Examining the genes identified as significantly, differentially expressed by RNA-Seq in PATRIC

Differential expression using PATRIC's new RNA-Seq pipeline has characterized the *Acinetobacter baumannii* genes below as being significantly expressed. In this exercise you will learn how to examine information that might be related to these genes in PATRIC.

Q value <0.05

fig|1310581.3.peg.696
fig|1310581.3.peg.1428
fig|1310581.3.rna.90
fig|1310581.3.peg.89
fig|1310581.3.peg.1468
fig|1310581.3.peg.2426
fig|1310581.3.peg.3061
fig|1310581.3.peg.3660
fig|1310581.3.peg.3045
fig|1310581.3.peg.1171
fig|1310581.3.peg.1944
fig|1310581.3.peg.2174
fig|1310581.3.rna.91
fig|1310581.3.peg.295
fig|1310581.3.peg.1156
fig|1310581.3.rna.53
fig|1310581.3.rna.52
fig|1310581.3.peg.33
fig|1310581.3.peg.112
fig|1310581.3.peg.2173
fig|1310581.3.peg.379
fig|1310581.3.peg.730
fig|1310581.3.peg.2031

0.05<Q value <0.01

fig|1310581.3.peg.3020
fig|1310581.3.peg.3001
fig|1310581.3.peg.2601
fig|1310581.3.peg.2507
fig|1310581.3.peg.1609
fig|1310581.3.peg.3430
fig|1310581.3.peg.2479
fig|1310581.3.peg.1185
fig|1310581.3.peg.515
fig|1310581.3.peg.2327
fig|1310581.3.rna.54
fig|1310581.3.peg.2185
fig|1310581.3.peg.2156
fig|1310581.3.peg.3232

I. **Searching for information on individual genes**

1. Enter the first locus tag into the global search box and hit return.

2. This will return the search results page. You can see that fig|1310581.3.peg.696 has been annotated as Bacterioferritin-associated ferredoxin. Click on that name

3. This takes you to the landing page for that gene. It is in the *A. baumannii* 34654 genome.

4. There is not any experimental evidence associated with this genome, but you should click through the tabs and associated links to see what information is available. You can click on the Genome Browser tab.

5. This allow you to compare the PATRIC (blue) and RefSeq (green) annotations.
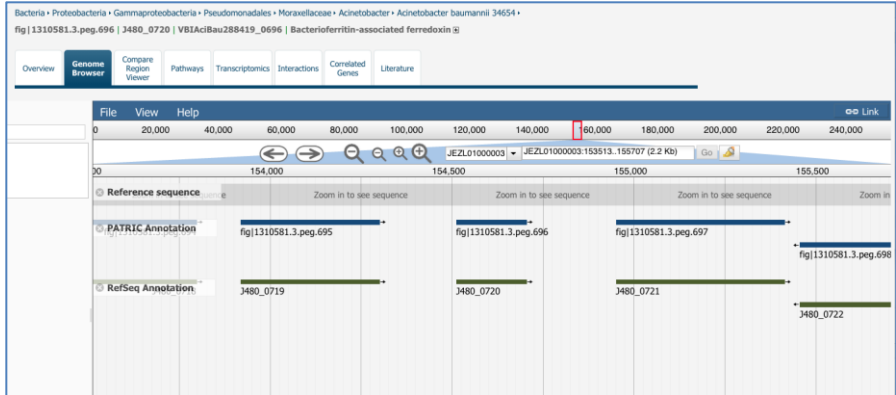
6. You can also look at associated information in other resources by clicking on the names of the sites under External Tools. As an example, click on "NCBI CDD Search."

7. This opens a page at Conserved Domain Database for this particular gene. You can see that the top hit is to Bacterioferritin-associated ferredoxin, which confirms the product description.
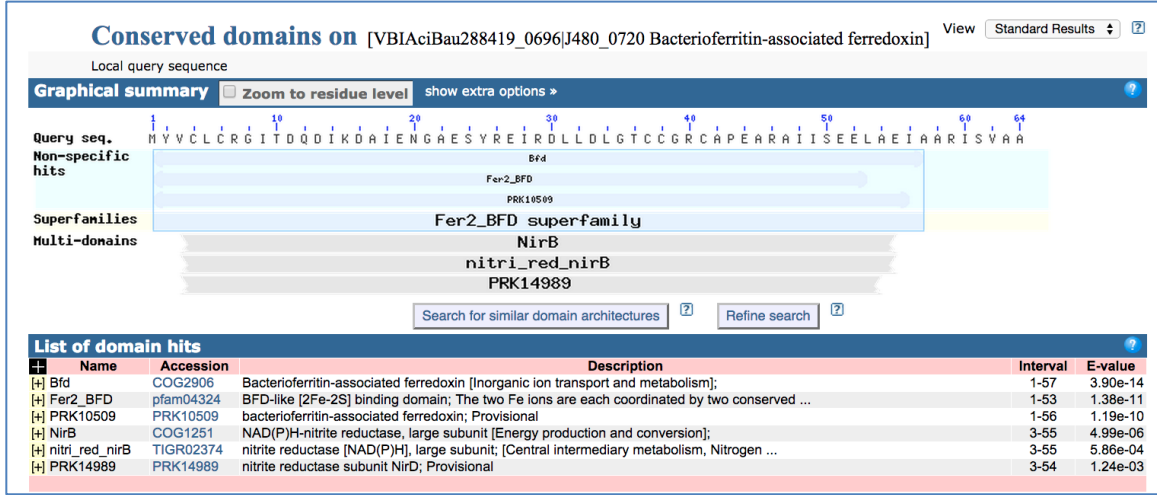
Assignment: Thirty-six genes were identified by the RNA-Seq as being significantly differentially expressed. Examine each of those genes in PATRIC, clicking on the tabs and links to the external resources. In particular, pay attention to the name given at PATRIC and how they are described in those resources.

II. Saving a list of genes to private workspace.
Sometimes it is easier to upload an entire gene list into your PATRIC workspace so that you can either examine it, or refer to it at a later time. The following steps show you how to save an entire list of genes into your private workspace.
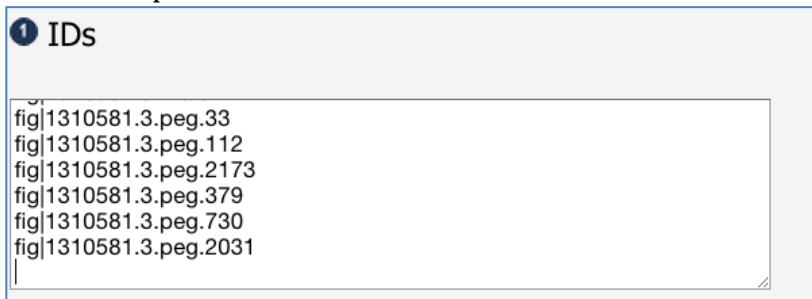
1. Click on the TOOLS tab and then click on "ID Mapping."
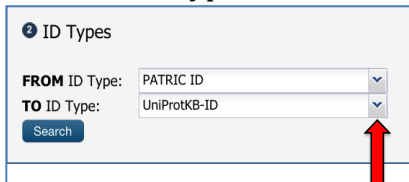

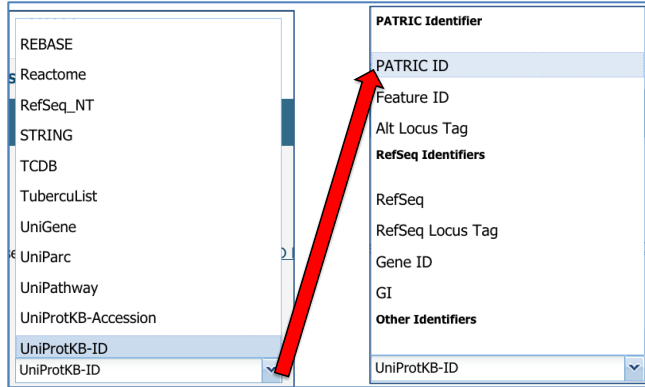2. This will open up the ID Mapping tool.
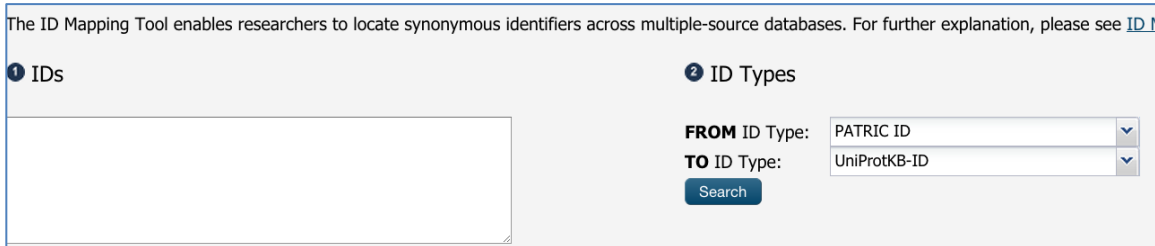
3. Cut and paste the first set of IDs into the ID text box.

4. Under ID Types, click on the down arrow that follows "UniProtKB-ID."

5. This will open up a box that shows all the available IDs. Scroll up to the top of the box to find PATRIC ID. Click on that.

6. Once you have put the IDs in and changed the To ID Type to PATRIC ID, click on the blue Search button.

3. This will return a table with those IDs and other information.

22 features found
To learn how to filer, sort, manipulate, refine, and save data within PATRIC feature tables, please see Feature Table FAQs.

	Workspace	View	Download	Tools	Columns
	Add Feature(s)	FASTA DNA / FASTA Protein	Table / FASTA	Pathway Summary / MAP IDs to... / Multiple Seq Alignment	Show/Hide ▾ Default

|	Genome Name ▲	PATRIC ID	RefSeq Locus Tag	Alt Locus Tag	PATRIC ID
☐	Acinetobacter baumannii 34654	fig|1310581.3.peg.3061	J480_3177	VBIAciBau288419_3061	fig|1310581.3.peg.
☐	Acinetobacter baumannii 34654	fig|1310581.3.peg.730	J480_0758	VBIAciBau288419_0730	fig|1310581.3.peg
☐	Acinetobacter baumannii 34654	fig|1310581.3.peg.1171	J480_1219	VBIAciBau288419_1171	fig|1310581.3.peg.
☐	Acinetobacter baumannii 34654	fig|1310581.3.peg.1428	J480_1490	VBIAciBau288419_1428	fig|1310581.3.peg.
☐	Acinetobacter baumannii 34654	fig|1310581.3.peg.1468	J480_1532	VBIAciBau288419_1468	fig|1310581.3.peg.
☐	Acinetobacter baumannii 34654	fig|1310581.3.peg.1944	J480_2021	VBIAciBau288419_1944	fig|1310581.3.peg.
☐	Acinetobacter baumannii 34654	fig|1310581.3.peg.2031	J480_2113	VBIAciBau288419_2031	fig|1310581.3.peg.
☐	Acinetobacter baumannii 34654	fig|1310581.3.peg.2173	J480_2266	VBIAciBau288419_2173	fig|1310581.3.peg.
☐	Acinetobacter baumannii 34654	fig|1310581.3.peg.2174	J480_2267	VBIAciBau288419_2174	fig|1310581.3.peg.
☐	Acinetobacter baumannii 34654	fig|1310581.3.peg.2426	J480_2523	VBIAciBau288419_2426	fig|1310581.3.peg.
☐	Acinetobacter baumannii 34654	fig|1310581.3.peg.3045	J480_3161	VBIAciBau288419_3045	fig|1310581.3.peg.
☐	Acinetobacter baumannii 34654	fig|1310581.3.peg.1156	J480_1204	VBIAciBau288419_1156	fig|1310581.3.peg.
☐	Acinetobacter baumannii 34654	fig|1310581.3.peg.3660	J480_3787	VBIAciBau288419_3660	fig|1310581.3.peg.
☐	Acinetobacter baumannii 34654	fig|1310581.3.peg.33	J480_0034	VBIAciBau288419_0033	fig|1310581.3.peg
☐	Acinetobacter baumannii 34654	fig|1310581.3.peg.89	J480_0090	VBIAciBau288419_0089	fig|1310581.3.peg
☐	Acinetobacter baumannii 34654	fig|1310581.3.peg.112	J480_0113	VBIAciBau288419_0112	fig|1310581.3.peg
☐	Acinetobacter baumannii 34654	fig|1310581.3.peg.295	J480_0308	VBIAciBau288419_0295	fig|1310581.3.peg
☐	Acinetobacter baumannii 34654	fig|1310581.3.peg.379	J480_0392	VBIAciBau288419_0379	fig|1310581.3.peg
☐	Acinetobacter baumannii 34654	fig|1310581.3.rna.52		VBIAciBau288419_r052	fig|1310581.3.rna

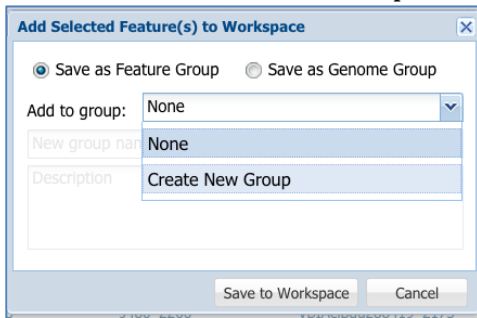4. You will need to resize the table to show all the results.

5. To select all the genes, click the box in front of the column named Genome Name.
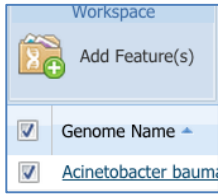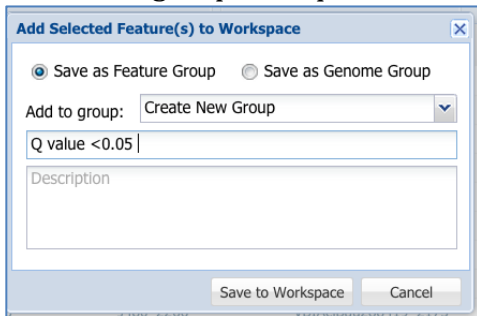
6. This will open a pop-up window. Click the down arrow next to the box that contains the word "None."
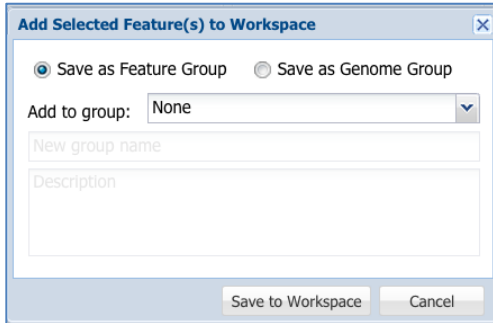
7. Click on "Create New Group."

8. Give the group a unique name and then click the "Save to Workspace" button.

Your gene group has now been saved to your private workspace.

Assignment: Create another gene group using the second set of genes.