

# BV-BRC Test Report

## V5. Heatmap

<b>Item to test</b>	Heatmap
<b>URL</b>	<a href="https://www.bv-brc.org/workspace/public/PATRIC@patricbrc.org/PATRIC%20Workshop/RNA-Seq/Acinetobacter_AMR_treatments">https://www.bv-brc.org/workspace/public/PATRIC@patricbrc.org/PATRIC%20Workshop/RNA-Seq/Acinetobacter_AMR_treatments</a>
<b>Prerequisites</b>	None
<b>Tester(s)</b>	Rebecca Wattam
<b>References</b>	<a href="https://www.bv-brc.org/docs/quick_references/services/rna_seq_analysis_service.html">https://www.bv-brc.org/docs/quick_references/services/rna_seq_analysis_service.html</a>
<b>Test date</b>	7-Feb-22 (original - passed), 10-May-2022 (follow-up - passed)
<b>Test Result</b>	<b>Passed</b>

### Overview

- Test the Heatmap using an example expression data set.
- Test zoom.
- Test filter (genome, keyword, log ratio, z-score).
- Test row/column rearrangement.
- Test clustering.
- Test show significant/all genes.
- Test flyovers and links.
- Test area selection and corresponding data access.

### Test Results

- Test results were verified by inspection.
- All visualization functions performed as expected.

Expression Data Set: [last time you used PATRIC workshop RNA-Seq example]

Services

RNA-Seq Analysis  

The RNA-Seq Analysis Service provides services for aligning, assembling, and testing differential expression on RNA-Seq c  
For further explanation, please see the RNA-Seq Analysis Service [Quick Reference Guide](#) and [Tutorial](#).

### Parameters

STRATEGY  
Tuxedo

TARGET GENOME  
Acinetobacter baumannii 34654

OUTPUT FOLDER  
↓↑

OUTPUT NAME  
Output Name

### Groups/Conditions

ON

Condition Name

COL	<span style="color: red;">■</span>	×
MERO	<span style="color: green;">■</span>	×
MHB	<span style="color: blue;">■</span>	×

### Paired read library

READ FILE 1  
↓↑

READ FILE 2  
↓↑

CONDITION

### Selected libraries

Place read files here using the arrow buttons.

P(MERO_...fq.gz, MERO_...fq.gz)		<span style="color: green;">■</span>	×
P(COL_7...fq.gz, COL_7...fq.gz)		<span style="color: red;">■</span>	×
P(MHB_R1.fq.gz, MHB_R2.fq.gz)		<span style="color: blue;">■</span>	×

 Transcriptomics Genes

Table Heatmap

Filter By  
↑ ↓ ↑↓

- Title
- Strain
- COL vs MERO
- COL vs MHB
- MERO vs MHB

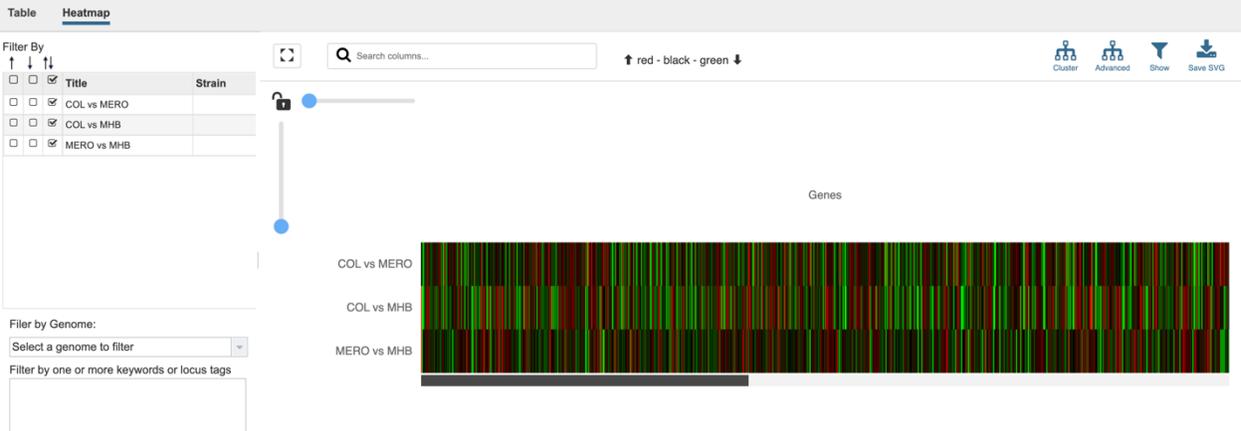
Filter by Genome:  
Select a genome to filter

Filter by one or more keywords or locus tags

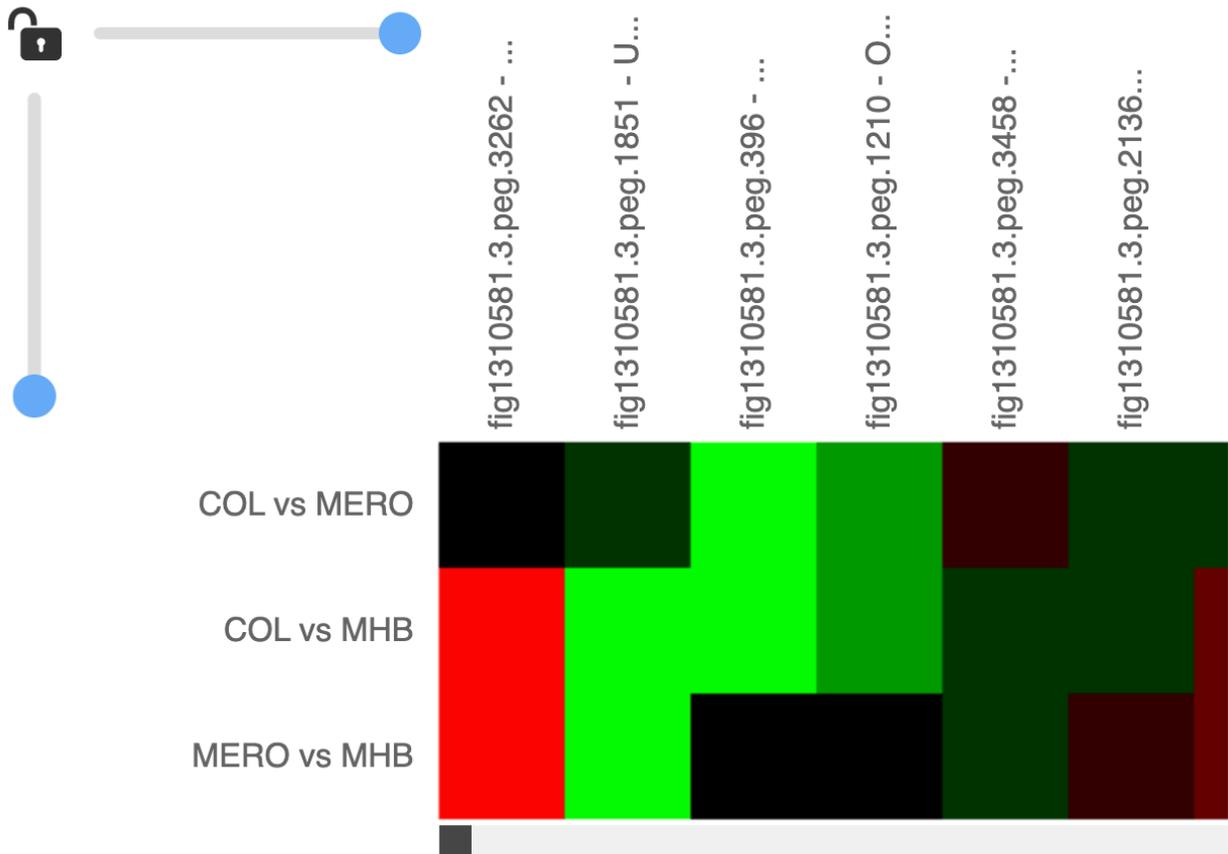
Filter by |Log Ratio|: 0

BRC ID	RefSeq Locus Tag	Gene Symbol	Product	Comparisons	Up	Down
<input type="checkbox"/>	figj1310581.3.pi.J480_3379		hypothetical protein	2	2	0
<input type="checkbox"/>	figj1310581.3.pi.J480_1924		UDP-glucose 6-dehydrogenase (EC 1.1.3	3	0	3
<input type="checkbox"/>	figj1310581.3.pi.J480_0409		Bsu YqfO NIF3/CutA domain	2	0	2
<input type="checkbox"/>	figj1310581.3.pi.J480_1261		Osmosensitive K+ channel histidine kina	2	0	2
<input type="checkbox"/>	figj1310581.3.pi.J480_3578		Putative two-domain glycosyltransferase	3	1	2
<input type="checkbox"/>	figj1310581.3.pi.J480_2221	pqqD	Coenzyme PQQ synthesis protein D	3	1	2
<input type="checkbox"/>	figj1310581.3.pi.J480_1253		hypothetical protein	3	2	1
<input type="checkbox"/>	figj1310581.3.pi.J480_1829	maiA	Maleylacetoacetate isomerase (EC 5.2.1	3	3	0
<input type="checkbox"/>	figj1310581.3.pi.J480_1438		Acyl-CoA dehydrogenase, short-chain sp	3	2	1
<input type="checkbox"/>	figj1310581.3.pi.J480_0448		hypothetical protein	3	3	0
<input type="checkbox"/>	figj1310581.3.pi.J480_1748		Phenylacetic acid degradation protein Pa	3	0	3
<input type="checkbox"/>	figj1310581.3.pi.J480_2425		Arginyl-tRNA--protein transferase (EC 2.:	3	1	2
<input type="checkbox"/>	figj1310581.3.pi.J480_2623		Lipid A phosphoethanolamine transferase	3	0	3
<input type="checkbox"/>	figj1310581.3.pi.J480_2880	recJ	Single-stranded-DNA-specific exonuclea	3	0	3
<input type="checkbox"/>	figj1310581.3.pi.J480_0509	ddc	L-2,4-diaminobutyrate decarboxylase (EC	3	3	0
<input type="checkbox"/>	figj1310581.3.pi.J480_1950		putative membrane protein	3	1	2
<input type="checkbox"/>	figj1310581.3.pi.J480_3874	hflX	Ribosome LSU-associated GTP-binding	3	3	0

1 - 200 of 2306 results

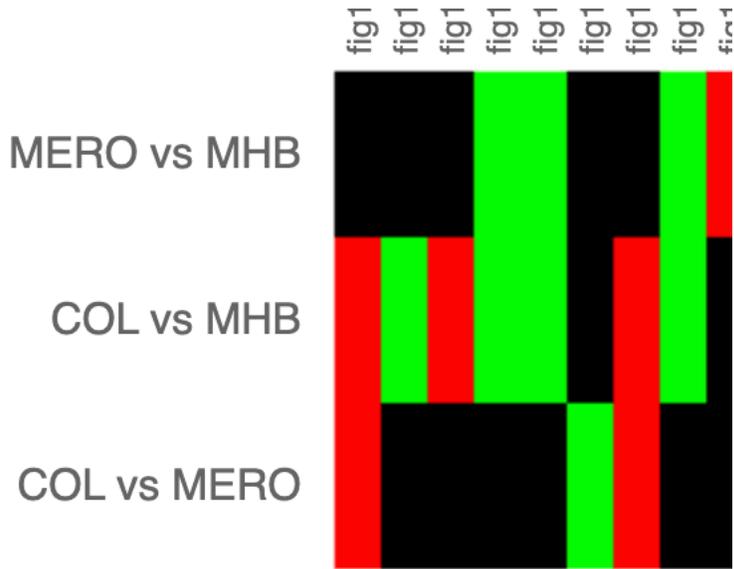
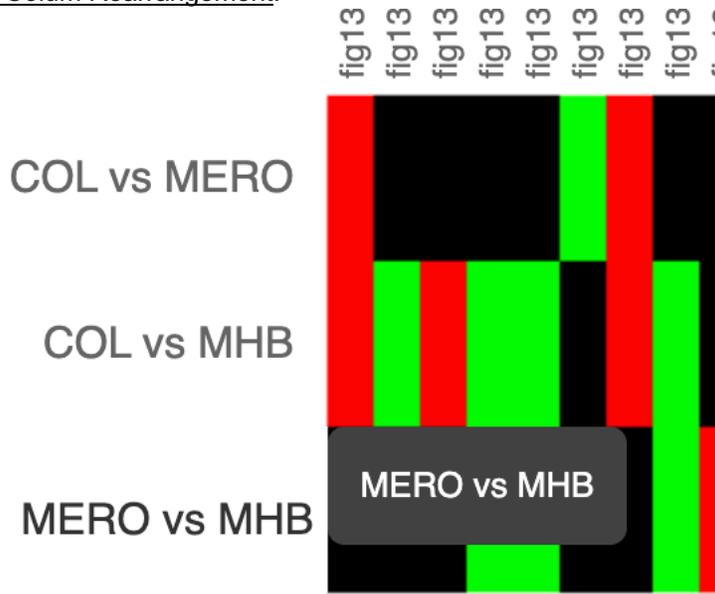


Zoom:





Row/Column Rearrangement:



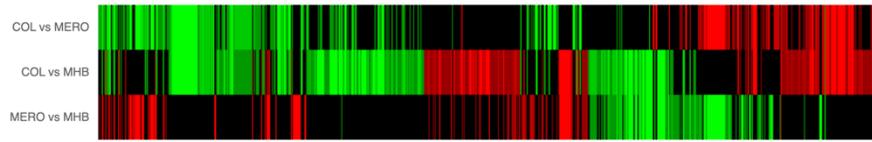
## Clustering:

Filter by Genome:  
 Acinetobacter baumannii 34654 (2306)

Filter by one or more keywords or locus tags

Filter by |Log Ratio|: 2

Filter by |Z-score|: 0



## Show significant/all genes:

**CBV-BRC** BETA ORGANISMS SEARCHES TOOLS & SERVICES WORKSPACES HELP All Data Types Find a gene, genome, microarray, etc

Transcriptomics Genes

Table Heatmap

COL vs MERO  
 COL vs MHB  
 MERO vs MHB

Filter by Genome:  
 Select a genome to filter

Filter by one or more keywords or locus tags

Filter by |Log Ratio|: 3

Filter by |Z-score|: 0

**Filter**

BRC ID	RefSeq Locus Tag	Gene Symbol	Product	Comparisons	Up	Down
<input checked="" type="checkbox"/>	fig 1310581.3.p.J480_3379		hypothetical protein	2	2	0
<input checked="" type="checkbox"/>	fig 1310581.3.p.J480_1924		UDP-glucose 6-dehydrogenase (EC 1.1.3)	3	0	2
<input checked="" type="checkbox"/>	fig 1310581.3.p.J480_0409		Bsu YqfO NIF3/CutA domain	2	0	2
<input checked="" type="checkbox"/>	fig 1310581.3.p.J480_1829	maiA	Maleylacetoacetate isomerase (EC 5.2.1.3)	3	1	0
<input checked="" type="checkbox"/>	fig 1310581.3.p.J480_0507		probable periplasmic protein NMA1059	3	0	2
<input checked="" type="checkbox"/>	fig 1310581.3.p.J480_1821	hutU	Urocanate hydratase (EC 4.2.1.49)	3	2	0
<input checked="" type="checkbox"/>	fig 1310581.3.p.J480_1262	kdpC	Potassium-transporting ATPase C chain	2	0	1
<input checked="" type="checkbox"/>	fig 1310581.3.p.J480_0912	nuoE	NADH-ubiquinone oxidoreductase chain	2	0	1
<input checked="" type="checkbox"/>	fig 1310581.3.p.J480_3638		Non-heme chloroperoxidase (EC 1.11.1.2)	2	0	1
<input checked="" type="checkbox"/>	fig 1310581.3.p.J480_2573		hypothetical protein	2	0	2
<input checked="" type="checkbox"/>	fig 1310581.3.p.J480_3195		Inner-membrane proton/drug antiporter (I)	3	1	1
<input checked="" type="checkbox"/>	fig 1310581.3.p.J480_0053		FIGfam138462: Acyl-CoA synthetase, AA	3	0	1
<input checked="" type="checkbox"/>	fig 1310581.3.p.J480_3101		Quinone oxidoreductase (EC 1.6.5.5)	3	0	1
<input checked="" type="checkbox"/>	fig 1310581.3.p.J480_2711		hypothetical protein	3	0	2
<input checked="" type="checkbox"/>	fig 1310581.3.p.J480_0058		3-oxoacyl-[ACP] synthase	3	0	1
<input checked="" type="checkbox"/>	fig 1310581.3.p.J480_0090		Ferrichrome-iron receptor	3	1	0
<input checked="" type="checkbox"/>	fig 1310581.3.p.J480_4176		hypothetical protein	2	0	1

**1 - 200 of 490 results**

DOWNLOAD  
 HIDE  
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 FEATURES  
 FASTA  
 ID MAP  
 PTHWY  
 GROUP

Feature List View (490 Genomic Features)

Feature List Overview Features

Genome ID	Genome Name	Accession	Feature Type	BRC ID	RefSeq Locus Tag	Start	End	Strand	Length (NA)	Gene Symbol	Product
<input type="checkbox"/>	1310581.3	Acinetobacter baumannii 34654	JEZL01000001	CDS	fig 1310581.3.pe J480_0006	3856	4365	+	510		hypothetical protein
<input type="checkbox"/>	1310581.3	Acinetobacter baumannii 34654	JEZL01000001	CDS	fig 1310581.3.pe J480_0011	7037	9793	-	2757	acnA	Aconitate hydratase (EC 4.2.1.3)
<input type="checkbox"/>	1310581.3	Acinetobacter baumannii 34654	JEZL01000001	CDS	fig 1310581.3.pe J480_0017	15662	16234	+	573		Transcriptional regulator, AcrR family
<input type="checkbox"/>	1310581.3	Acinetobacter baumannii 34654	JEZL01000001	CDS	fig 1310581.3.pe J480_0028	28568	29908	+	1341		Macrolide-specific efflux protein MacA
<input type="checkbox"/>	1310581.3	Acinetobacter baumannii 34654	JEZL01000001	CDS	fig 1310581.3.pe J480_0029	29911	31905	+	1995		Macrolide export ATP-binding/permease
<input type="checkbox"/>	1310581.3	Acinetobacter baumannii 34654	JEZL01000001	CDS	fig 1310581.3.pe J480_0030	31916	32473	+	558		Efflux transport system, outer membrane
<input type="checkbox"/>	1310581.3	Acinetobacter baumannii 34654	JEZL01000001	CDS	fig 1310581.3.pe J480_0031	32525	33322	+	798		Efflux transport system, outer membrane
<input type="checkbox"/>	1310581.3	Acinetobacter baumannii 34654	JEZL01000001	CDS	fig 1310581.3.pe J480_0032	33392	34258	-	867	fabI	Enoyl-lacyl-carrier-protein] reductase [N
<input type="checkbox"/>	1310581.3	Acinetobacter baumannii 34654	JEZL01000001	CDS	fig 1310581.3.pe J480_0039	38307	38963	-	657		4'-phosphopantetheinyl transferase (EC
<input type="checkbox"/>	1310581.3	Acinetobacter baumannii 34654	JEZL01000001	CDS	fig 1310581.3.pe J480_0040	38988	39422	-	435		Excinuclease ATPase subunit
<input type="checkbox"/>	1310581.3	Acinetobacter baumannii 34654	JEZL01000001	CDS	fig 1310581.3.pe J480_0041	39434	40660	-	1227		FIG138576: 3-oxoacyl-[ACP] synthase (I
<input type="checkbox"/>	1310581.3	Acinetobacter baumannii 34654	JEZL01000001	CDS	fig 1310581.3.pe J480_0042	40660	41385	-	726		3-oxoacyl-[ACP] reductase (EC 1.1.1.10
<input type="checkbox"/>	1310581.3	Acinetobacter baumannii 34654	JEZL01000001	CDS	fig 1310581.3.pe J480_0043	41409	41834	-	426		3-hydroxydecanoyl-[ACP] dehydratase (I
<input type="checkbox"/>	1310581.3	Acinetobacter baumannii 34654	JEZL01000001	CDS	fig 1310581.3.pe J480_0044	41834	43036	-	1203		3-oxoacyl-[ACP] synthase (EC 2.3.1.41)
<input type="checkbox"/>	1310581.3	Acinetobacter baumannii 34654	JEZL01000001	CDS	fig 1310581.3.pe J480_0045	43033	43578	-	546		hypothetical protein
<input type="checkbox"/>	1310581.3	Acinetobacter baumannii 34654	JEZL01000001	CDS	fig 1310581.3.pe J480_0046	43581	44876	-	1296		FIG022199: FAD-binding protein
<input type="checkbox"/>	1310581.3	Acinetobacter baumannii 34654	JEZL01000001	CDS	fig 1310581.3.pe J480_0047	44906	47164	-	2259		FIG021862: membrane protein, exporter

1 - 200 of 490 results

# Flyovers/Links:

CBV-BRC <sup>BETA</sup> ORGANISMS SEARCHES TOOLS & SERVICES WORKSPACES HELP All Data Types Find a gene, genome, microarray, etc. All terms

Transcriptomics Genes

Table Heatmap

COL vs MERO  
 COL vs MHB  
 MERO vs MHB

Search columns... ↑ red - black - green ↓

Cluster Advanced Show Save SVG

Genes

Filter by Genome:  
Select a genome to filter

Filter by one or more keywords or locus tags

Filter by |Log Ratio|: 3

Filter by |Z-score|: 0

Filter

COL vs MERO  
COL vs MHB  
MERO vs MHB

Title: COL vs MERO  
Gene: fig1310581.3.peg.281 - Universal stress protein  
Log ratio: -11.8109852658

Uploads Jobs 0 0 3761

Comparison: COL vs MERO  
Product: fig1310581.3.peg.281 - Universal stress protein

Download Heatmap Data Download Genes Show Genes Add Proteins to Group Cancel

COL vs MERO  
COL vs MHB  
MERO vs MHB

**F** Feature View

Bacteria » Proteobacteria » Gammaproteobacteria » Pseudomonadales » Moraxellaceae » Acinetobacter » Acinetobacter baumannii » Acinetobacter baumannii 34654  
 fig|1310581.3.peg.281 | J480\_0291 | Universal stress protein

- Overview**
- Genome Browser
- Compare Region Viewer
- Transcriptomics
- Interactions
- Domain and Motifs
- Protein Structures

**fig|1310581.3.peg.281**



Genome	
Genome ID	1310581.3
Genome Name	Acinetobacter baumannii 34654
Taxon ID	1310581
Source	
Annotation	PATRIC
Feature Type	CDS
Identifiers	
BRC ID	fig 1310581.3.peg.281
Database Cross References	
RefSeq Locus Tag	J480_0291
Protein ID	EXD26013.1
Location	
Start	12110
End	12547
Strand	-
Location	complement(12110..12547)
Sequences	
NA Length	438

Functional Properties

PATRIC Local Family	PLF_469_00002795
PATRIC Global Family	PGF_06961731
FIGfam	FIG00017615
Identical Proteins	<a href="#">View (new tab)</a>
Identical Genes	<a href="#">View (new tab)</a>
GO Terms	-

Not supported by SSGCID/CSGID

Area Selection and Data Access:

Number of comparisons selected: 1  
 Number of features selected: 38

Download Heatmap Data   Download Genes   Show Genes   Add Proteins to Group   Cancel

Feature List View  
 ( 38 Genomic Features )

Feature List Overview   **Features**

Genome ID	Genome Name	Accession	Feature Type	BRC ID	RefSeq Locus Tag	Start	End	Strand	Length (NA)	Gene Symbol	Product
<input type="checkbox"/>	1310581.3	Acinetobacter baumannii 34654	JEZL01000001	CDS	fig 1310581.3.pe J480_0107	111423	112265	+	843	thyA	Thymidylate synthase (EC 2.1.1.45)
<input type="checkbox"/>	1310581.3	Acinetobacter baumannii 34654	JEZL01000001	CDS	fig 1310581.3.pe J480_0282	290902	291258	-	357		hypothetical protein
<input type="checkbox"/>	1310581.3	Acinetobacter baumannii 34654	JEZL01000002	CDS	fig 1310581.3.pe J480_0291	12110	12547	-	438		Universal stress protein
<input type="checkbox"/>	1310581.3	Acinetobacter baumannii 34654	JEZL01000002	CDS	fig 1310581.3.pe J480_0394	130361	130549	+	189		hypothetical protein
<input type="checkbox"/>	1310581.3	Acinetobacter baumannii 34654	JEZL01000002	CDS	fig 1310581.3.pe J480_0409	146120	146437	+	318		Bsu YqfO NIF3/CutA domain
<input type="checkbox"/>	1310581.3	Acinetobacter baumannii 34654	JEZL01000003	CDS	fig 1310581.3.pe J480_0633	71832	72233	-	402		Nudix hydrolase family protein PA3470
<input type="checkbox"/>	1310581.3	Acinetobacter baumannii 34654	JEZL01000003	CDS	fig 1310581.3.pe J480_0634	72248	72829	-	582		Lysine decarboxylase family
<input type="checkbox"/>	1310581.3	Acinetobacter baumannii 34654	JEZL01000003	CDS	fig 1310581.3.pe J480_0642	77435	77605	-	171		hypothetical protein
<input type="checkbox"/>	1310581.3	Acinetobacter baumannii 34654	JEZL01000003	CDS	fig 1310581.3.pe J480_0664	102384	102803	+	420		hypothetical protein
<input type="checkbox"/>	1310581.3	Acinetobacter baumannii 34654	JEZL01000003	CDS	fig 1310581.3.pe J480_0666	103429	104784	-	1356		Peptidase S8 and S53, subtilisin, kexin, i
<input type="checkbox"/>	1310581.3	Acinetobacter baumannii 34654	JEZL01000003	CDS	fig 1310581.3.pe J480_0667	104820	105131	-	312		hypothetical protein; putative signal pept
<input type="checkbox"/>	1310581.3	Acinetobacter baumannii 34654	JEZL01000003	CDS	fig 1310581.3.pe J480_0811	240295	240438	+	144		Msl2237 protein
<input type="checkbox"/>	1310581.3	Acinetobacter baumannii 34654	JEZL01000004	CDS	fig 1310581.3.pe J480_0895	73577	73801	-	225		hypothetical protein
<input type="checkbox"/>	1310581.3	Acinetobacter baumannii 34654	JEZL01000006	CDS	fig 1310581.3.pe J480_1281	57934	58356	+	423		Glycine-rich cell wall structural protein pr
<input type="checkbox"/>	1310581.3	Acinetobacter baumannii 34654	JEZL01000006	CDS	fig 1310581.3.pe J480_1360	138776	139009	+	234		Bsr8028 protein
<input type="checkbox"/>	1310581.3	Acinetobacter baumannii 34654	JEZL01000007	CDS	fig 1310581.3.pe J480_1383	2048	2392	+	345		hypothetical protein
<input type="checkbox"/>	1310581.3	Acinetobacter baumannii 34654	JEZL01000007	CDS	fig 1310581.3.pe J480_1522	134348	134821	+	474		General secretion pathway protein M