## Hydramacin-1 in Action – Scrutinising the Barnacle Model

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	MBC	LD90	Aggregation
Gram-negative bacteria			
C. freundii NCTC 9750	7.1	0.9	+
B. cepacia ATCC 17759	>14.3	>14.3	-
<i>E. coli</i> ATCC 25922	0.9	0.2	+
K. pneumoniae ATCC 13883	0.9	0.5	+
P. mirabilis ATCC 21100	14.3	0.9	-
Ps. aeruginosa NCTC 11446	>14.3	14.3	+
S. marcescens NCTC 10211	>14.3	1.8	+
Y. enterocolitca NCTC 11176	0.9	0.2	+
Gram-positive bacteria			
S. aureus ATCC 6538	>14.3	>14.3	+
S. hemolyticus ATCC 29970	1.8	0.9	-
B. megaterium ATCC 14581	0.2	0.1	+
E. faecalis ATCC 29212	14.3	0.9	+
S. epidermidis ATTC 14990	>14.3	>14.3	+
S. hominis ATTC 27844	>14.3	3.6	-
S. pneumoniae ATTC 33400	>14.3	>14.3	-
Str. pyogenes ATCC 12344	>14.3	7.1	+



Figure SI 1



Figure SI 1





Figure SI 1

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**Figure SI 1: Aggregation of bacteria by HM1** – Depicted are the micrographs of several Gramnegative and Gram-positive bacteria in absence (left panels) or presence (right panels) of sub-lethal dosages of HM-1 after 10 min of incubation. HM1 led to the formation of cell aggregates of (a) *C. freundii* NCTC 9750, (b) *K. pneumoniae* ATCC 13883, (d) *Ps. aeruginosa* NCTC 11446, (e) *S. marcescens* NCTC 10211, (f) *Y. enterocolitca* NCTC 11176, (g) *S. aureus* ATCC 6538, (i) *B. megaterium* ATCC 14581, (j) *E. faecalis* ATCC 29212, and (k) *S. epidermidis* ATTC 14990. In comparison, untreated control samples (left panels) show a uniform distribution of bacterial cells. (c) displays *P. mirabilis* ATCC 21100 as representative for Gram-negative bacteria and (h) shows *S. hemolyticus* ATCC 29970 as representative for Gram-positive bacteria which did not show cell aggregation in presence of HM1. Black bar = 100 µm.