Supplemental Material

Table S1: Data collection and refinement statistics for the *S. aureus* FabI, 3'NADPH , AFN-1252 ternary complex

Data collection	
Space Group	I4122
No. of molecules in AU	1
Resolution (Å)	50.0 - 1.80 (1.85 - 1.80)
a, b, c (Å)	a = b = 126.3, c = 80.9
α, β, γ (°)	90, 90, 90
Unique data	30598 (3003)
Completeness	100 (99.9)
Average redundancy	9.7 (4.5)
R_{sym}	9.6 (52.9)
$<I/\sigma(I)>$	38.8 (3.4)
Refinement statistics	
R-factor[a]	16.9
R_{free}	20.2
Average main chain / side chain B-factor (Å^2)	21.0
Average solvent / 3'NADPH / AFN-1252 B-factor (Å^2)	36.3 / 22.2 / 23.5
Covalent bond lengths (Å)	0.013
Bond angles (°)	1.702
[a]R-factor – Σhkl‖Fobs| - |Fcalc‖/Σhkl|Fobs Fobs|	

AFN-1252 – Mode of action, *in vitro* activity and *in vivo* efficacy of a selective anti-staphylococcal FabI inhibitor. N. Kaplan et al.

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Table S2. Oligonucleotide primers used for polymerase chain amplification and sequencing of *S. aureus* and *S. epidermidis* FabI genes.

Name of Primer	Sequence 5'→ 3'
S. aureus FABI FOR 1	CCCATTCGGAGGAGACATCA
S. aureus FABI FOR 2	GGGAATCGCTAATAAGCGTAGT
S. aureus FABI FOR 3	GCATTAGACTTAGGTCCTGA
S. aureus FABI REV 1	CCTTCAAGTTGGTGTGCAAT
S. aureus FABI REV 2	CAAGTGGCGTTACAGGTGAA
S. aureus FABI REV 3	GATGTTGGCAATATTGATGGTG
S. epidermidis FABI FOR 1	CCCAGTTGGTGTTGTTGAAG
S. epidermidis FABI FOR 2	GCGAATAAACGTAGTATCGCA
S. epidermidis FABI FOR 3	AGCAAGTTTAGAGGCGAATG
S. epidermidis FABI REV 1	CTGCAACAAGAATGAGTGTG
S. epidermidis FABI REV 2	GTGATCTTTCAAGTGGTGTAAC
S. epidermidis FABI REV 3	GTAGGCCAGATTGATGGTGT