Finding genes associated with antibiotic resistance in *Pseudomonas* and *Klebsiella*

This exercise demonstrates two different ways to look for antibiotic resistance genes in PATRIC. The first is to do a direct search with the gene name and a popular Pseudomonas strain. The second is to use PATRIC's specialty gene search. We will begin with the mexA gene in *Pseudomonas aeruginosa* strain PAO1. This strain of *P. aeruginosa* is one of NCBI's reference strains and PATRIC has incorporated 46 transcriptomic experiments for this genome.

I. Searching for a specific gene in a specific strain of *Pseudomonas*

1. Search for the gene name (mexA) and the strain (PAO1) in the global search box on PATRIC and hit return.



2. This will open up the search results page. You can see that there are 12 features that match the search criteria. This page shows the top three results.



3. To see all the results, click on the number that follows the word "Features."



4. This will display all the genes that match the search criteria.

Show	ing 12 feature(s) for: <i>mexA PAO1</i>
	Select all (12) displayed feature(s)Show Toolbar
	472024.472053mexA Pseudomonas aeruginosa PAO1H2O sig_peptide OU9_00435
	RND multidrug efflux membrane fusion protein MexA mexA Pseudomonas aeruginosa PAO1H2O CDS OU9_00435
	multidrug resistance protein mexA mexA Pseudomonas aeruginosa PAO1-VE13 CDS N297_436 N297_436
	multidrug resistance protein mexA mexA Pseudomonas aeruginosa PAO1-VE2 CDS N296_436 N296_436
	RND multidrug efflux membrane fusion protein MexA precursor mexA Pseudomonas aeruginosa PAO1 CDS PA0425 PA0425
	multidrug resistance protein mexA mexA Pseudomonas aeruginosa PAO581 CDS M801_436 M801_436
	RefSeq Cos V563_05235
	RND efflux system, membrane fusion protein CmeA mexA Pseudomonas aeruginosa PAO1-VE2 CDS fig 1367493.3.peg.446 N296_436 VBIPseAer310614_0446
	RND efflux system, membrane fusion protein CmeA mexA Pseudomonas aeruginosa PAO1-VE13 CDS fig 1367494.3.peg.446 N297_436 VBIPseAer305084_0446
	RND efflux system, membrane fusion protein CmeA mexA

5. To find the gene in the PAO1 strain, click on the blue product description (RND multidrug efflux membrane fusion protein MexA precursor).



6. This will take you to the landing page for the mexA gene in the PAO1 strain. Look carefully at the page. It includes summary information across the very top, tabs across the top of the page just above the tables, links to different information along the left-hand side, and boxes with summary information.

Bacteria · Proteobacteria · Gammaproteobac fig 208964.12.peg.447 PA0425 VBI	teria • Pseudomo PseAer58763_	onadales • Pse 0447 mex/	udomona A RND e	daceae + Ps efflux syst	eudomon em, mer	as • Pseudom nbrane fusio	ionas aerugin on protein C	osa PAO1 ►		
Overview Genome Region Pa	thways Transcr	iptomics Inte	eractions	Correlated Genes	Literat	ure				
Add PATRIC Feature to Workspace	Gene ID	PATRIC I	D : fig 208	964.12.peg.•	447 Refs	eq: <u>PA0425</u>	Alt Locus Ta	g: VBIPseAer58763_0447		
iew NT Sequence	w NT Sequence Protein ID RefSeq					77 80 IDs a	re mapped		mexA	
iew AA Sequence										
xternal Tools									CDS	
he SEED Viewer	Annotation			Start	End	NT	AA	Product		
ICBI CDD Search	Annotation	LOCUS Tay	Start		LIIU	Length	Length	Floduce		
TRING: Protein-Protein Interactions	PATRIC	VBIPseAer58	763_0447	472042	473175	1134	377	RND efflux system, membrane fusion protein Cme		
TITCH: Chemical-Protein Interactions	RefSeq	q PA0425		472024	473175	1152	383	RND multidrug efflux membrane fusion protein I precursor		
ecent PubMed Articles										
	Functional I	Properties								
2015 Apr 28 Expression of the mexA Gene	GO Assignmen	nts	-							
Requires the DNA Helicase RecG in Pseudomonas aeruginosa PAQ1	EC Assignment	ts	-							
Heo A and Park W	FIGfam Assign	iments	FIG01304	998						
	Pathway Assignments		-							
Reduced production of OprM may	Structure		Not suppo	rted by SSG	CID/CSGI	2				
promote oprD mutations and lead to imipenem resistance in Pseudomonas	Protein Interac	ctions	Host-pat	hogen inte	ractions:	0 All inter	ractions: 0			

7. We'll explore the tabs for this gene. Click on the second tab (Genome Browser).



8. This will open up the genome browser, which shows the PATRIC annotation (generated by RAST and with the blue lines) and RefSeq annotation (green lines).

File	View	Help										ee Link
0	500,000	1,000,000	1,500,000	2,000,000	2,500,000	3,000,000	3,500,000	4,000,000	4,500,000	5,000,000	5,500,000	6,000,000
			$ \bigcirc \bigcirc$	Q	Q & 🕀	NC_00251	6 - NC_0025	16:471043474	176 (3.13 Kb)	Go 🔏		
4	71,250					472,500					473,750	
© Refe	Reference sequence Zoom in to see sequence Zoom in to see sequence											
© PAT	RIC Anno	ation64.12.pe	:g.446	fig 20	8964.12.peg.44	47		fig 20896	4.12.peg.448		-	
© Refs	Seq Annot	ation		PA0425	;			-				
PA04	123								PA0426			

9. Click on the 5th tab (Transcriptomics)



10. This is where you will find a summary of all the transcriptomics experimental evidence we have in PATRIC for this particular gene. The top of the page has a filter that allows you to search for specific results. Below are two summary graphs that display the information, followed by a table with the title and other information on the experiment, including the log ratio and Z score for the gene in that particular experiment.



11. Along the top, you can filter on different levels of expression. Change the log ratio from 0 to 1, and then click on the filter button.



12. The results of the filter will show you the experimental conditions where your gene matches that value, and also shows the experimental conditions where the gene is more significantly expressed.



13. Return to the tabs and click the 7th one (Correlated Genes)



18. This will open the page that shows correlated expression with the mexA gene. The top row contains the mexA gene itself. The second row, with the highest correlation to the mexA gene is mexB.

Co	rrelation Cutoff:	0.4 Y Corre	lation:	positive 💙	Filter							
10 fea	D features found											
Workspace View			Download		Tools	Columns						
×.	Add Feature(s)	FASTA DNA		Table - FASTA -	MAP ID	Summary 🔛 Multiple Seq Alignment	Show/Hide - Defau	ult				?
	(Genome Name			PATRIC ID	Alt Locus Tag	RefSeq Locus Tag		Gene Symbol	Product Description	Correlat	tion 🕆
	Pseudom	onas aeruginosa PAO1		fig 20	8964.12.peg.447	VBIPseAer58763_0447	PA0425		mexA	RND efflux system, membrane fusion protein CmeA	1.00	00
	Pseudom	onas aeruginosa PAO1		fig 20	8964.12.peg.448	VBIPseAer58763_0448	PA0426		mexB	RND efflux system, inner membrane transporter C	0.58	81
	Pseudom	onas aeruginosa PAO1		fig 208	964.12.peg.3056	VBIPseAer58763_3056	PA2915			Zn-dependent hydrolases, including glyoxylases	0.47	70
	Pseudom	onas aeruginosa PAO1		fig 208	964.12.peg.2958	VBIPseAer58763 2958	PA2821			Glutathione S-transferase family protein	0.44	42
	Pseudom	onas aeruginosa PAO1		fig 20	8964.12.peg.449	VBIPseAer58763_0449	PA0427		oprM	RND efflux system, outer membrane lipoprotein Cm	0.43	36
	Pseudom	onas aeruginosa PAO1		fig 20	8964.12.peg.106	VBIPseAer58763 0106	PA0102			Carbonic anhydrase (EC 4.2.1.1)	0.42	20
	Pseudom	onas aeruginosa PAO1		fig 208	964.12.peg.5260	VBIPseAer58763 5260	PA5018		msrA	Peptide methionine sulfoxide reductase MsrA (EC 1	0.40	06
	Pseudom	onas aeruginosa PAO1		fig 20	8964.12.peg.58	VBIPseAer58763_0058	PA0055			Uncharacterized protein conserved in bacteria	0.40	06
	Pseudom	onas aeruginosa PAO1		fig 208	964.12.peg.3262	VBIPseAer58763 3262	PA3110			DedD protein	0.40	00
	Pseudom	onas aeruginosa PAO1		fig 208	964.12.peg.3204	VBIPseAer58763 3204	PA3053			2-hydroxy-6-oxo-6-phenylhexa-2,4-dienoate hydrol	0.40	00

19. Go back to the 1st tab (Overview).

Bacteria · Proteobacteria · Gammaproteobacter

fig | 208964.12.peg.447 | PA0425 | VBIPs

Overview	Genome Browser	Compare Region Viewer	Path						
	Eesture to W	/orkspace							
View NT Sequence									
View AA Seq	uence								
External To	ools								
The SEED Vi	ewer								
NCBI CDD S	earch								
STRING: Protein-Protein Interactions									
STITCH: Che	emical-Prote	in Interaction	าร						

20. Along the upper left hand side, under "External Tools" there are a number of hyperlinks to other resources that have information about the mexA gene. These include SEED, Conserved Domain Database (CDD), String and Stitch. Clicking on any of the title will open a new tab on your browser to the other resources, and will land on the mexA gene there.



21. This page also shows the most recent publications about the gene, with hyperlinks to PubMed for researchers get access to the paper.



22. To find the related proteins in the same family you will need to look in the Functional Properties table on the gene page for the FIGFam Assignment. Click on the hyperlink to the protein family page by clicking on FIG01304998.

Functional Properties									
GO Assignments	-								
EC Assignments	-								
FIGfam Assignments	FIG01304998								
Pathway Assignments	-								
Structure	Not supported by SSGCID/CSGID								
Protein Interactions	Host-pathogen interactions: $\underline{0}$	All interactions: 0							

23. This will take you to a table that shows all the members of the protein family that contains mexA, and includes a large number of the genomes currently in PATRIC.

Prote	ein Family Memk	bers								
Кеуи	vord:		Filter Table	I						
1960	7 features found	in FIG01304998								
	Workspace	View	Downlo	ad		Tools	Columns			
8	Add Feature(s)	FASTA DNA FASTA Protein	Table	-	A Pathway Summ	ary 🛗 Multiple Seq Alignment	Show/Hide -	Default		
	Genome Name				D	RefSeq Locus Tag	Alt Locus Tag	Gene Symbol		
	Acinetobacter bauma	nnii 470922		fig 1310808.3.peg.2326 1707 2400 VBIAciBau281795 2326						
	Enterobacter sp. B50	9		fig 1377;	19.3.peg.3893		VBIEntSp64224 3893			
	Acinetobacter nosoco	mialis 28F		fig 1147:	131.5.peg.1506		VBIAciNos231591_1506			
	Xanthomonas axonop	odis pv. manihotis str. I	BSBF 2538	fig 11856	575.3.peg.72		VBIXanAxo245698 0072			
	Delftia sp. 670			fig 15372	702.3.peg.27	<u>GY15 00115</u>				
	Salmonella enterica s	ubsp. enterica serovar C	holeraesuis	fig 321314.9.peg.3877			VBISalEnt136302_3877			
	Salmonella enterica s	ubsp. enterica serovar C	holeraesuis	fig 90413	39.4.peg.2130		VBISalEnt174419 2130			
Salmonella enterica subsp. enterica serovar Choleraesuis					fig 997330.3.peg.2430 VBISalEnt302986 2430					
	Salmonella enterica s	ubsp. enterica serovar C	holeraesuis	fig 93814	12.3.peg.3456		VBISalEnt312252_3456			

24. If you wanted to find if any Klebsiella genomes contained mexA genes in this same protein family you could enter "Klebsiella" in the Keyword search at the top of the table and click on the "Filter Table" button.

Protein Fa	mily Membe	ers								
Keyword:	Klebsiella		Filter Table							
19607 feat	19607 features found in FIG01304998									
Works	Download									

25. This will show you the number of genes across all the Klebsiella genomes that are members of this family. Note that the number along the top of the table has changed.

Protein Family Members												
Keywor	rd: Klebsiella		Filter Table									
816 features found in FIG01304998												
1	Workspace	View		Download								
		m	Table	•								
	Add Feature(S)	🔊 FASTA Protein	>	FASTA	•							
G	enome Name			PA	TRI							
K	Klebsiella pneumoniae BIDMC 47											
K	Klebsiella pneumoniae											
K	Klebsiella pneumoniae subsp. rhinoscleromatis ATCC 13884 f											
К	lebsiella pneumonia	e subsp. pneumoniae Kp	03210	fiq	123							

26. You can add a column to show additional information, by clicking on the down arrow next to the Show/Hide icon.



30. Click on the box in front of Length (AA) to see the length of the protein, measured in amino acids.



31. This will open up a new column that shows the lengths of the Klebsiella proteins that are included in this family.

Length (AA)	Product Description
68	RND efflux system, membrane fusion protein CmeA
74	RND efflux system, membrane fusion protein CmeA
74	RND efflux system, membrane fusion protein CmeA
138	RND efflux system, membrane fusion protein CmeA
177	RND efflux system, membrane fusion protein CmeA
177	RND efflux system, membrane fusion protein CmeA
187	RND efflux system, membrane fusion protein CmeA
187	RND efflux system, membrane fusion protein CmeA
210	RND efflux system, membrane fusion protein CmeA
214	RND efflux system, membrane fusion protein CmeA
214	DND - 40

30. You can generate a multiple sequence alignment to see similarities and differences in these proteins by first clicking on the box right in front of the column "Genome Name."



32. This will select all of the 20 genes that you see in the table that contains the protein family members.



33. In the Tools section above the table, click on the icon for "Multiple Sequence Alignment."



34. This will open up a new window that contains an alignment (right side) and a gene tree (left side) for those first 20 proteins.

Protein Alignment		
No. of Members: 20	Min AA Length: 68	Printable Alignment For all 20 members
No. of Species: 14	Max AA Length: 310	Printable Tree For all 20 members (Newick File)
Draw tree as phylogram + Label tree with	genome names \$	55% conserved per position (shaded bl
	1 11 21 31 41 51 61 71	81 91 101 111 121 131 141
Hebsiells_pneumonise_BIDMC_47		
Websiella_pneumoniae_UCI_61	HL TAL GAMML SF	-LL VGCDDS VAQNAAP PAPTVS AAKVLVKS I SQWDS F NOT I EAVES VQL RPRVS GY
Nebsiella_pnoumoniae_UCI_17	MSGTTLKRNFVEGSDVEAGQSLYQTDPATYQAAWNSAKGDEAKAEAAAATAHLTVKRYVPLLGTKYTSQQEY	DQAYATARQADADY I AT KAAYETAR I NLAYTKY ISPUS OF I GKSSYTERAL Y I NOQSD -ALAHVQQLDP I YYD
Nebsiella_preumoniae_subsp_preumoniae_85055	MSGIILKRNFVEGS DVEAGQSLYQIDPATYQAAWNS AKGDEAKAEAAAAIAHLTVKRYVPLLGTKYIS QQEY	DQAVATARQADADY I ATKAAVETAR I NLAYTKVIISRI SOR I GKSSVITERAAVI NOQSD -ALATIVQQLDP I WD
Nebsiella preumoniae 1953	MSGTTLKRNFVEGS DVEAGQSLYQTDPATYQAAWNS AKGDEAKAEAAAATAHLTVKRYVPLLGTKYTS QQEY	DQAVATARQADADVI AT KAAVETAR I NLAYTKVISPUS (BIGKSS VIEDALVINOQS DI-ALADVQQL DPI VVD
Nahuialla maumoniaa ISC21	MSGTTLKRNFVEGS DVEAGQS LYQTDP ATYQAAWNS AKGDE AKAE AAAATAHLTVKRYVPLLGTKYTS QQEY	DQAVATARQADADY I ATKAAYETAR I NLAYTKY <mark>USPUS OF I GKS S VIEBALYI NO</mark> QS DI-ALAHVQQLDP I <mark>YY</mark> D
Mahaialla securezian 1919	MS GTTLEKRNFVEGS DVEAGQS LYQTDP ATYQAAWNS AKGDEAKAEAAAATAHETYKRYVPLEGTKYTS QQEY	DQAVATARQADADVI AT KAAVETAR I NEAVTKVISPIS OF I GKSS VIEBALVI NOQS DI-ALADVQQEDPI VVD
National Processing Statements	MSGTTLKRNFVEGS DVEAGQS LYQTDP ATYQAAWNS AKGDEAKAEAAAATAHLTVKRYVPLLGTKYTS QQEY	DQAVATARQADADVI ATKAAVETAR I NLAYTKVIISRIIS OFI GKSSVITERALVI NOQSD - ALAHVQQLDPI I VID
Nebsiella_preumoniae_1546	MSGTTLKRNFVEGS DVEAGQSLYQTDPATYQAAWNS AKGDEAKAEAAAATAHLTVKRYVPLLGTKYTSQQEY	DQAVATARQADADY I ATKAAYETAR I NLAYTKYISRIS GI I GKSSYI EVALYI NGQSD - ALAHVQQLDP I YYD
Nebsiella_preumoniae_1533	MSGTTLKRNFVEGSDVEAGQSLYQTDPATYQAAWNSAKGEEAKAEAAAATAHLTVKRYVPLLGTKYTSQQEY	DQAVATARQADADVI ATKAAVETAR I NLAYTKVI SPIS DI GKSSVI EVALVTNOQSD - ALADVQQLDP I YVD
Nebsiella_pneumoniae_BIDMC_47	· · · · · · · · · · · · · · · · · · ·	
Nebsiells_preumonise_subsp _pneumonise_Kp03210		
Nebsiella_pneumoniae_subsprhinosoleromatis_ATCC_13004		
Nebsiells_preumoniae		
Hebsiella_pneumoniae_UCL_61		
Klebsiella_pneumoniae_1539		
Hiebsiella_pneumoniae_IS10		
Nebsiella preumoniae 1553		MOAAOLNEDETKVIAR DOASRALLISS NEVER DTASVITULVSOKTV
Eshriella neuropiae mban, posuropiae 04054		
Nebslelle en		MARINE AS RAL TO SPREAM OT AS AT THE VS OKT WHAT

II. Looking more broadly at antibiotic resistance genes-Specialty Gene landing page for *Pseudomonas*

1. Enter Pseudomonas into the text box for the global search and hit return



2. This will open up the search results page that divides the results into Features (aka genes), Genomes, Taxonomy and Experiments.



3. Scroll down to the Taxonomy results and click on the name "Pseudomonas."



4. This will take you to the landing page for the genus *Pseudomonas*.

Bacteria · Proteobacteria · Gammaproteobacteria · Pseudomonadales · Pseudomonadaceae · Pseudomonas ⊞ Data · Domo Down												ata Overview Tutorial » ownload genome data »		
Overview Taxono	my	Phylogeny	Genome List	Feature Table	Feature Specia Table Gene		tein hilies	Pathways	Transcriptomics	Interactions	Diseases	Literature	•	
Search Tools		Тахо	onomy Sum	mary										
GE Genome Finder			Тахо	nomy ID		<u>286</u>								
FF Feature Finder				cellular organisms > Bacteria > Proteobacteria > Gammaproteob Lineage Resudemonadaceae > Resudemonas						ammaproteobac	acteria > Pseudomonadales >			
CP Comparative Pa	CP Comparative Pathway Tool													
PFS Protein Family S	Sorter		Exte	External Links Immune Epitope Database and Analysis Resource										
-			Sum	Summary Terms - Click on number to view genomes associated with term (see PATRIC FAQs)										
Experiment Summ	nary		Geno	Genome Status WGS (<u>1049</u>), Complete (<u>94</u>)										
Transcriptomics from G	GEO	349	Refe	rence Genome		Representative (<u>30</u>), Reference (<u>1</u>)								
Transcriptomics from		426	Antir	microbial Resista	ance	Susceptible (125), Resistant (36), show all 182 genomes								
ArrayExpress	ArrayExpress		Antir	nicrobial Resista	AMD Danal	(125)								
Proteomics from PRIDI	E	0	Evide	ence		AMK Panel (123)								
Structure from NCBI		2277	Isola	tion Country		USA (259), France (79), show all 845 genomes								

5. Click on the tab called "Specialty Genes."

Overview	Taxonomy	Phylogeny	Genome List	Feature Table	Specialty Genes

6. This will take you to the Specialty Genes landing page for Pseudomonas. On the left side there is a dynamic filter, and on the right a table that shows the genes. The table shows if the evidence came from literature or BLAST, the type of property associated with the gene (i.e. virulence, antibiotic resistance, human homolog, or drug target), various locus tags, the gene that has the actual evidence associated with it, the gene name, the product description, a link to the PubMed reference (if there is one), the percent identity of the Pseudomonas gene to the gene with the evidence, and the E-value from the BLAST hit.

Filter By «	Specialty Gene	5											
keyword Clear All	395387 recor	ds found											
Property (395063)	Workspace	e View		Download	Tools			Columns				He	elp
Virulence Factor (207124)	Add Feat	FASTA DNA		Table -	😽 Pathway Summary 🛛 🔠	Multiple Seq Align	nment da st	now/Hide •	Default				TRIC FAOs
Human Homolog (84845)		🔊 FASTA Protei	n 🕑	FASTA -	🐪 MAP IDs to 👻		10		berdure			•	
Antibiotic Resistance (37411)	Evidence	Property	Source	Genome Name -	PATRIC ID	RefSeq Loc	Alt Locus Tag	Source ID	Gene	Product	Pubmed	Identity	E-value
Source (395063)	BLASTP	Virulence Factor	VFDB	Pseudomonas aerugi	fig/983918.3.peg.5774	PA13_2 VBI	IPseAer186653 5	VFG0114		Leader peptidase (Pr		99	0.0
Human (84845)	BLASTP	Virulence Factor	Victors	Pseudomonas aerugi	fig/983918.3.peg.5774	PA13_2 VBI	IPseAer186653 5	4208		Leader peptidase (Pr	PubMed	99	0.0
Victors (72360)	BLASTP	Virulence Factor	VFDB	Pseudomonas aerugi	fig 983918.3.peg.2405	PA13 1 VBI	IPseAer186653 2	VFG1226		twitching motility pro		100	6e-76
DrugBank (56502)	BLASTP	Virulence Factor	VFDB	Pseudomonas aerugi	fig 983918.3.peg.4647	PA13_2 VBI	IPseAer186653 4	VFG2071		Uncharacterized prot		100	6e-119
CARD (24026)	BLASTP	Human Homolog	Human	Pseudomonas aerugi	fig/983918.3.peg.2072	PA13 1 VBI	IPseAer186653 2	NP 071		Methylcrotonyl-CoA c		65	0.0
TTD (9181)	BLASTP	Virulence Factor	VFDB	Pseudomonas aerugi	fig 983918.3.peg.2336	PA13 1 VBI	IPseAer186653 2	VFG0209		Type III secretion ne		99	1e-168
PATRIC_VF (839)	BLASTP	Virulence Factor	VFDB	Pseudomonas aerugi	fig 983918.3.peg.4642	PA13_2 VBI	3IPseAer186653 4	VFG2076		ClpB protein		99	0.0
Evidence (395387)	BLASTP	Virulence Factor	Victors	Pseudomonas aerugi	fig 983918.3.peg.4642	PA13 2 VBI	3IPseAer186653 4	4231		ClpB protein	PubMed	99	0.0
BLASTP (215879)	BLASTP	Drug Target	DrugBank	Pseudomonas aerugi	fig/983918.3.peg.3098	PA13_1 VBI	IPseAer186653_3	6537		Protocatechuate 3,4		82	5e-123
Literature (179508)	BLASTP	Virulence Factor	VFDB	Pseudomonas aerugi	fig 983918.3.peg.2097	PA13 1 VBI	IPseAer186653 2	VFG1264	flhF	Flagellar biosynthesi		99	0.0
Filter BLAST Hits by:	BLASTP	Virulence Factor	VFDB	Pseudomonas aerugi	fig 983918.3.peg.2354	PA13 1 VBI	IPseAer186653 2	VFG0192		Flagellum-specific AT		99	0.0

7. In the dynamic filter, click on Antibiotic Resistance. This will filter the table to show all the genes that meet that search criterion.

Filter By	«	Spe	ecialty Gene	25	
keyword	Clear All	374	111 record	ls foun	d
Property (395063)			Workspace	е	
clear		<u>~</u>			🏅 FAST
Virulence Factor (207124)		A (Add Feat	ure(s)	S FAST
Human Homolog (84845)					,
Drug Target (65683)			Evidence		Property
Antibiotic Resistance (37411)					

8. When you look at the column "Gene," you can see that many of the genes do not have a gene name, although they do have a product, or functional description. Click once on the "Gene" column head.

Evidence	Property	Source	Genome Name 🔺	PATRIC ID	RefSeq Loc	Alt Locus Tag	Source ID	Gene
BLASTP	Antibiotic Resistance	CARD	Pseudomonas aeru	fig 983918.3.peg.2	<u>PA13 1</u>	VBIPseAer186653	NC_00	
BLASTP	Antibiotic Resistance	CARD	Pseudomonas aeru	fig 983918.3.peg.4	<u>PA13 2</u>	VBIPseAer186653	NC_00	
BLASTP	Antibiotic Resistance	CARD	Pseudomonas aeru	fig 983918.3.peg.3	<u>PA13 2</u>	VBIPseAer186653	NC_00	
BLASTP	Antibiotic Resistance	CARD	Pseudomonas aeru	fig 983918.3.peg.5	<u>PA13 3</u>	VBIPseAer186653	NC_00	
BLASTP	Antibiotic Resistance	CARD	Pseudomonas aeru	fig 983918.3.peg.5	<u>PA13 2</u>	VBIPseAer186653	NC_00	

9. This will resort the table and show you the genes that have an associated gene name.

Gene 🔺	Product	Pubmed	Identity	E-value
MexF	Multidrug efflux tra	PubMed	95	0.0
MexF	Multidrug efflux tra		87	0.0
aadA1	Streptomycin 3"-O	PubMed	100	0.0
aadA1	Streptomycin 3"-O		100	0.0
acrA	Multidrug efflux RN		98	0.0
acrA	Multidrug efflux RN		99	0
acrA	Multidrug efflux RN		100	0.0
acrA	Multidrug efflux RN		99	0.0
acrB	RND efflux system,	PubMed	81	0
acrB	Multidrug efflux RN	PubMed	99	0.0
a cr D	Multidaya offlux DN		00	0.0

12. Examine the first row and the associated data and evidence for that gene.

										-		
Evidence	Property	Source	Genome Name	PATRIC ID	RefSeq Loc	Alt Locus Tag	Source ID	Gene 🔺	Product	Pubmed	Identity	E-value
BLASTP	Antibiotic Resistance	ARDB	Pseudomonas pseu	fig 1182590.4.peg	<u>BN5 0</u>	VBIPsePse244945	<u>YP 001</u>	MexF	Multidrug efflux tra	PubMed	95	0.0

13. Find the PATRIC ID and click on it.

fig|1182590.4.peg....

14. This takes you to the landing page for that gene.

Bacteria · Proteobacteria · Gammaproteobact	erla • Pseudomor	adales • Ps	eudomonada	aceae • Pseudo	monas • Pse	udomonas pseur	doalcaligenes Cl	ECT 5344 ·
fig 1182590.4.peg.1503 BN5_01487	VBIPsePse244	945_150	3 MexF M	Multidrug eff	lux transpo	rter MexF 🗄		
Overview Genome Region Pate	hways Transcrip	tomics In	teractions	Genes L	iterature			
Add PATRIC Feature to Workspace View NT Sequence	Gene ID	PATRIC VBIPsePs	ID: fig 11825 ie244945_150	590.4.peg.1503 13	RefSeq: B≬	15_01487 Alt Lo	cus Tag:	MexF
View AA Sequence	Protein ID	RefSeq	CCH37584.1					
External Tools								
The SEED Viewer	Annotation Locus Tag		ig	Start	End	NT Length	AA Length	Product
NCBI CDD Search	PATRIC	VBIPsePs	e244945_1503	3 15886	6 162045	3180	1059	Multidrug efflux transporter MexF
STRING: Protein-Protein Interactions	RefSeq	RefSeq BN5_0148		15886	6 162045	3180	1059	RND multidrug efflux transporter
Recent PubMed Articles	Functional P	ropertie	s					
No nubmed record is available	GO Assignment	5	-					
Please try PMC or Google Scholar	EC Assignments		-					
	FIGfam Assignm	nents	FIG001024	65				
	Pathway Assign	ments	-					
	Structure		Not support	ted by SSGCID	CSGID			
	Protein Interact	ions	Host-path	ogen interact	ions: 0 All	interactions: 0		

15. Scroll down to the bottom of the page and you will see a description of the evidence that linked this gene to antibiotic resistance. It gives the specific source information, including the strain that the original gene was in, and also includes the PubMed link so that you can examine the evidence directly.

0	Special Pr	roperties								
	Evidence	Property	Source	Source ID	Organism	PubMed	Subject Coverage	Query Coverage	Identity	E- value
	BLASTP	Antibiotic Resistance	ARDB •	YP_001187672 >	Pseudomonas mendocina ymp	<u>9044268</u> •	100	100	95	0.0
	BLASTP	Antibiotic Resistance	CARD •	NC_002516.2.882884.p01	Pseudomonas aeruginosa PAO1		100	100	87	0.0

III. Assignment: Find other genes and explore them using PATRIC

You can do similar searches to find other genes of interest. Below is a list of the genes important in antibiotic resistance. For each gene, see if you can find it in the PAO1 genome, and if not, search more broadly in *Pseudomonas* or *Klebsiella*. Are any of the genes not found in either of those genera, but found in other genera of bacteria in PATRIC? Are there any genes that you can't find in any genome in PATRIC?

mexA mexB tolC oprD ampC Aminooglycoside AAC Aminoglycoside APH Aminoglycoside ANT tetM tet0 tetQ cfr erm qnrA qnrB qnrS gyrA gyrB parC parE mecA vanA vanB vanE vanG pmrA pmrB phoP

phoQ