

## A) Color scale

Scoring : Very Weak Weak Middle Strong Very Strong

🔗 CARD Database

Gene Name:	bacA
Best Hit ID	AACT6093.1
Similarity:	<span>51.1%</span>
Coverage:	<span>99%</span>
Bitscore:	<span>244.2</span>
evalue:	<span>5.8e-66</span>

AMR profile:

bacA is a gene that recycles undecaprenyl pyrophosphate during cell wall biosynthesis which confers resistance to bacitracin

🔗 peptide antibiotic [Class]  
determinant of resistance to peptide antibiotics. Enzymes, other proteins or other gene products shown clinically to confer resistance to peptide antibiotics..

🔗 restructuring of bacterial cell wall conferring antibiotic resistance [Mechanism]  
gene conferring antibiotic resistance via molecular bypass. Genes involved in restructuring of the cell wall.

Description of the color scale

Alignment scores are shown in colors depicting the quality of the sequence similarity.

## B) MGE Evidence

Scoring : Very Weak Weak Middle Strong Very Strong

🔗 Plasmids

Type:	Plasmids
Count:	18
Similarity:	<span>58.48% ± 10.17</span>
Bitscore:	<span>333.04 ± 61.23</span>
Coverage:	<span>100% ± 1</span>
Description:	aminoglycoside 3'-phosphotransferase
Gene Adame ID:	proteinplasmid:117403

Number of Plasmids that contain the ARG

Evidence of the ARG being carried by a MGE

## C) Pathogen Evidence

Scoring : Very Weak Weak Middle Strong Very Strong

🔗 Pathogenic Genomes

Pathogen Score: 11.2%

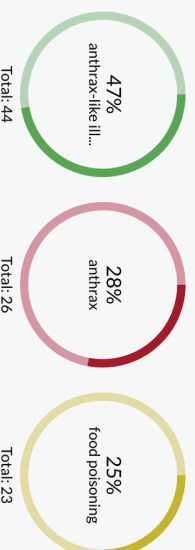
The gene entry AOA142GAB7 (uPPP) has been aligned to the PATRIC database using strict cutoffs to ensure the existence of the gene (>90% identity, >90% coverage).

507 genomes contain this particular gene (AOA142GAB7). From those, 57 (11.2%) genomes are labeled as pathogens.

Disease and Antimicrobial Resistance More information about

Genomes causing diseases

This figure shows the distribution of the bacterial genomes that are reported to cause or be involved in any diseases and contain the gene AOA142GAB7.



Genomes with Antimicrobial Resistance phenotype

This figure shows the existing antimicrobial resistance phenotype from the genomes.

