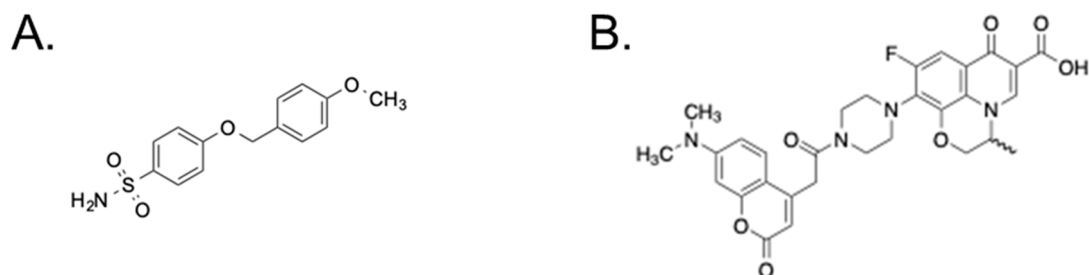


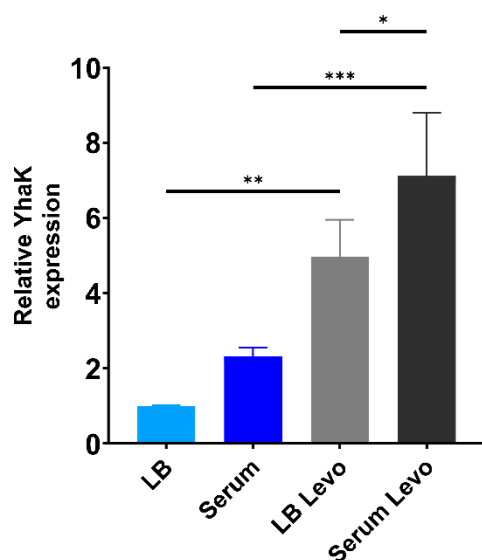
## Supplementary Materials

### Supplemental Figure S1.



**Supplemental Figure S1. Chemical structures.** Shown are the structures of DMACA-Olfoxacin (Panel A) and AE0003 (Panel B).

### Supplemental Figure S2.



**Supplemental Figure S2. Quantitative real time PCR measures of YhaK transcription.** Shown are the relative expression levels of *yhaK* within *A. baumannii* strain 98-37-09 during growth in LB or human serum  $\pm$  0.2  $\mu\text{g ml}^{-1}$  levofloxacin. All data normalized to LB grown

cells in the absence of antibiotic. Standard deviation shown; statistical difference (One-way ANOVA, \*  $P \leq 0.05$ , \*\*  $P \leq 0.01$  and \*\*\*  $P \leq 0.001$ ).

## Supplemental Figure S3

YhaK	--MITRTARQCGQADYGWLQARYTFSFGHY--FDPKLLGYASLRVLNQEV LAPGAAFPQRTYPKVDILNVILDG-EAEYRDSSEGNHVQA	85
YhhW	--MIYLRKANERGHANHGWLDSWHTFSFANY--YDNFMGFSA LRVINDDVIEAGQGFTHPHKDMELITYVLEG-TVEHQDSMGNKEQV	85
A1S_3277	MKKFLGAYQNNHMHVVDGFPVYNLFSYDRLGQTLSPFLLDYAAPYNFSPTEQQGVGSHPHRGFE TVTIA YQG-EVTHKDSGGGTI	89
hPirin	-----MGSSKKVTL SVLSREQSEG VGARVRRSIGRP ELKNLDPFLLFDEFKGGRPGGFPDHPHRGFE TVSYLLEGGSMAHEDFCGHTGKM	85
YhaK	SAGEALLSTQPGVSYSEHN-LSKDKP---LTRMQLWLDACPQRENPLIQKLALNMGK-QQLIASPEG-----AMGSLQLRQQ	158
YhhW	PAGEFQIMSAGTGIRHSEYN-PSSTER---LHLYQIWIIMPEENGITPRYEQRRFD AVQ GKQLV LSPDA-----RDGSLKVHQD	159
A1S_3277	KTGDVQWMTAGAGVLHEEFHSPFEAEHGGLFEMVQLWVNLPSHSMTPGKYQAIEAKDIPDIALDEHGSHLRVIAGEYADAKGAATTFS	179
hPirin	NPGLQWMTAGRGILHAEMPCSEEP AHG-----LQLWVNLRSSEKMVEPQYQELKSEEIPKPSKDGVTVAVISG--EALGIKSKVYTRTP	168
YhaK	VVLHHIVLDKGESANFQLHGPR-AYLQSIHGKFHALTHHEEKAALTCGDGAFIR-DEANITLVADSPRLALLIDL PV-----	246
YhhW	MELYRWALLKDEQSVHQIAAERRVWIQVVKGNVTIN-----GVKASTSDGLAIW-DEQAISIHADSDSEVLLFDLPV-----	243
A1S_3277	LNVDGKLVKGQKHTLYVPEGHTTLVVVLEGAVVVN---DTNRLEGKTVAILSR-EGVEFSLNAEEDTKFLVLTGQPLNEPIEGYGP FVM	265
hPirin	TLYLD FKLDPGAKHSQPIPKGWT SFIYTISGDVYIGPDDAQKIEPHHTAVLGEGBSVQVENKDKPRSHFVLIAGEPLREPVIQHGP FVM	258
YhaK	-----	233
YhhW	-----	231
A1S_3277	NTKAEIMEAINDFN RGKFGSIMQEG-----	290
hPirin	NTNEEISQAILDFRNAKNGFERAKTWKSKIGN	290

**Supplemental Figure S3. ClustalW alignment of *Escherichia coli* pirin-like protein YhaK, *E. coli* 2,3 dioxygenase YhhW, human pirin protein (hPirin), and *A. baumannii* YhaK pirin-like protein (A1S\_3277).** Matching amino acid residues are highlighted in yellow, while the location of four conserved metal binding residues (His57, His59, His101, and Glu103) are highlighted by red boxes and corresponding notation. Amino acid positions are from *E. coli* YhhW.