

# **Targeting drug-resistant enteric bacteria *in vivo* using live engineered probiotics**

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# There is an urgent need for new antimicrobial compounds to target drug-resistant bacteria!

## Priority 1: CRITICAL<sup>#</sup>

*Acinetobacter baumannii*, carbapenem-resistant

*Pseudomonas aeruginosa*, carbapenem-resistant

*Enterobacteriaceae\**, carbapenem-resistant, 3<sup>rd</sup> generation  
cephalosporin-resistant

## Priority 2: HIGH

*Enterococcus faecium*, vancomycin-resistant

*Staphylococcus aureus*, methicillin-resistant, vancomycin  
intermediate and resistant

*Helicobacter pylori*, clarithromycin-resistant

*Campylobacter*, fluoroquinolone-resistant

*Salmonella* spp., fluoroquinolone-resistant

*Neisseria gonorrhoeae*, 3<sup>rd</sup> generation cephalosporin-resistant,  
fluoroquinolone-resistant

# THE LANCET

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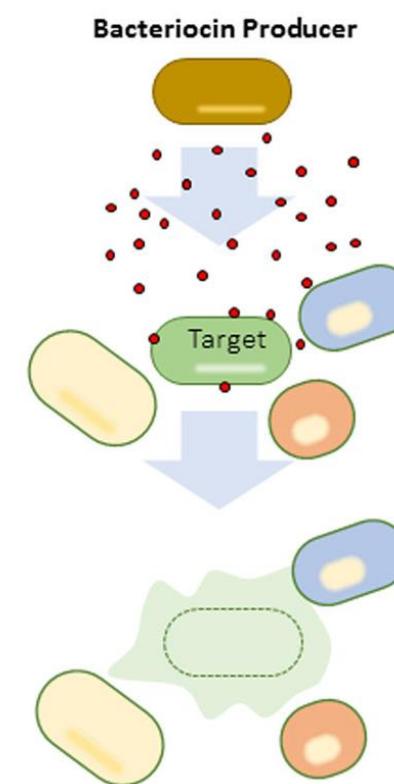
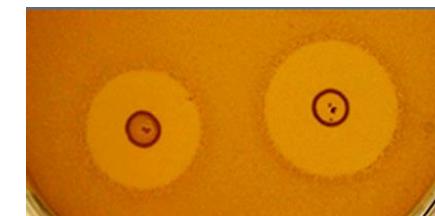
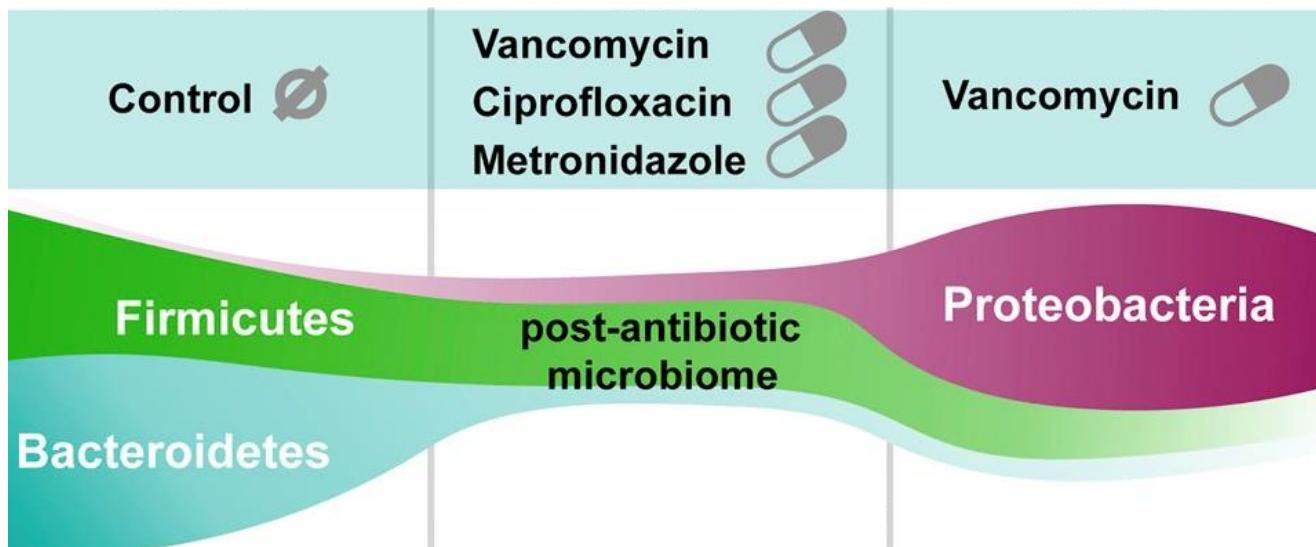
## Global burden of bacterial antimicrobial resistance in 2019: a systematic analysis

Antimicrobial Resistance Collaborators <sup>†</sup> • Show footnotes

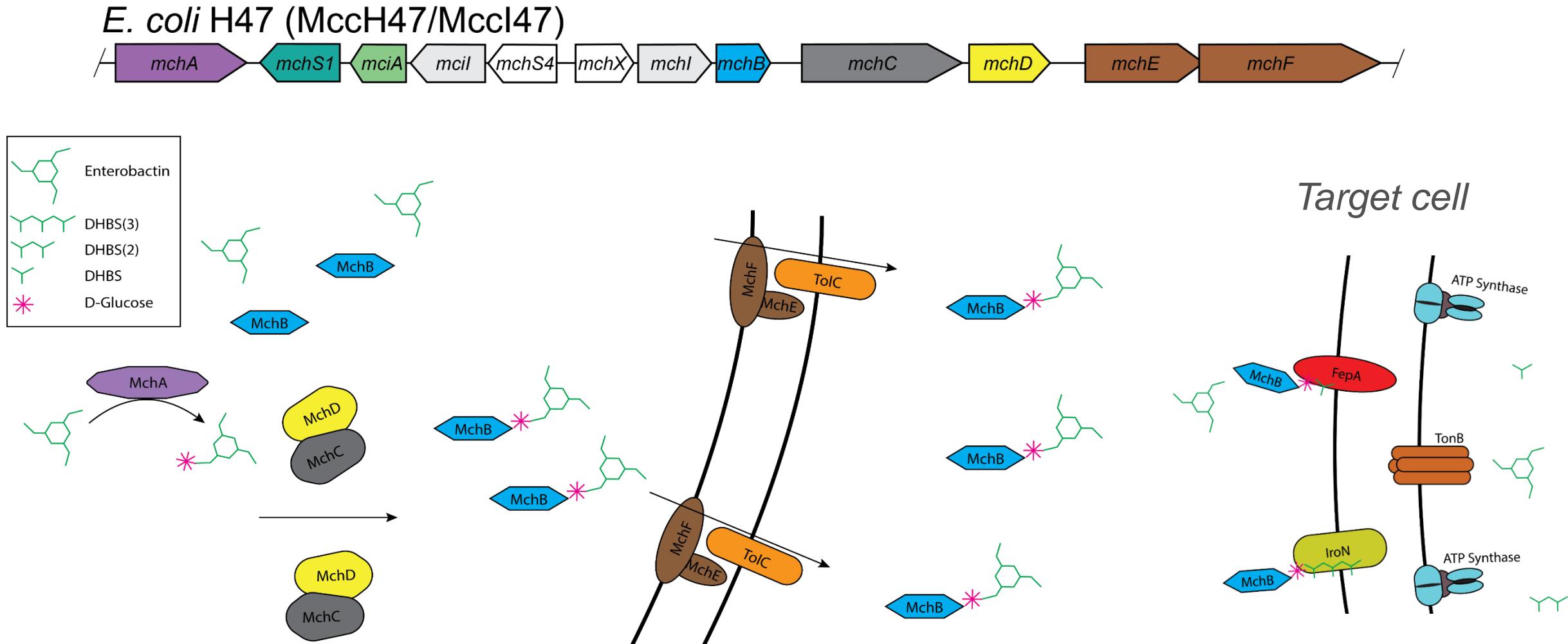
ower respiratory infections accounted for more than 1·5 million deaths associated with resistance in 2019, making the most burdensome infectious syndrome. The six leading pathogens for deaths associated with resistance (*Escherichia coli*, followed by *Staphylococcus aureus*, *Klebsiella pneumoniae*, *Streptococcus pneumoniae*, *Acinetobacter baumannii*, and *Pseudomonas aeruginosa*) were responsible for 929 000 (660 000–1 270 000) deaths attributable to AMR and 3·57 million (2·62–4·78) deaths associated with AMR in 2019. One pathogen–drug combination, meticillin-resistant *S aureus*, caused more than 100 000 deaths attributable to AMR in 2019, while six more each caused

# The Drawbacks of Antibiotics

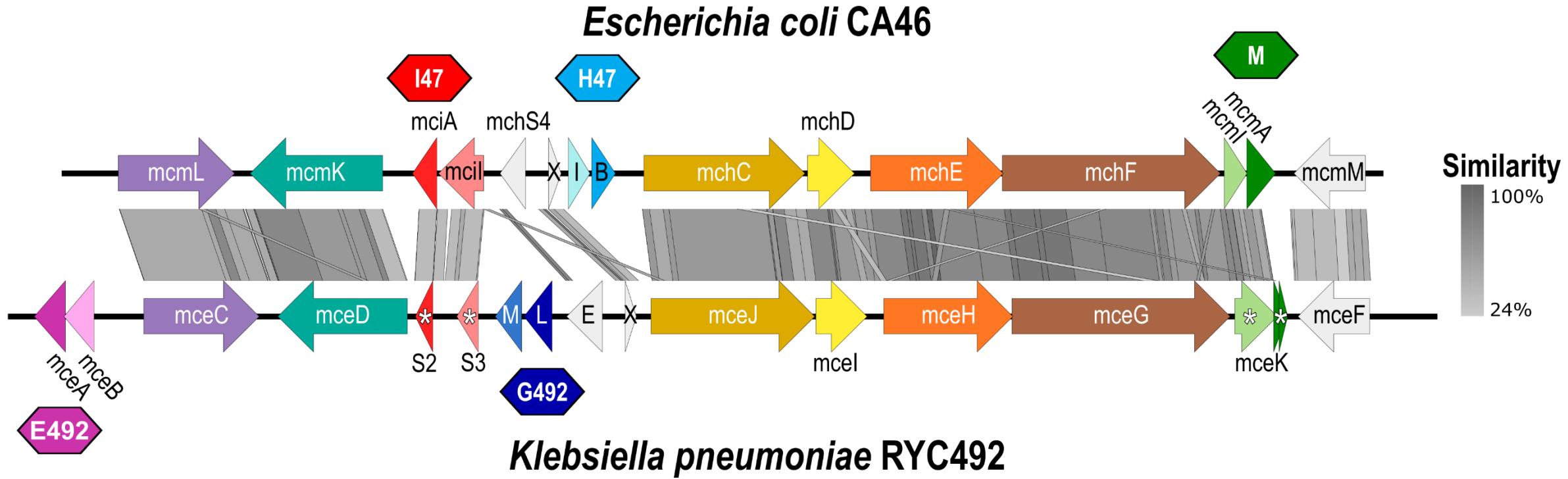
1. Broad spectrum
2. Systemic application



# Class IIb Microcins – Trojan Horse AMPs



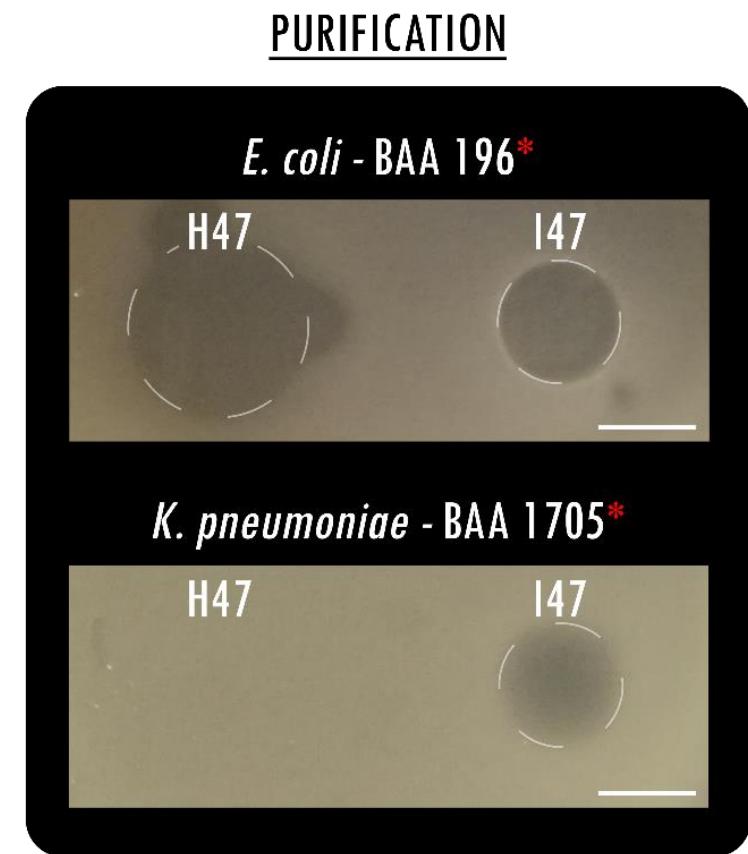
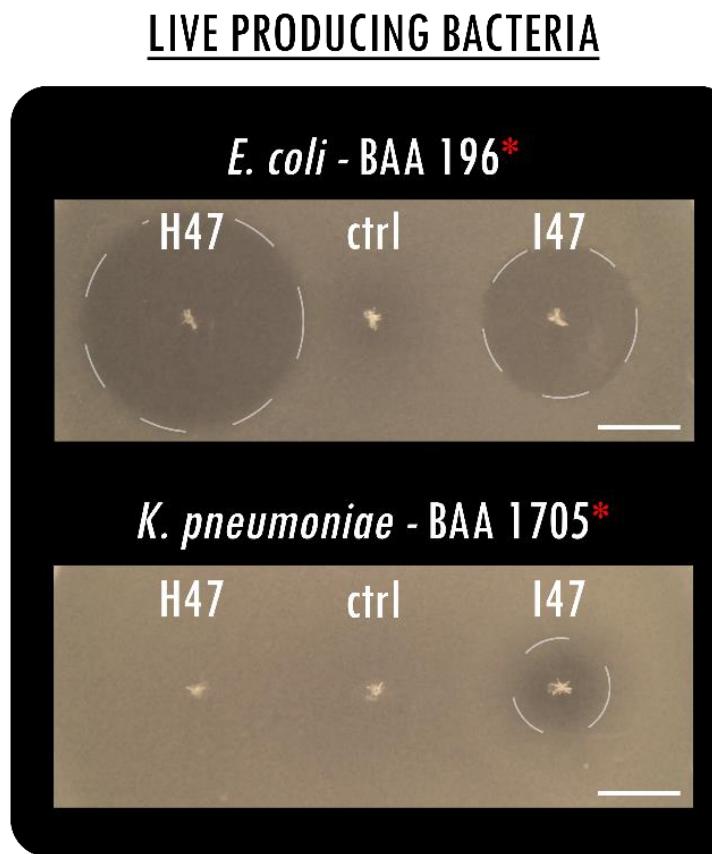
# Class IIb Microcins – Trojan Horse AMPs



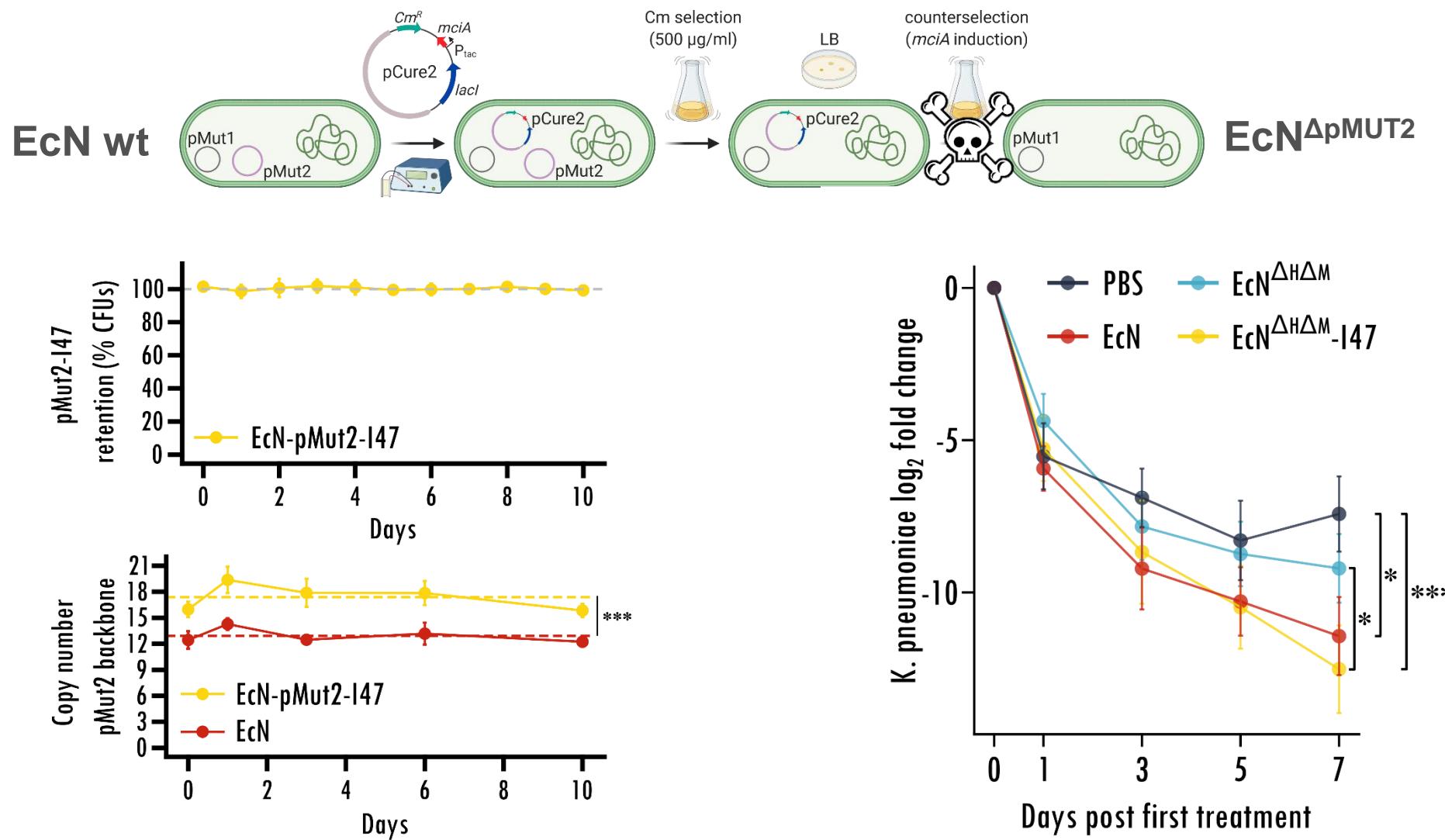
# Narrow-Spectrum Antimicrobials

Bacterial species	Strain	H47 ( $\mu\text{M}$ ) <sup>3</sup>	I47 ( $\mu\text{M}$ ) <sup>2</sup>
<i>Enterobacter cloacae</i>	BAA 2341	>113	17
<i>Escherichia coli</i>	25922	5	0.2
<i>Escherichia coli</i>	BAA 196	2	0.6
<i>Escherichia coli</i>	DH5 $\alpha$	1	0.3
<i>Klebsiella oxytoca</i>	51983	>113	>28
<i>Klebsiella oxytoca</i>	700324	>113	>28
<i>Klebsiella pneumoniae</i>	BAA 1705	>113	5
<i>Klebsiella pneumoniae</i>	BAA 2146	>113	4
<i>Klebsiella pneumoniae</i>	BAA 2342	>113	2
<i>Klebsiella pneumoniae</i>	BAA 2524	>113	2
<i>Proteus mirabilis</i>	29906	5	>28
<i>Salmonella Typhimurium</i>	19585	9	1
<i>Salmonella Typhimurium</i>	29630	7	1
<i>Salmonella Typhimurium</i>	BAA 190	13	2
<i>Salmonella Typhi</i>	700931	11	ND
<i>Salmonella Typhi</i>	19214	13	ND
<i>Shigella flexneri</i>	2457T	2	0.1
<i>Shigella flexneri</i>	M90T	4	0.1

Members of *Staphylococcus*, *Acinetobacter*, and *Pseudomonas* were tested but MICs exceeded 113  $\mu\text{M}$ . Multidrug-resistant isolate

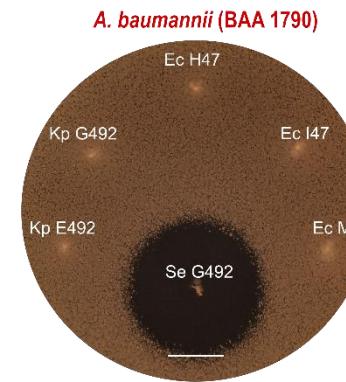
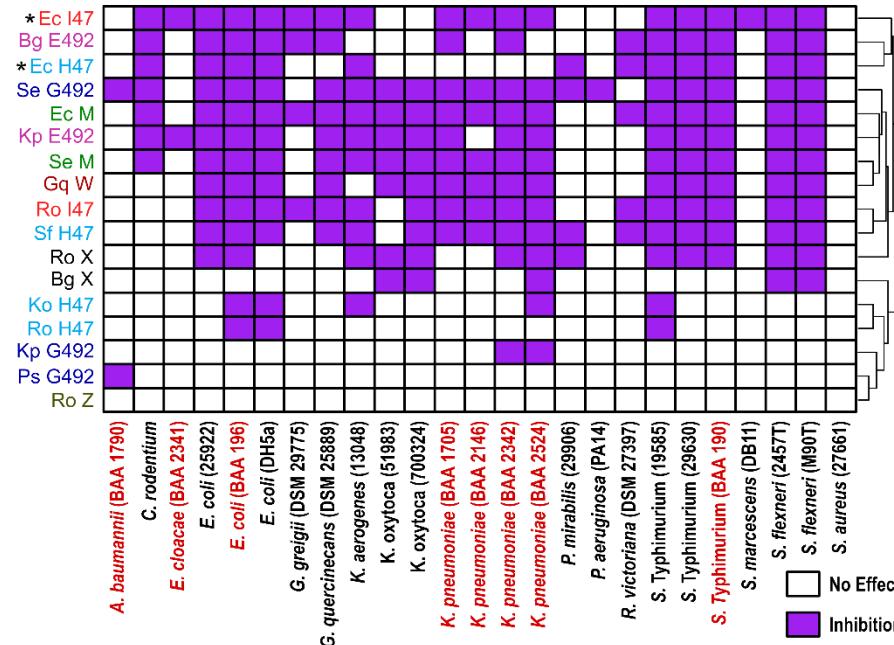
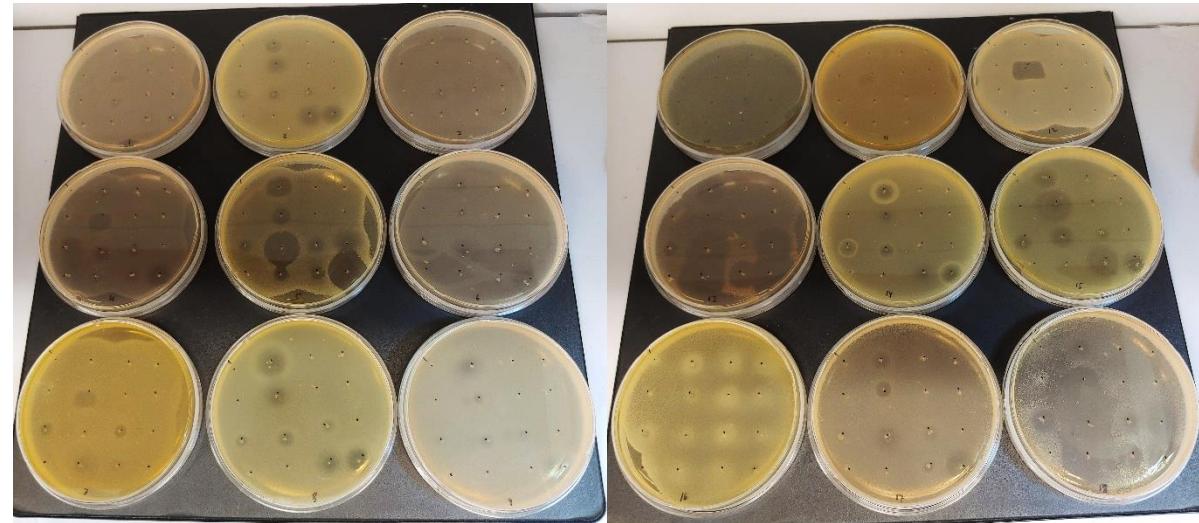


# Selective Reduction of *K. pneumoniae* Colonization

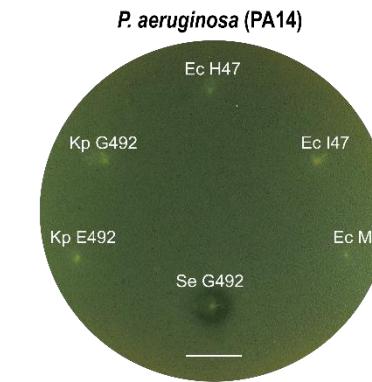


# Identification of Potent Novel Class IIb Microcins

	1	5	10	15	-30	-25	-20	-15	-10	-5	-1		
Kp E492A	M	R	E	I	S	Q	K	D	L	A	F	G	A
Bg E492A	M	R	A	L	N	V	Y	E	I	K	M	A	A
Kp G492A	M	R	A	L	T	E	N	D	F	A	V	S	G
Se G492A	M	R	A	L	T	D	N	E	V	F	S	V	G
Ps G492A	M	R	A	L	S	A	N	D	L	L	S	V	G
Ec H47A	M	R	E	I	T	E	S	Q	L	R	Y	I	S
Sf H47A	M	K	E	L	T	S	S	Q	L	N	Y	I	S
Ko H47A	M	R	E	L	T	Q	Y	Q	M	E	N	V	G
Ro H47A	M	R	E	L	T	Q	D	Q	I	E	N	V	G
Ec I47A	M	R	E	I	S	D	N	M	L	D	S	V	K
Ro I47A	M	R	E	L	D	V	K	M	L	A	F	K	G
Gq WA	M	R	E	L	S	M	L	D	I	T	L	A	K
Bg XA	M	R	E	I	S	H	V	E	L	S	A	I	S
Ro XA	M	I	P	I	S	D	T	E	L	S	M	I	S
Ro ZA	M	R	Q	L	T	E	S	E	L	V	A	S	G
Ec MA	M	R	K	L	S	E	N	I	K	Q	I	S	G
Se MA	M	R	N	L	T	L	N	E	L	K	S	I	S



*A. baumannii* (BAA 1790)



*P. aeruginosa* (PA14)

Mortzfeld *et al.*, under review

# Acknowledgements



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**UMass Chan**  
MEDICAL SCHOOL



Bucci Lab

**Poster Session C**  
**Saturday 12/09**  
**4:35pm – 6:00pm**

Reboldi Lab

Andrea Reboldi  
Simona Ceglia



National Institute of  
Allergy and  
Infectious Diseases



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