

Fig. S1. Cytotoxicity of the compounds towards J774 macrophages. J774 cells were incubated with 0.5 % DMSO or compounds at 50 μ M for 24 h. Data are presented as means \pm SD of three wells from one representative experiment of three.

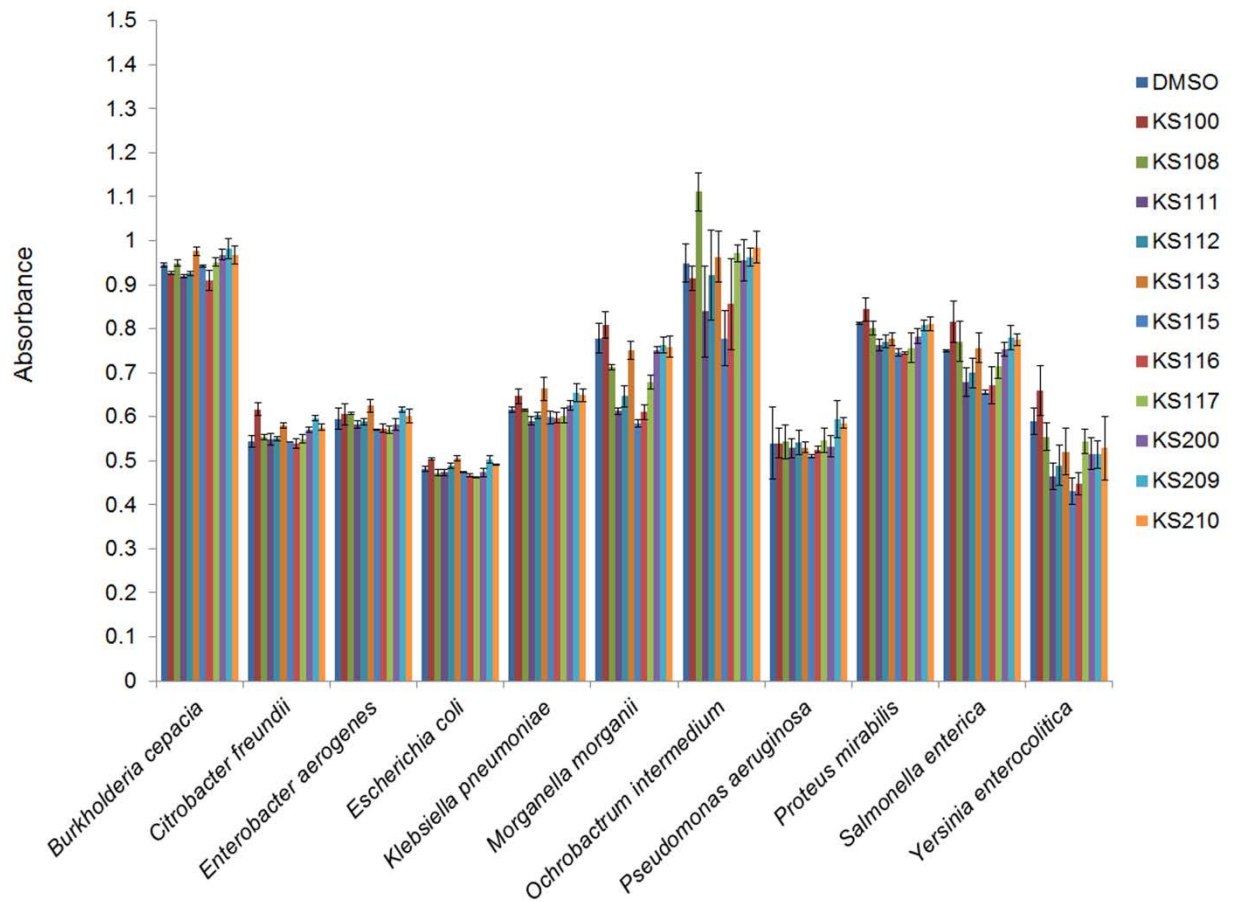


Fig. S2. Effects of the compounds on the growth of strains of selected Gram-negative species. Bacterial strains were incubated with 0.5 % DMSO or compounds at 50 μ M for 18 h. Experiments were carried out in triplicates, and the means \pm SD from one representative experiment of three are shown. The addition of compounds did in no case significantly affect the growth of the bacterial strains in comparison to cultures with DMSO only ($P > 0.05$).

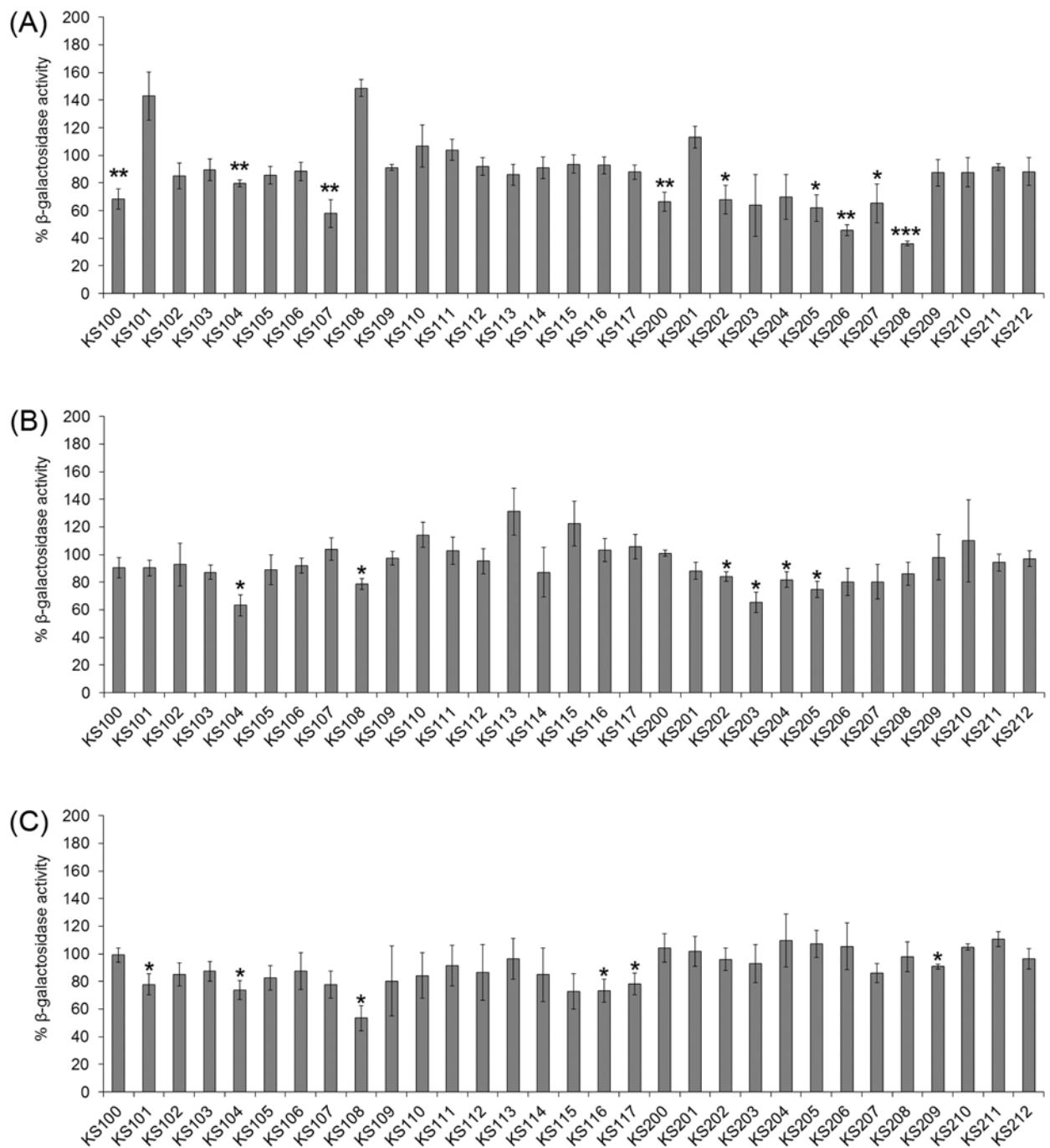


Fig. S3. KS100 and KS200 and the analogues inhibitory effects on the Bacterial-2-hybrid interactions between VipA-VipB (A), AaiA-AaiB (B), or HsiB2-HsiC2 (C) were tested by assessing the β-galactosidase activity and expressed as percentages relative to the control with DMSO only. Data are presented as means ± SD of three wells from one representative experiment of three. * $P < 0.05$, ** $P < 0.01$ and *** $P < 0.001$.

Table S1. Strains and plasmids used in this study.

Strain or plasmid	Relevant genotype or phenotype	Reference
Strain		
<i>Escherichia coli</i>		
KDZif1ΔZ	<i>araD(gpt-lac)5, rpsL (Str^R), ΔspoS3::cat (Cm^R) [F' lacI^q (Z321[-61] lacZYA*) Km^R]</i>	(1)
CCUG 10979	clinical isolate	http://www.ccug.se
536	UPEC isolate (O6:K15:H31), Sm ^R	(2)
363	clinical isolate, Km ^R	this study
Top10	F- <i>mcrA</i> , Δ(<i>mrr-hsdRMS-mcrBC</i>), φ80 <i>lacZ</i> ΔM15, Δ <i>lacX74</i> , <i>recA1</i> , <i>deoR</i> , <i>araD139</i> , Δ(<i>ara-leu</i>)7679, <i>galU</i> , <i>galK</i> , <i>rpsL</i> (Str ^R), <i>endA1</i> , <i>nupG</i>	Invitrogen
DH5α F'IQ	F-φ80 <i>lacZ</i> ΔM15 Δ(<i>lacZYA-argF</i>) U169 <i>recA1 endA1 hsdR17</i> (rk-, mk+) <i>phoA</i> <i>supE44 λ- thi-1 gyrA96 relA1/F' proAB+</i> <i>lacIqZ</i> ΔM15 <i>zzf::Tn5</i> [Km ^R].	Invitrogen
<i>Vibrio cholerae</i>		
V52	O37 serotype	(3)
<i>Burkholderia cepacia</i>		
CCUG 13226	clinical isolate	http://www.ccug.se
<i>Citrobacter freundii</i>		
CCUG 418	clinical isolate	http://www.ccug.se

Enterobacter aerogenes

CCUG 1429 clinical isolate <http://www.ccug.se>

Klebsiella pneumonia

CCUG 225 clinical isolate <http://www.ccug.se>

Morganella morganii

CCUG 6328 clinical isolate <http://www.ccug.se>

Ochrobactrum intermedium

CCUG 39736 clinical isolate <http://www.ccug.se>

Proteus mirabilis

CCUG 26767 clinical isolate <http://www.ccug.se>

Pseudomonas aeruginosa

1824 clinical isolate (4)

PAK wild type (5)

Salmonella enterica

CCUG 19369 clinical isolate <http://www.ccug.se>

Yersinia enterocolitica

CCUG 8233 clinical isolate <http://www.ccug.se>

Plasmid

pCR®4-TOPO® TA cloning vector, Km^R, Cb^R Invitrogen

pACTR-AP-Zif Zif/ω Bacterial 2-Hybrid reporter vector, (1)
Tet^R

pJEB794 pACTR-AP-Zif encoding VipA, Tet^R (6)

pACTR-MglA-Zif	pACTR-AP-Zif encoding MglA, Tet ^R	(7)
pMOL135	pACTR-AP-Zif encoding IglA, Tet ^R	(8)
pMOL139	pACTR-AP-Zif encoding IglB, Tet ^R	(8)
pSK201	pACTR-AP-Zif encoding ECP0238, Tet ^R	this study
pSK202	pACTR-AP-Zif encoding PA1657, Tet ^R	this study
pBRGP ω	Zif/ ω Bacterial 2-Hybrid reporter vector, Cb ^R	(1)
pJEB799	pBRGP ω encoding VipB, Cb ^R	(6)
pBRSpA- ω	pBRGP ω encoding SspA, Cb ^R	(7)
pMOL133	pBRGP ω encoding IglA, Cb ^R	(8)
pMOL134	pBRGP ω encoding IglB, Cb ^R	(8)
pSK203	pBRGP ω encoding ECP0237, Cb ^R	this study
pSK204	pBRGP ω encoding PA1658m, Cb ^R	this study

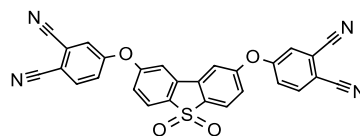
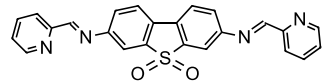
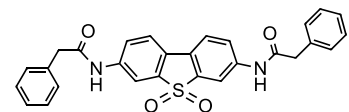
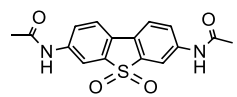
Table S2. Oligonucleotides used in this study

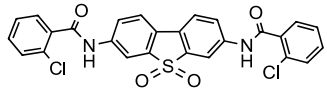
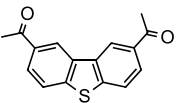
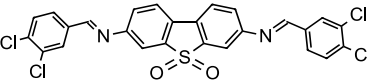
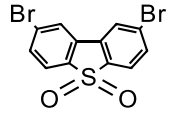
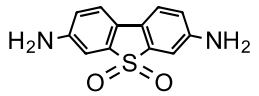
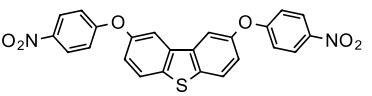
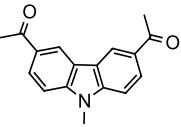
Insert	Oligonucleotide pairs
ECP0237	ECP_0237_F: 5'- <i>CAT ATG TCA GTA AAG GAA GAA ATT GC</i> -3' (<i>NdeI</i>) and ECP_0237_NotI_R: 5'- <i>GCG GCC GCT TCC TTA TCC AGT CGT CC</i> 3' (<i>NotI</i>)
ECP0238	ECP_0238_F: 5'- <i>CAT ATG ATA GCA GTA AAA GAT ATA ACT GAT</i> -3' (<i>NdeI</i>) and ECP_0238_NotI_R: 5'- <i>GCG GCC GCT TTC TGA ACG GCG ATA CC</i> -3' (<i>NotI</i>)
PA1657	PA1657_F: 5'- <i>CAT ATG ATG GCC AAA GAA GGC TCG GTA</i> -3' (<i>NdeI</i>) and PA1657_NotI_R: 5'- <i>GCG GCC GCG GCG TCC TGG GAG GGG</i> -3' (<i>NotI</i>)
PA1658m	PA1658_F: 5'- <i>CAT ATG ATG AGC ACC AGT GCC GCA CAG</i> -3' (<i>NdeI</i>) and PA1658_NotIm_R: 5'- <u>CTT CG GA CCG GCG GCT GCC ACG</u> -3' PA1658_NotIm_F5'- <u>GCG CCA TTC GTG GCA GCC GCC</u> -3' and PA1658_NotI_R: 5'- <i>GCG GCC GCC TCT TTG TCC AGC TTG CCG A</i> -3' (<i>NotI</i>)

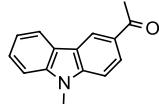
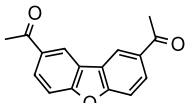
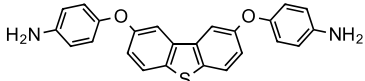
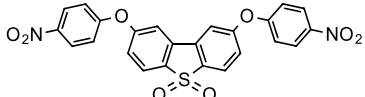
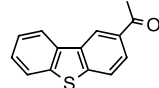
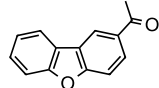
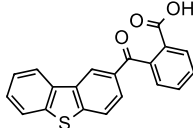
The oligonucleotide sequences in italics represent the incorporated *NdeI* and *NotI* restriction sites used for cloning of the PCR amplified DNA fragments.

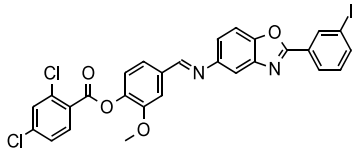
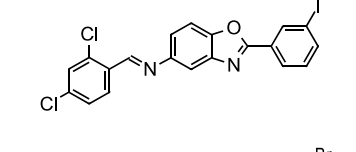
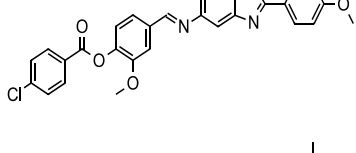
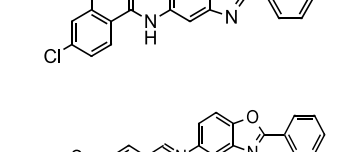
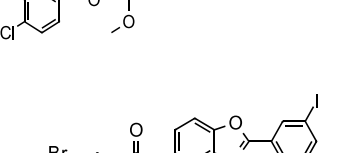
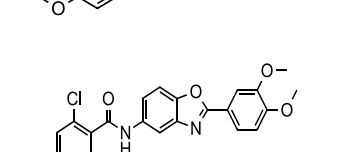

Underlined sequences indicate the complementary sequences in the overlap PCR primers. In the primers that were used to generate amino acid substitutions, the nucleotides substituted are indicated in boldface.

Table S3. Structures, *in silico* calculations, effects on VipA-VipB interaction, Hcp secretion, phospholipase activity and cytotoxicity.

ID	logP ^a	logS ^b	Caco-2 ^c	MDCK ^d	SASA ^e	B2H (%) ^f	Hcp secretion ^g	PLA ₁ (%) ^h	LDH release(%) ⁱ	Cytotoxicity ^j	Structure
KS100	1.4	-7.0	10	0	750	68.4±7.4 ^{***k}	4	42.5±3.4	13.4±0.6	1	
KS101	3.7	-5.8	430	200	758	142.9±17.3 [*]	3	96.9±1.8	16.2±1.2 ^{**}	3	
KS102	4.1	-6.8	230	100	821	85.0±9.3	4	80.2±5.9	37±3.6 ^{***}	5	
KS103	0.3	-3.2	120	50	603	89.6±7.9	5	42.2±5.0	14.6±0.7 [*]	4	

KS104	4.1	-7.2	230	370	798	$79.6 \pm 2.4^{**}$	2	86.1 ± 1.2	$18.2 \pm 3.1^*$	4	
KS105	2.7	-3.7	1000	890	518	85.6 ± 6.6	5	57.1 ± 2.9	$19.2 \pm 0.5^{***}$	4	
KS106	7.0	-9.6	1100	10000	858	88.4 ± 6.8	4	52.6 ± 3.1	12.6 ± 0.6	4	
KS107	2.7	-5.9	1500	5300	472	$57.9 \pm 10.2^{**}$	2	48.4 ± 3.3	14.7 ± 1.7	4	
KS108	0.3	-2.7	100	40	445	$148.5 \pm 6.1^{***}$	5	88.4 ± 2.2	14.6 ± 3.1	1	
KS109	5.7	-8.9	140	110	726	91.1 ± 2.3	3	37.6 ± 4.0	$14.7 \pm 1.1^*$	3	
KS110	4.1	-3.9	980	490	535	106.7 ± 15.2	4	98.0 ± 0.4	$66.2 \pm 8.1^{***}$	5	

KS111	3.4	-3.7	3100	1700	473	103.9±7.8	4	90.1±1.6	15.4±0.8*	1	
KS112	2.1	-3.1	1000	500	495	72.0±6.2	4	85.8±0.1	14.4±1.2	1	
KS113	5.0	-7.3	670	570	678	85.9±7.8	4	16.9±4.7	14.1±1.3	1	
KS114	3.2	-5.7	20	10	743	90.9±7.8	4	40.3±3.6	14.8±2.0	4	
KS115	3.4	-3.7	3200	3100	456	93.6±6.5	4	84.2±1.4	14.4±2.9	1	
KS116	2.7	-3.2	3200	1700	432	72.7±6.1	4	79.6±0.6	14.7±1.0*	1	
KS117	4.2	-5.5	140	180	575	87.8±5.0	4	98.9±1.7	13.7±1.3	1	

KS200	7.6	-11.5	2700	10000	896	66.4±6.8**	2	94.1±0.7	24.5±3.0**	2	
KS201	6.6	.8.1	5600	10000	684	113.2±8.0	1	41.2±6.1	19.0±1.8**	2	
KS202	7.2	-10.0	2600	8900	929	67.7±10.4*	3	87.7±0.9	23.9±1.1***	5	
KS203	5.6	-9.1	2600	10000	682	63.7±22.3	3	59.9±4.4	44.1±2.9***	5	
KS204	7.2	-10.7	2600	9800	893	69.8±16.1	3	53.9±4.0	22.7±2.9**	4	
KS205	5.8	-10.3	2400	10000	732	61.9±9.6*	2	55.8±6.8	49.9±1.6***	5	
KS206	4.6	-6.3	2600	2700	698	45.7±3.8**	1	48.9±3.1	19.1±1.1***	4	

KS207	5.2	-7.3	2400	7700	702	65.2±13.9*	3	74.3±3.3	54.7±0.8***	5	
KS208	5.1	-7.2	2500	3800	763	36.1±1.9***	2	45.3±4.2	29.5±2.6***	5	
KS209	7.4	-9.5	2500	10000	882	87.3±9.8	3	56.1±2.9	11.4±2.3	1	
KS210	7.2	-9.1	2700	6800	893	87.8±10.7	3	40.8±4.1	12±0.1**	1	
KS211	7.6	-9.9	2700	10000	896	91.4±2.6	2	63.7±0.3	13.5±2.6	3	
KS212	6.1	-9.1	5600	10000	682	88.2±10.0	4	71.0±4.0	24.5±3.0**	5	

^a The octanol/water partition coefficient. A high value indicates a more hydrophobic compound.

^b The water solubility. A high value indicates a water soluble compound.

^c Caco-2 cell membrane permeability. A high value indicates a permeability similar to that of permeable molecules out of 126 drugs (9, 10) (<25 low, >500 marked).

^d MDCK-cell membrane permeability. A high value indicates a permeability similar to that of permeable molecules out of 52 drugs (11) (<25 low, >500 marked).

^e The solvent accessible surface area.

^f Effects on the VipA-VipB interaction. The values of β -galactosidase activity were shown as percentage vs. the control with DMSO only. Means \pm SD values are shown. A low value indicates a strong inhibition.

^g Hcp secretion. A high value indicates a strong inhibition (*i.e.*, no band could be detected in the Western blot analysis).

^h Inhibition of phospholipase A₁ activity. The values of inhibitory effect on phospholipase activity were shown as the control with DMSO only. Means \pm SD values are shown. A high value indicates a strong inhibition.

ⁱ LDH release. The values of LDH release were shown as percentage vs. the control with DMSO only. Means \pm SD values are shown. A high value indicates poor cell membrane integrity. The values of samples treated with DMSO or not treated were 12.6 ± 0.3 % and 10.7 ± 0.5 %, respectively.

^j Cell morphology. A high value indicates that a high proportion of cells showed abnormal morphology (*i.e.* rounding up of the cells and detachment).

^k Significance of β -galactosidase activity and LDH release was determined using a two-tailed t-test (* $P < 0.05$, ** $P < 0.01$, and *** $P < 0.001$).

References

1. **Vallet-Gely I, Donovan KE, Fang R, Joung JK, Dove SL.** 2005. Repression of phase-variable cup gene expression by H-NS-like proteins in *Pseudomonas aeruginosa*. Proc Natl Acad Sci U S A **102**:11082-11087.
2. **Berger H, Hacker J, Juarez A, Hughes C, Goebel. W.** 1982. Cloning of the chromosomal determinants encoding hemolysin production and mannose-resistant hemagglutination in *Escherichia coli*. J. Bacteriol. **152**:1241-1247.
3. **Pukatzki S, Ma AT, Sturtevant D, Krastins B, Sarracino D, Nelson WC, Heidelberg JF, Mekalanos JJ.** 2006. Identification of a conserved bacterial protein secretion system in *Vibrio cholerae* using the *Dictyostelium* host model system. Proc Natl Acad Sci U S A **103**:1528-1533.
4. **Rzhepishevskaya O, Ekstrand-Hammarström B, Popp M, Björn E, Bucht A, Sjöstedt A, Antti H, Ramstedt M.** 2011. The antibacterial activity of Ga³⁺ is influenced by ligand complexation as well as the bacterial carbon source. Antimicrob Agents Chemother **55**:5568-5580.
5. **Bröms JE, Forsberg Å, Francis MS.** 2003. PcrH of *Pseudomonas aeruginosa* is essential for secretion and assembly of the type III translocator. J Infect Dis. **188**:1909-1921.
6. **Bröms JE, Ishikawa T, Wai SN, Sjöstedt A.** 2013. A functional VipA-VipB interaction is required for the type VI secretion system activity of *Vibrio cholerae* O1 strain A1552. BMC Microbiol **13**:96.
7. **Charity JC, Costante-Hamm MM, Balon EL, Boyd DH, Rubin EJ, Dove SL.** 2007. Twin RNA polymerase-associated proteins control virulence gene expression in *Francisella tularensis*. PLoS Pathog **3**:e84.
8. **Bröms JE, Meyer L, Lavander M, Larsson P, Sjöstedt A.** 2012. DotU and VgrG, core components of type VI secretion systems, are essential for *Francisella tularensis* LVS pathogenicity. PLoS One **7**:e34639.
9. **Stenberg P, Norinder U, Luthman K, Artursson P.** 2001. Experimental and computational screening models for the prediction of intestinal drug absorption. J Med Chem **44**:1927-1937.
10. **Yazdaniyan M, Glynn SL, Wright JL, Hawi A.** 1998. Correlating partitioning and caco-2 cell permeability of structurally diverse small molecular weight compounds. Pharm Res **15**:1490-1494.
11. **Irvine JD, Takahashi L, Lockhart K, Cheong J, Tolan JW, Selick HE, Grove JR.** 1999. MDCK (Madin-Darby canine kidney) cells: A tool for membrane permeability screening. J Pharm Sci **88**:28-33.