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## **Supplemental Information**

## **Discovery of a Novel DNA Gyrase-Targeting**

## Antibiotic through the Chemical Perturbation

## of Streptomyces venezuelae Sporulation

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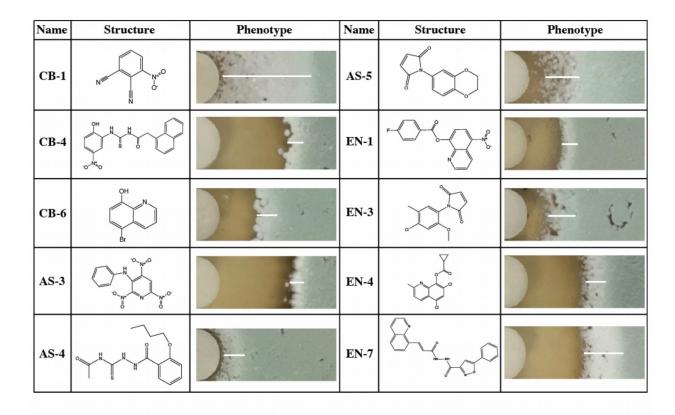
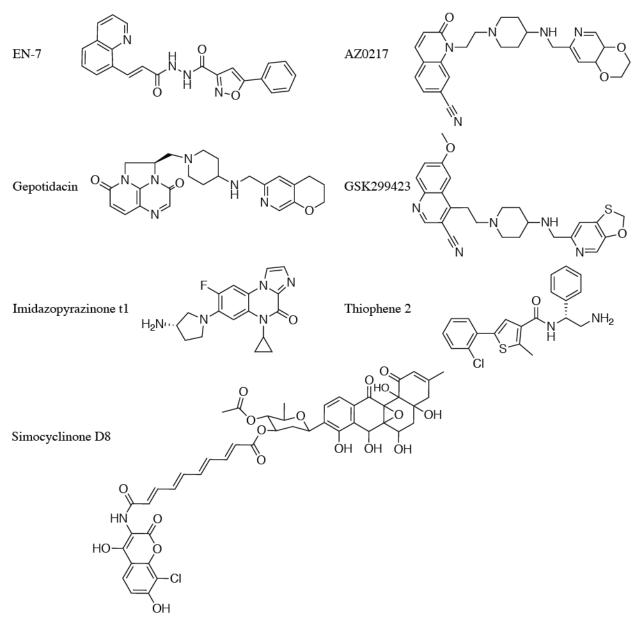
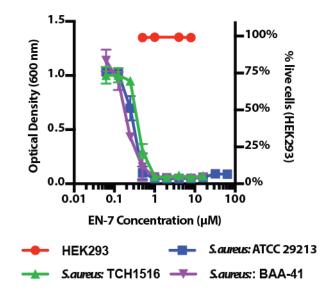


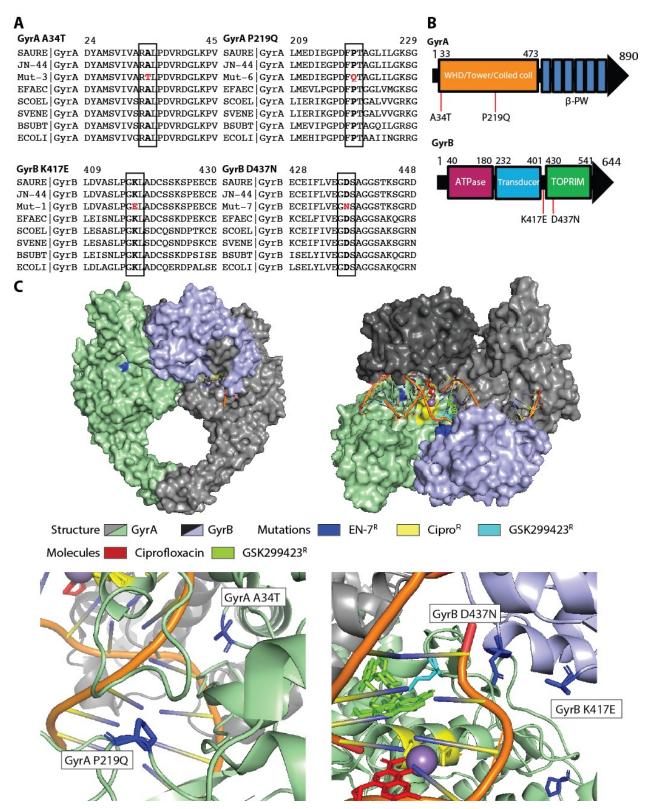
Figure S1, related to Figure 1. Chemical structures and inhibition of *S. venezuelae* sporulation by the screening hits. 10  $\mu$ L of each molecule was added to the drug disk, placed on a lawn of *S. venezuelae* spores and incubated at 30 °C for 48 hours before imaging. The EN-1 and AS-5 stocks were 10 mM while the remaining were at 2.5 mM. A white horizontal line has been added for visual reference.



**Figure S2, related to Figure 2**. Chemical structures of EN-7 with other investigational gyrase inhibitors

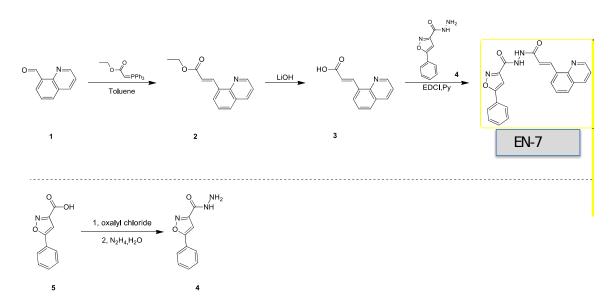


**Figure S3, related to Table 1.** EN-7 inhibits growth of Gram-positive *S. aureus* while having no effect on human cell lines, such as HEK293.



**Figure S4, related to Table 2.** Analysis of EN-7-resistance gyrase mutations. (A) Amino acid alignment of the two GyrA and two GyrB mutations found in the EN-7 resistant *S. aureus* strains against published *S. aureus* (SAURE), parent strain (JN-44), *Enterococcus faecalis* (EFAEC), *Streptomyces coelicolor* (SCOEL),

Streptomyces venezuale (SVENE), Bacillus subtilis (BSUBT), and Escherichia coli (ECOLI) sequences. (B) Location of EN-7 resistant mutations on linear GyrA and GyrB domain structure. (C) Location of EN-7 resistant mutations mapped to a published gyrase crystal structure. The structural information was created by overlaying a *S. aureus* gyrase structure with GSK299423 (2XCS) and a *S. aureus* gyrase structure with ciprofloxacin (2XCT). Ciprofloxacin is depicted in the structure as red while GSK299423 is green. Resistance determinants for EN-7 (blue), ciprofloxacin (yellow), and GSK299423 (teal) are also depicted.



**Figure S5, related to STAR Method, Synthesis and characterization of EN-7** 

Strain	C0117	C0023	C0112	C0017	C0032	C0018	C0019	C0024		
MIC (µM)	> 128	-	4	-	> 128	> 128	-	-		
Resistance elements								-	Product	Inhibit ed antibiot ic s
parE P585S									Modified topoisomerase IV	No reference
ErmA									Ribosomal RNA methyltransferase	Macrolides
ANT(4')-Ib									Nucleotidyltransferase	Aminoglyclosides
ANT(9)-Ia									Nucleotidyltransferase	Aminoglyclosides
blaZ									Beta-lac tamases	Beta-lactams
SAT-4									Acetyltransferase	N uc leoside s
mphC									Phosphotransferase	Macrolides
APH(3')-IIIa									Phosphotransferase	Macrolides
bcrA									ABC efflux pump	Bacitracin
gyrB K66Q						Γ			Modified gyrase	No reference
gyrA R246C									Modified gyrase	No reference
gyrA T457A									Modified gyrase	No reference
gyrA D459N					F		F	Γ	Modified gyrase	No reference
gyrA S85P									Modified gyrase	Fluoroquinolones
gyrA S84L					F				Modified gyrase	Fluoroquinolones
mecI									PBP2A	Be ta-la cta ms
mprF					Γ	Γ	T		Modified phosphatidylglycerol	Daptomycin
tet38					Γ	Γ	Γ	Γ	MFS efflux pump	Te trac yc line
Sav1866					Γ	Γ	Γ	Γ	ABC efflux pump	Multidrug
norB					Γ	Γ			MFS efflux pump	Fluoroquinolones & Tetracycline
norA						F			MFS efflux pump	Fluoroquinolones & Tetracycline
murA					F	F	F	F	UDP-N-acetylglucosamine enolpyruvyl transferase	Fosfomycin
mgrA						F			MFS efflux pump	Multidrug
mepR					F	F	F		MATE transporter	Tetracycline
mepA						F	F		MATE transporter	Tetracycline
mecRI					F	F	F	F	PBP2A	Be ta-la cta ms
mecC					F	F	F	F	PBP2A	Beta-lactams
lmrB							T		ABC efflux pump	Lincosamides
EF-Tu						T	T		Elongation factor Tu	Kirromyein
cls									Cardiolipin synthetase	Daptomycin
dfrC						T	T		Dihydrofolate reductase	Trimethoprim
ileS							T		Isoleucyl-tRNA synthetase	Mupirocin
arlS									MFS efflux pump	Fluoroquinolones
alaS									Alanyl-tRNA synthetase	Novobiocin
arlR									MFS efflux pump	Fluoroquinolones

**Table S1, related to Table 1.** EN-7 inhibits growth of extensively resistant *S. aureus* clinical strains. Blue boxes indicates that the corresponding antibiotic resistance gene was found within the clinical strain's genome. A white box indicates that the gene was absent in the genome.