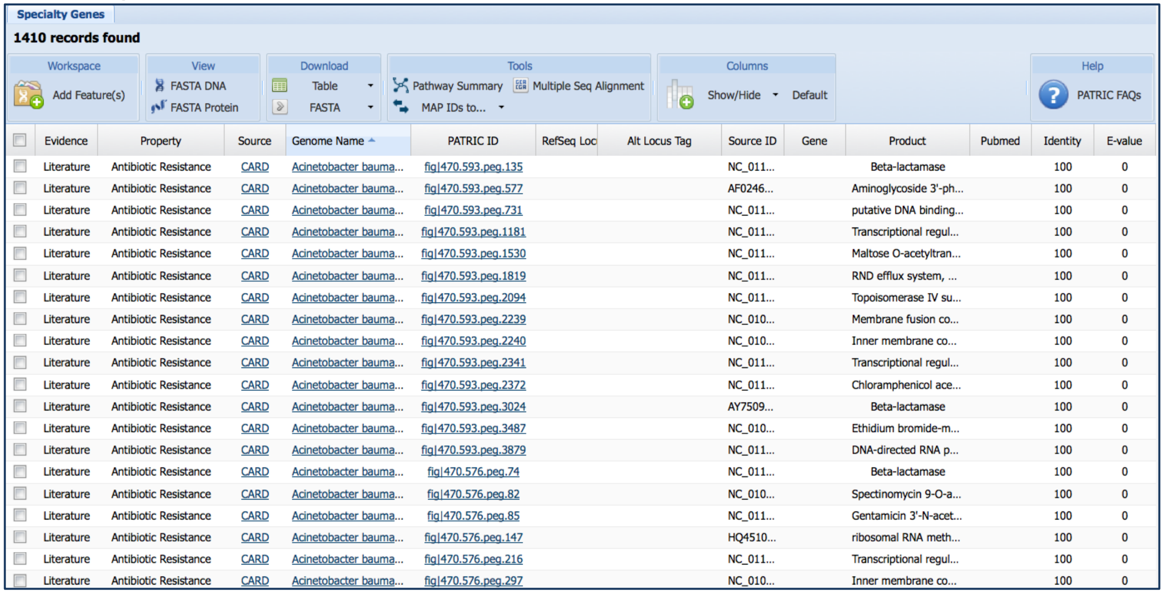
% Subject Coverage >= 100

% Identity >= 100

10. Each of these filters will be reflected in the changing number at the top of the table on the right.

1410 records found

11. The genes are reflected in the table.

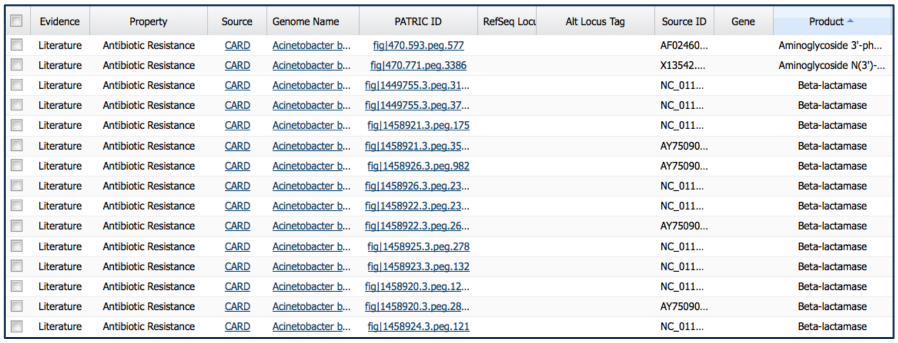


1410 records found

☐	Evidence	Property	Source	Genome Name	PATRIC ID	RefSeq Loc	Alt Locus Tag	Source ID	Gene	Product	Pubmed	Identity	E-value
☐	Literature	Antibiotic Resistance	CARD	Acinetobacter bauma...	fig|470.593.peg.135			NC_011...		Beta-lactamase		100	0
☐	Literature	Antibiotic Resistance	CARD	Acinetobacter bauma...	fig|470.593.peg.577			AF0246...		Aminoglycoside 3'-ph...		100	0
☐	Literature	Antibiotic Resistance	CARD	Acinetobacter bauma...	fig|470.593.peg.731			NC_011...		putative DNA binding...		100	0
☐	Literature	Antibiotic Resistance	CARD	Acinetobacter bauma...	fig|470.593.peg.1181			NC_011...		Transcriptional regul...		100	0
☐	Literature	Antibiotic Resistance	CARD	Acinetobacter bauma...	fig|470.593.peg.1530			NC_011...		Maltose O-acetyltran...		100	0
☐	Literature	Antibiotic Resistance	CARD	Acinetobacter bauma...	fig|470.593.peg.1819			NC_011...		RND efflux system, ...		100	0
☐	Literature	Antibiotic Resistance	CARD	Acinetobacter bauma...	fig|470.593.peg.2094			NC_011...		Topoisomerase IV su...		100	0
☐	Literature	Antibiotic Resistance	CARD	Acinetobacter bauma...	fig|470.593.peg.2239			NC_010...		Membrane fusion co...		100	0
☐	Literature	Antibiotic Resistance	CARD	Acinetobacter bauma...	fig|470.593.peg.2240			NC_010...		Inner membrane co...		100	0
☐	Literature	Antibiotic Resistance	CARD	Acinetobacter bauma...	fig|470.593.peg.2341			NC_011...		Transcriptional regul...		100	0
☐	Literature	Antibiotic Resistance	CARD	Acinetobacter bauma...	fig|470.593.peg.2372			NC_011...		Chloramphenicol ace...		100	0
☐	Literature	Antibiotic Resistance	CARD	Acinetobacter bauma...	fig|470.593.peg.3024			AY7509...		Beta-lactamase		100	0
☐	Literature	Antibiotic Resistance	CARD	Acinetobacter bauma...	fig|470.593.peg.3487			NC_010...		Ethidium bromide-m...		100	0
☐	Literature	Antibiotic Resistance	CARD	Acinetobacter bauma...	fig|470.593.peg.3879			NC_011...		DNA-directed RNA p...		100	0
☐	Literature	Antibiotic Resistance	CARD	Acinetobacter bauma...	fig|470.576.peg.74			NC_011...		Beta-lactamase		100	0
☐	Literature	Antibiotic Resistance	CARD	Acinetobacter bauma...	fig|470.576.peg.82			NC_010...		Spectinomycin 9-O-a...		100	0
☐	Literature	Antibiotic Resistance	CARD	Acinetobacter bauma...	fig|470.576.peg.85			NC_011...		Gentamicin 3'-N-acet...		100	0
☐	Literature	Antibiotic Resistance	CARD	Acinetobacter bauma...	fig|470.576.peg.147			HQ4510...		ribosomal RNA meth...		100	0
☐	Literature	Antibiotic Resistance	CARD	Acinetobacter bauma...	fig|470.576.peg.216			NC_011...		Transcriptional regul...		100	0
☐	Literature	Antibiotic Resistance	CARD	Acinetobacter bauma...	fig|470.576.peg.297			NC_010...		Inner membrane co...		100	0

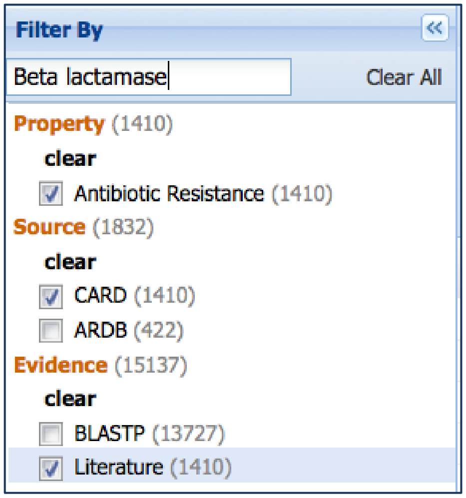
12. To sort the genes by name, click once on the Product column head.

13. This will sort the gene alphabetically by their product description.



☐	Evidence	Property	Source	Genome Name	PATRIC ID	RefSeq Locu	Alt Locus Tag	Source ID	Gene	Product ▲
☐	Literature	Antibiotic Resistance	CARD	Acinetobacter b...	fig|470.593.peg.577			AF02460...		Aminoglycoside 3'-ph...
☐	Literature	Antibiotic Resistance	CARD	Acinetobacter b...	fig|470.771.peg.3386			X13542....		Aminoglycoside N(3')-...
☐	Literature	Antibiotic Resistance	CARD	Acinetobacter b...	fig|1449755.3.peg.31...			NC_011...		Beta-lactamase
☐	Literature	Antibiotic Resistance	CARD	Acinetobacter b...	fig|1449755.3.peg.37...			NC_011...		Beta-lactamase
☐	Literature	Antibiotic Resistance	CARD	Acinetobacter b...	fig|1458921.3.peg.175			NC_011...		Beta-lactamase
☐	Literature	Antibiotic Resistance	CARD	Acinetobacter b...	fig|1458921.3.peg.35...			AY75090...		Beta-lactamase
☐	Literature	Antibiotic Resistance	CARD	Acinetobacter b...	fig|1458926.3.peg.982			AY75090...		Beta-lactamase
☐	Literature	Antibiotic Resistance	CARD	Acinetobacter b...	fig|1458926.3.peg.23...			NC_011...		Beta-lactamase
☐	Literature	Antibiotic Resistance	CARD	Acinetobacter b...	fig|1458922.3.peg.23...			NC_011...		Beta-lactamase
☐	Literature	Antibiotic Resistance	CARD	Acinetobacter b...	fig|1458922.3.peg.26...			AY75090...		Beta-lactamase
☐	Literature	Antibiotic Resistance	CARD	Acinetobacter b...	fig|1458925.3.peg.278			NC_011...		Beta-lactamase
☐	Literature	Antibiotic Resistance	CARD	Acinetobacter b...	fig|1458923.3.peg.132			NC_011...		Beta-lactamase
☐	Literature	Antibiotic Resistance	CARD	Acinetobacter b...	fig|1458920.3.peg.12...			NC_011...		Beta-lactamase
☐	Literature	Antibiotic Resistance	CARD	Acinetobacter b...	fig|1458920.3.peg.28...			AY75090...		Beta-lactamase
☐	Literature	Antibiotic Resistance	CARD	Acinetobacter b...	fig|1458924.3.peg.121			NC_011...		Beta-lactamase

14. You can use the filter on the left to sort for specific names. In the text box at the top of the filter, enter the words “Beta lactamase” and hit return.



Filter By

Beta lactamase

Property (1410)

☑ Antibiotic Resistance (1410)

Source (1832)

☑ CARD (1410)

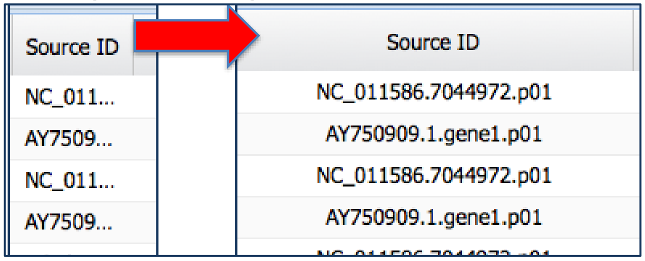
☐ ARDB (422)

Evidence (15137)

☐ BLASTP (13727)

☑ Literature (1410)

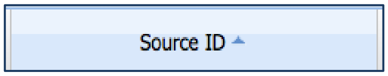
15. The experimental evidence that validates Beta lactamase as being important in antibiotic resistance could come from experiments that researchers have done on different genomes, which would mean that the source of the experimental data could come from different genes. To see the source of the evidence you will need to expand the Source column head by grabbing the right side of the header and then moving it to the right.



Source ID
NC_011...
AY7509...
NC_011...
AY7509...

Source ID
NC_011586.7044972.p01
AY750909.1.gene1.p01
NC_011586.7044972.p01
AY750909.1.gene1.p01

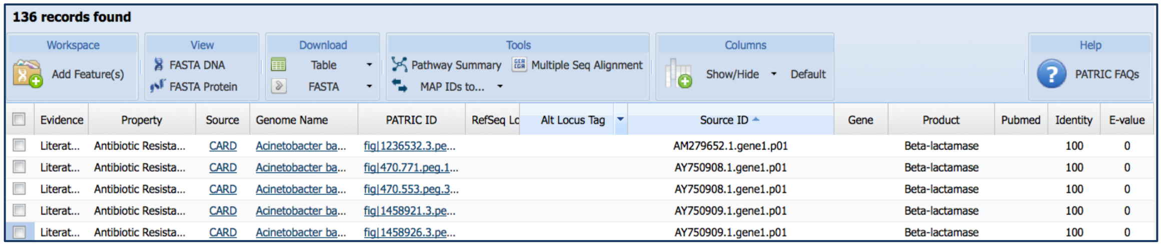
16. Click on the Source ID column head to sort the results.



17. Resize the page to see all the genes with the Beta lactamase description. Enter 150 in the text box at the bottom of the table and hit return.

Show 150 per page

16. You can see that there are several sources of the experimental evidence that define Beta lactamase as being important in antibiotic resistance.



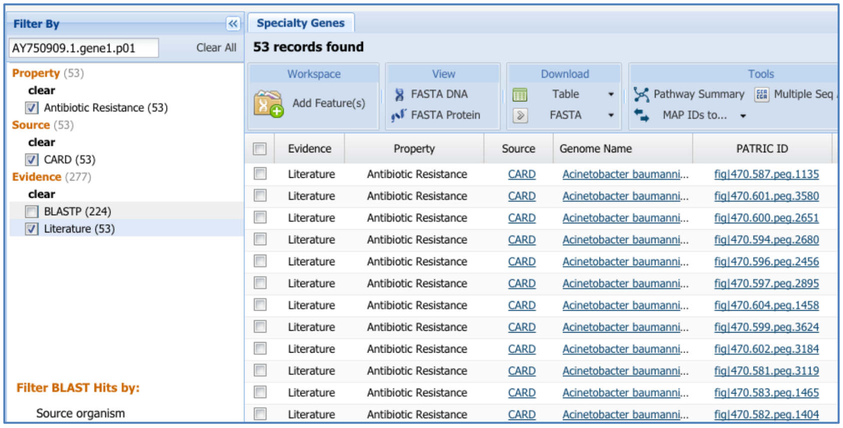
136 records found

☐	Evidence	Property	Source	Genome Name	PATRIC ID	RefSeq Lc	Alt Locus Tag	Source ID	Gene	Product	Pubmed	Identity	E-value
☐	Literat...	Antibiotic Resista...	CARD	Acinetobacter ba...	fig|1236532.3.pe...			AM279652.1.gene1.p01		Beta-lactamase		100	0
☐	Literat...	Antibiotic Resista...	CARD	Acinetobacter ba...	fig|470.771.peg.1...			AY750908.1.gene1.p01		Beta-lactamase		100	0
☐	Literat...	Antibiotic Resista...	CARD	Acinetobacter ba...	fig|470.553.peg.3...			AY750908.1.gene1.p01		Beta-lactamase		100	0
☐	Literat...	Antibiotic Resista...	CARD	Acinetobacter ba...	fig|1458921.3.pe...			AY750909.1.gene1.p01		Beta-lactamase		100	0
☐	Literat...	Antibiotic Resista...	CARD	Acinetobacter ba...	fig|1458926.3.pe...			AY750909.1.gene1.p01		Beta-lactamase		100	0

17. Many of these genes have "AY750909.1.gene1.p01" as the source. In the text box, enter "AY750909.1.gene1.p01" and hit return

AY750909.1.gene1.p01

18. This will show the genes that had AY750909.1.gene1.p01 as the gene that had the original evidence linking it to antibiotic resistance.



AY750909.1.gene1.p01

Property (53)
clear
☑ Antibiotic Resistance (53)
Source (53)
clear
☑ CARD (53)
Evidence (277)
clear
☐ BLASTP (224)
☑ Literature (53)

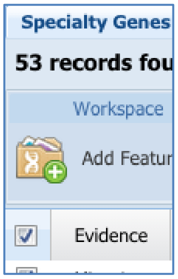
53 records found

☐	Evidence	Property	Source	Genome Name	PATRIC ID
☐	Literature	Antibiotic Resistance	CARD	Acinetobacter baumanni...	fig|470.587.peg.1135
☐	Literature	Antibiotic Resistance	CARD	Acinetobacter baumanni...	fig|470.601.peg.3580
☐	Literature	Antibiotic Resistance	CARD	Acinetobacter baumanni...	fig|470.600.peg.2651
☐	Literature	Antibiotic Resistance	CARD	Acinetobacter baumanni...	fig|470.594.peg.2680
☐	Literature	Antibiotic Resistance	CARD	Acinetobacter baumanni...	fig|470.596.peg.2456
☐	Literature	Antibiotic Resistance	CARD	Acinetobacter baumanni...	fig|470.597.peg.2895
☐	Literature	Antibiotic Resistance	CARD	Acinetobacter baumanni...	fig|470.604.peg.1458
☐	Literature	Antibiotic Resistance	CARD	Acinetobacter baumanni...	fig|470.599.peg.3624
☐	Literature	Antibiotic Resistance	CARD	Acinetobacter baumanni...	fig|470.602.peg.3184
☐	Literature	Antibiotic Resistance	CARD	Acinetobacter baumanni...	fig|470.581.peg.3119
☐	Literature	Antibiotic Resistance	CARD	Acinetobacter baumanni...	fig|470.583.peg.1465
☐	Literature	Antibiotic Resistance	CARD	Acinetobacter baumanni...	fig|470.582.peg.1404

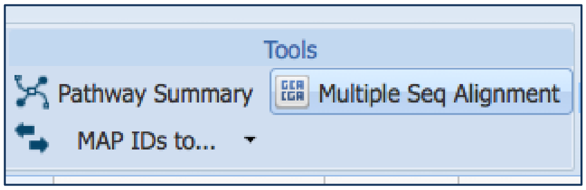
19. Resize the table to see all the genes

Show 53 per page

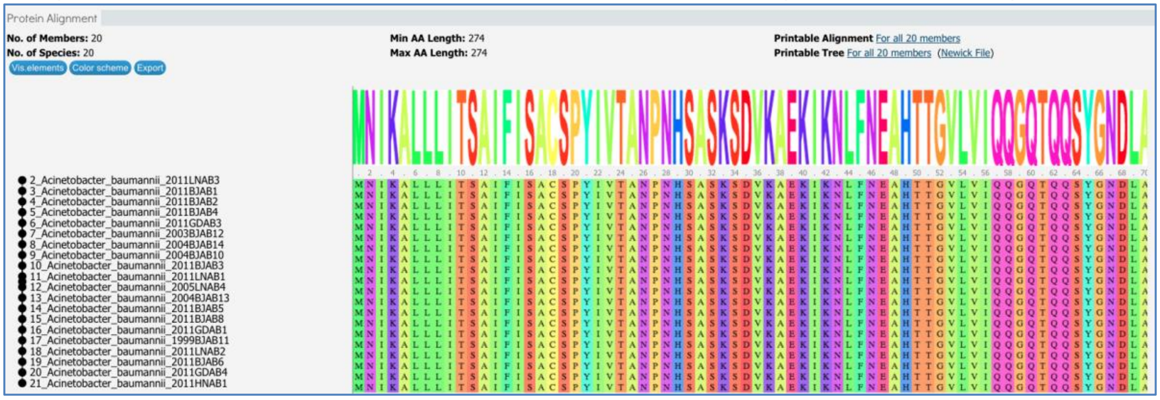
20. Let's look at a multiple sequence alignment for these genes. To do this you must first select all of them. Click in the box in the column head in front of the word "Evidence." This will select all the genes.



21. Above the table in the box labeled “Tools” click “Multiple Sequence Alignment.”



22. This will open a new window with the multiple sequence alignment from all the genes that were selected. Included is a gene tree showing the relationships among the genes selected on the left, and a multiple sequence alignment on the right.



No. of Members: 20
No. of Species: 20
Min AA Length: 274
Max AA Length: 274
Printable Alignment For all 20 members
Printable Tree For all 20 members (Newick File)

```
. 2 . 4 . 6 . 8 . 10 . 12 . 14 . 16 . 18 . 20 . 22 . 24 . 26 . 28 . 30 . 32 . 34 . 36 . 38 . 40 . 42 . 44 . 46 . 48 . 50 . 52 . 54 . 56 . 58 . 60 . 62 . 64 . 66 . 68 . 70
2_Acinetobacter_baumannii_2011LNAB3     MNIKALLLITSAIFISACSPYIVTANPNHSASKSDVKAEKIKNLFNEAHTTGVLVIQQGQTQQSYGNDLA
3_Acinetobacter_baumannii_2011BJAB1     MNIKALLLITSAIFISACSPYIVTANPNHSASKSDVKAEKIKNLFNEAHTTGVLVIQQGQTQQSYGNDLA
4_Acinetobacter_baumannii_2011BJAB2     MNIKALLLITSAIFISACSPYIVTANPNHSASKSDVKAEKIKNLFNEAHTTGVLVIQQGQTQQSYGNDLA
5_Acinetobacter_baumannii_2011BJAB4     MNIKALLLITSAIFISACSPYIVTANPNHSASKSDVKAEKIKNLFNEAHTTGVLVIQQGQTQQSYGNDLA
6_Acinetobacter_baumannii_2011GDAB3     MNIKALLLITSAIFISACSPYIVTANPNHSASKSDVKAEKIKNLFNEAHTTGVLVIQQGQTQQSYGNDLA
7_Acinetobacter_baumannii_2003BJAB12    MNIKALLLITSAIFISACSPYIVTANPNHSASKSDVKAEKIKNLFNEAHTTGVLVIQQGQTQQSYGNDLA
8_Acinetobacter_baumannii_2004BJAB14    MNIKALLLITSAIFISACSPYIVTANPNHSASKSDVKAEKIKNLFNEAHTTGVLVIQQGQTQQSYGNDLA
9_Acinetobacter_baumannii_2004BJAB10    MNIKALLLITSAIFISACSPYIVTANPNHSASKSDVKAEKIKNLFNEAHTTGVLVIQQGQTQQSYGNDLA
10_Acinetobacter_baumannii_2011BJAB3    MNIKALLLITSAIFISACSPYIVTANPNHSASKSDVKAEKIKNLFNEAHTTGVLVIQQGQTQQSYGNDLA
11_Acinetobacter_baumannii_2011LNAB1    MNIKALLLITSAIFISACSPYIVTANPNHSASKSDVKAEKIKNLFNEAHTTGVLVIQQGQTQQSYGNDLA
12_Acinetobacter_baumannii_2005LNAB4    MNIKALLLITSAIFISACSPYIVTANPNHSASKSDVKAEKIKNLFNEAHTTGVLVIQQGQTQQSYGNDLA
13_Acinetobacter_baumannii_2004BJAB13   MNIKALLLITSAIFISACSPYIVTANPNHSASKSDVKAEKIKNLFNEAHTTGVLVIQQGQTQQSYGNDLA
14_Acinetobacter_baumannii_2011BJAB5    MNIKALLLITSAIFISACSPYIVTANPNHSASKSDVKAEKIKNLFNEAHTTGVLVIQQGQTQQSYGNDLA
15_Acinetobacter_baumannii_2011BJAB8    MNIKALLLITSAIFISACSPYIVTANPNHSASKSDVKAEKIKNLFNEAHTTGVLVIQQGQTQQSYGNDLA
16_Acinetobacter_baumannii_2011GDAB1    MNIKALLLITSAIFISACSPYIVTANPNHSASKSDVKAEKIKNLFNEAHTTGVLVIQQGQTQQSYGNDLA
17_Acinetobacter_baumannii_1999BJAB11   MNIKALLLITSAIFISACSPYIVTANPNHSASKSDVKAEKIKNLFNEAHTTGVLVIQQGQTQQSYGNDLA
18_Acinetobacter_baumannii_2011LNAB2    MNIKALLLITSAIFISACSPYIVTANPNHSASKSDVKAEKIKNLFNEAHTTGVLVIQQGQTQQSYGNDLA
19_Acinetobacter_baumannii_2011BJAB6    MNIKALLLITSAIFISACSPYIVTANPNHSASKSDVKAEKIKNLFNEAHTTGVLVIQQGQTQQSYGNDLA
20_Acinetobacter_baumannii_2011GDAB4    MNIKALLLITSAIFISACSPYIVTANPNHSASKSDVKAEKIKNLFNEAHTTGVLVIQQGQTQQSYGNDLA
21_Acinetobacter_baumannii_2011HNAB1    MNIKALLLITSAIFISACSPYIVTANPNHSASKSDVKAEKIKNLFNEAHTTGVLVIQQGQTQQSYGNDLA
```

Assignment

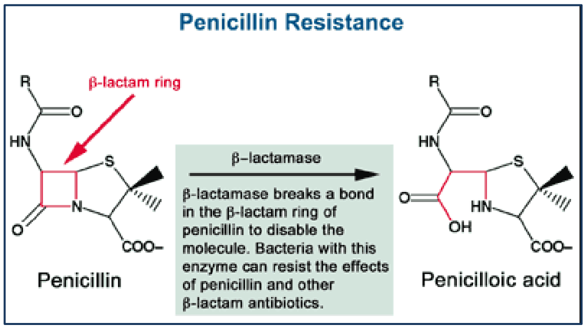
- Use the filter on the Specialty Gene landing page for *Acinetobacter baumannii* to find genes with lower Query coverage and check the multiple sequence alignment for some that have the same product description.
- Use the filter on the Specialty Gene landing page for *Acinetobacter baumannii* to find genes with lower Subject coverage and check the multiple sequence alignment for some that have the same product description.
- Use the filter on the Specialty Gene landing page for *Acinetobacter baumannii* to find genes with lower % Identity and check the multiple sequence alignment for some that have the same product description
- What happens when you compare genes with the same product description, but come from different sources?

Extra Assignment: Exploring the Beta lactamase gene family.

Beta-lactam antibiotics are structurally related to penicillin, which inhibits synthesis of the bacterial cell wall. Beta lactamase enzymes cleave the four-atom lactam ring, rendering these antibiotics harmless to the bacteria. Researchers found that the beta-lactamase OXA-23 gene in *A. baumannii* was flanked by insertion sequences, suggesting acquisition by horizontal transfer[7].

Using what you have learned above, please explore the Beta lactamases from *A. baumannii* in the following ways:

- How many different genes act as the source for the Beta lactamase genes you see in the Specialty Genes page for *A. baumannii*?
- Using the multiple sequence alignment and the gene tree tools, explore which alignments map to the specific Source ID genes.
- Using the genes in the Source ID, can you tell many Beta lactamase genes each of the genomes have?
- When you look at the genomes that result from filtering the Specialty Gene page data as described above, you will not see the *A. baumannii* AYE genome. Does the AYE genome have any genes that have the words “Beta lactamase” in the functional description? How many?
- If you are able to find Beta lactamase genes in the AYE genomes, generate an alignment with those genes and the genes you saw on the Specialty Gene page (Hint: You will have to add genes to different groups when you are in your Workspace). Do any of the AYE genes have strong homology to any of the genes we saw and built alignments for previously?
- Using the Compare Region Viewer and/or the Genome Browser, choose some of these Beta lactamase genes and see if they are flanked by insertion sequences (transposases or mobile elements).



β-lactamase breaks a bond in the β-lactam ring of penicillin to disable the molecule. Bacteria with this enzyme can resist the effects of penicillin and other β-lactam antibiotics.

References

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