Table S3 NewAMP database[1-9]

Sub-set	Name	Sequence	Bacterial Strain	MIC (μg/mL)
NewAMP_E	HJH-5[8]	KKLLRLLKVLLR	*E. coli* ATCC 25922	1.5
NewAMP_E	RaCa-2[3]	FFPIIARLAAKVIPSLVCAVTKKC	*E. coli* ATCC 25922	4-16
NewAMP_E	RaCa-6[3]	ATAWRIPPPGMQPIIPIRIRPLCGKQ	*E. coli* ATCC 25922	No inhibition
NewAMP_E	RaCa-8[3]	FPAIICKVSKNC	*E. coli* ATCC 25922	No inhibition
NewAMP_E	RaCa-10[3]	ALVAKIQKFPVFNTLKLCKLELEII	*E. coli* ATCC 25922	No inhibition
NewAMP_E	Hydr_2[5]	GVAKKLWIAAKKPAGAGSKFKLL-NH_2	*E. coli* ATCC 25922	512
NewAMP_E	Hydr_3[5]	GELKKLWQAGKLSEEDGGAFKAG-NH_2	*E. coli* ATCC 25922	512
NewAMP_E	Hydr_4[5]	FLPLIGRVFSGIL-NH_2	*E. coli* ATCC 25922	512
NewAMP_E	Hydr_5[5]	FLPLIGRVFSGIK-NH_2	*E. coli* ATCC 25922	512
NewAMP_E	Hydr_6[5]	FLPLIGRVLSGIA-NH_2	*E. coli* ATCC 25922	512
NewAMP_E	Hydr_7[5]	FLPLIGRVKSGIK-NH_2	*E. coli* ATCC 25922	512
NewAMP_E	Hydr_8[5]	FLPIKNRYASAAE-NH_2	*E. coli* ATCC 25922	512
NewAMP_E	KS22[4]	KLKKVTGKKMSKCMKCKIYVCS	*E. coli*	633.82
NewAMP_E	RD10[4]	RTLFVCRVGD	*E. coli*	291.34
NewAMP_E	FE23[4]	FTFYLPLFVCRRNPRPRRVSCRE	*E. coli*	728.36
NewAMP_E	Hm-AMP[2]	RLKRFKRVALRREKTARNFRSIVS	*E. coli* MG 1655	298.86
NewAMP_E	Hm-AMP2[2]	EKRWRRLIFNYF	*E. coli* MG 1655	7.95
NewAMP_E	Hm-AMP3[2]	VVKTGCQRRRMLPR	*E. coli* MG 1655	170.01
NewAMP_E	Hm-AMP5[2]	FIFSKLFLGLIKI	*E. coli* MG 1655	153.90
NewAMP_E	Hm-AMP7[2]	GLKITHTITVKGILGFLWVKIVAQK	*E. coli* MG 1655	276.44
NewAMP_E	Hm-AMP9[1]	WGKNLQMKSLYNNLTIGHYKRRF	*E. coli* MG 1655	286.84
NewAMP_E	hHK-1[8]	TGKASQFFGLM-NH_2	*E. coli* ATCC 25922	151.63
NewAMP_E	AH-1[8]	LKKWTGKASQFFGLM-NH_2	*E. coli* ATCC 25922	111.35
NewAMP_E	AH-3[8]	LKKWLKKWTGKASQFFGLM-NH_2	*E. coli* ATCC 25922	4.59
NewAMP_E	AH-4[8]	LKKWLKKWTLKASQFFGLM-	*E. coli* ATCC 25922	4.70

		NH_2		
NewAMP_E	AH-5[8]	LKKWLKKWTPKASQFFGLM-NH_2	*E. coli* ATCC 25922	4.67
NewAMP_P	RaCa-2[3]	FFPIIARLAAKVIPSLVCAVTKKC	*P. aeruginosa* ATCC 10148	128
NewAMP_P	RaCa-4[3]	FLTFPGMTFGKLLGK	*P. aeruginosa* ATCC 10148	No inhibition
NewAMP_P	RaCa-6[3]	ATAWRIPPPGMQPIIPIRIRPLCGKQ	*P. aeruginosa* ATCC 10148	No inhibition
NewAMP_P	RaCa-7[3]	FFPRVLPLANKFLPTIYCALPKSVGN	*P. aeruginosa* ATCC 10148	No inhibition
NewAMP_P	RaCa-8[3]	FPAIICKVSKNC	*P. aeruginosa* ATCC 10148	No inhibition
NewAMP_P	RaCa-9[3]	FYFPVSRKFGGK	*P. aeruginosa* ATCC 10148	No inhibition
NewAMP_P	RaCa-10[3]	ALVAKIQKFPVFNTLKLCKLELEII	*P. aeruginosa* ATCC 10148	No inhibition
NewAMP_P	RaCa-11[3]	SNRDFFKVNIFRLCG	*P. aeruginosa* ATCC 10148	No inhibition
NewAMP_P	PEP-38[1]	GLKDWVKKALGSLWKLANSQKAIISGKKS	*P. aeruginosa*	No inhibition
NewAMP_P	hHK-1[8]	TGKASQFFGLM-NH_2	*P. aeruginosa* ATCC 27853	151.63
NewAMP_P	AH-1[8]	LKKWTGKASQFFGLM-NH_2	*P. aeruginosa* ATCC 27853	222.71
NewAMP_P	AH-2[8]	LKKWTLKASQFFGLM-NH_2	*P. aeruginosa* ATCC 27853	114.94
NewAMP_P	AH-3[8]	LKKWLKKWTGKASQFFGLM-NH_2	*P. aeruginosa* ATCC 27853	9.18
NewAMP_P	AH-4[8]	LKKWLKKWTLKASQFFGLM-NH_2	*P. aeruginosa* ATCC 27853	4.70
NewAMP_P	AH-5[8]	LKKWLKKWTPKASQFFGLM-NH_2	*P. aeruginosa* ATCC 27853	4.67
NewAMP_S	HJH-3[8]	KLLKRKLLVTLR	*S. aureus* ATCC 29213	6.25
NewAMP_S	HJH-4[8]	KLLKRKLLVLLR	*S. aureus* ATCC 29213	3
NewAMP_S	HJH-5[8]	KKLLRLLKVLLR	*S. aureus* ATCC	1.5

			29213	
NewAMP_S	HJH-6[8]	KKLLKKLLRLLKVLLR	*S. aureus* ATCC 29213	0.75
NewAMP_S	GW18[6]	GWGAKRWGKRGWKWKRH W-$COONH_2$	*S. aureus* ATCC 6538	3.12
NewAMP_S	RaCa-2[3]	FFPIIARLAAKVIPSLVCAVTK KC	*S. aureus* ATCC 6538P	2-4
NewAMP_S	RaCa-4[3]	FLTFPGMTFGKLLGK	*S. aureus* ATCC 6538P	No inhibition
NewAMP_S	RaCa-6[3]	ATAWRIPPPGMQPIIPIRIRPLC GKQ	*S. aureus* ATCC 6538P	No inhibition
NewAMP_S	RaCa-7[3]	FFPRVLPLANKFLPTIYCALPK SVGN	*S. aureus* ATCC 6538P	No inhibition
NewAMP_S	RaCa-8[3]	FPAIICKVSKNC	*S. aureus* ATCC 6538P	No inhibition
NewAMP_S	RaCa-9[3]	FYFPVSRKFGGK	*S. aureus* ATCC 6538P	No inhibition
NewAMP_S	RaCa-10[3]	ALVAKIQKFPVFNTLKLCKLE LEII	*S. aureus* ATCC 6538P	No inhibition
NewAMP_S	RaCa-11[3]	SNRDFFKVNIFRLCG	*S. aureus* ATCC 6538P	No inhibition
NewAMP_S	WSKK11[9]	WSKKWKKKWKW-NH_2	*S. aureus* TISTR 746	8
NewAMP_S	KS22[4]	KLKKVTGKKMSKCMKCKIY VCS	*S. aureus*	633.82
NewAMP_S	RD10[4]	RTLFVCRVGD	*S. aureus*	291.34
NewAMP_S	FE23[4]	FTFYLPLFVCRRNPRPRRVSC RE	*S. aureus*	728.36
NewAMP_S	Hm-AMP1[2]	RLKRFKRVALRREKTARNFRS IVS	*S. aureus* ST 88	128.51
NewAMP_S	Hm-AMP3[2]	VVKTGCQRRRMLPR	*S. aureus* ST 88	170.01
NewAMP_S	Hm-AMP5[2]	FIFSKLFLGLIKI	*S. aureus* ST 88	153.90
NewAMP_S	Hm-AMP6[2]	WITLKRLGRCHPWGGHGH	*S. aureus* ST 88	211.15
NewAMP_S	Hm-AMP7[2]	GLKITHTITVKGILGFLWVKIV AQK	*S. aureus* ST 88	276.44
NewAMP_S	Hm-AMP8[2]	RAVIYKIPYNAIASRWIIAPKK C	*S. aureus* ST 88	267.53
NewAMP_S	Hm-AMP9[2]	WGKNLQMKSLYNNLTIGHYK RRF	*S. aureus* ST 88	286.84

NewAMP_S	Hm-AMP10[2]	VGALAGFLYWHFLRKGTKMVGK	*S. aureus* ST 88	248.00
NewAMP_S	hHK-1[8]	TGKASQFFGLM-NH_2	S. aureus ATCC 25923	151.63
NewAMP_S	AH-1[8]	LKKWTGKASQFFGLM-NH_2	S. aureus ATCC 25923	222.71
NewAMP_S	AH-2[8]	LKKWTLKASQFFGLM-NH_2	S. aureus ATCC 25923	229.89
NewAMP_S	AH-3[8]	LKKWLKKWTGKASQFFGLM-NH_2	S. aureus ATCC 25923	9.18
NewAMP_S	AH-4[8]	LKKWLKKWTLKASQFFGLM-NH_2	S. aureus ATCC 25923	4.70
Sub-set	**Name**	**Sequence**	**Erythrocyte**	**MHC(μg/mL) (% hemolysis)**
NewAMP_HE	HJH-1[8]	KLLKHKLLVTLA	*Erythrocyte*	382.72[a]
NewAMP_HE	HJH-2[8]	KLLKHKLLVTLR	*Erythrocyte*	382.72[a]
NewAMP_HE	HJH-3[8]	KLLKRKLLVTLR	*Erythrocyte*	382.72[a]
NewAMP_HE	HJH-4[8]	KLLKRKLLVLLR	*Erythrocyte*	382.72[a]
NewAMP_HE	HJH-6[8]	KKLLKKLLRLLKVLLR	*Erythrocyte*	3.95 (90%)
NewAMP_HE	Hm-AMP4[2]	FILYGLIRFGRLLRK	*Erythrocyte*	18.65 (77%)
NewAMP_HE	Hm-AMP8[2]	RAVIYKIPYNAIASRWIIAPKKC	*Erythrocyte*	535.06 (6.50%)
NewAMP_HE	hHK-1[8]	TGKASQFFGLM-NH_2	*Erythrocyte*	473.84 (5.05%)
NewAMP_HE	AH-1[8]	LKKWTGKASQFFGLM-NH_2	*Erythrocyte*	695.96 (1.01%)
NewAMP_HE	AH-3[8]	LKKWLKKWTGKASQFFGLM-NH_2	*Erythrocyte*	918.12 (7.88%)
NewAMP_HE	AH-5[8]	LKKWLKKWTPKASQFFGLM-NH_2	*Erythrocyte*	934.12 (2.94%)

a. % Hemolysis data was not reported in the original paper[8]; it was considered as non-hemolysis. Therefore, we have also classified them as non-hemolysis.