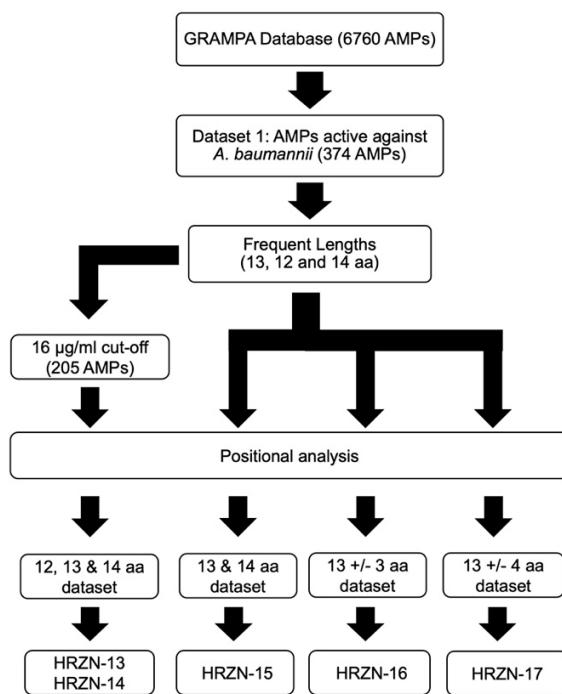
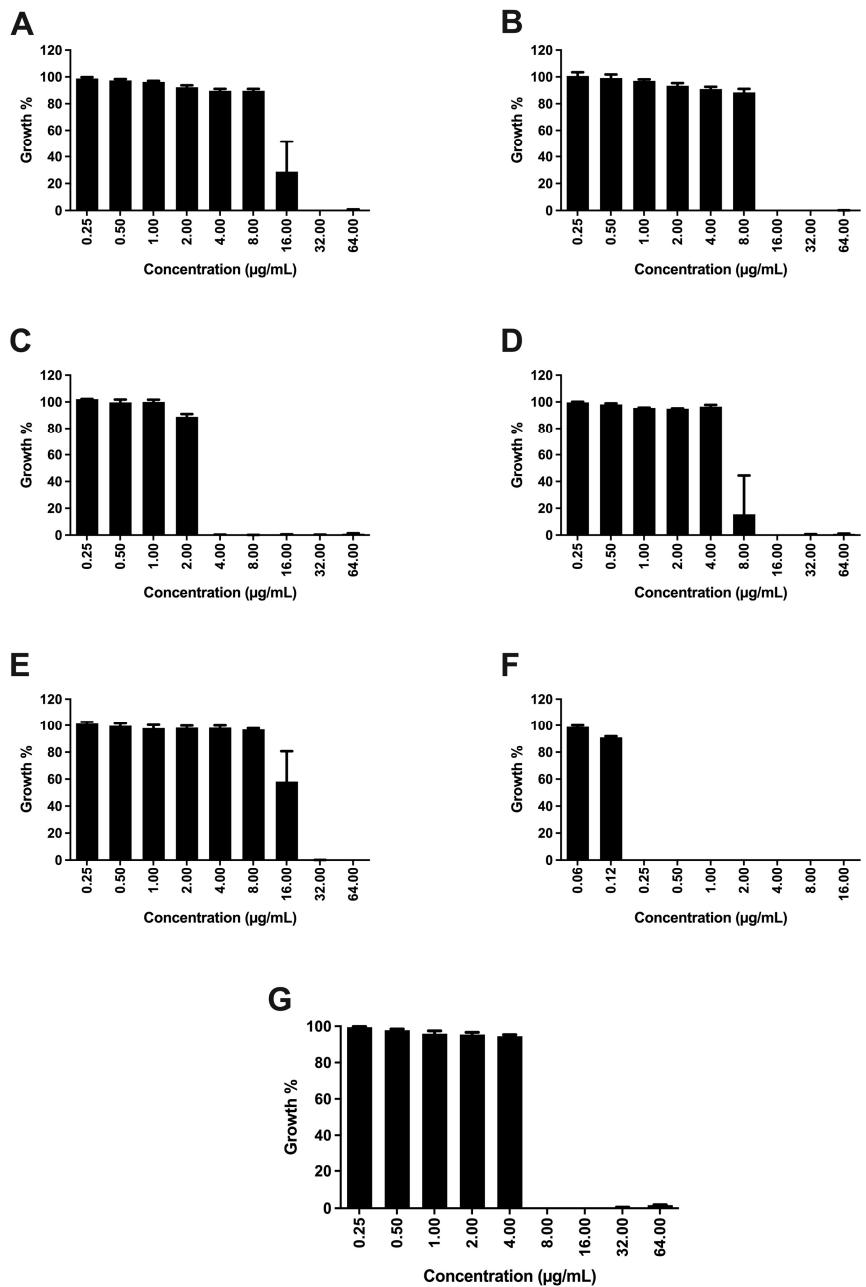


Supplemental Materials:

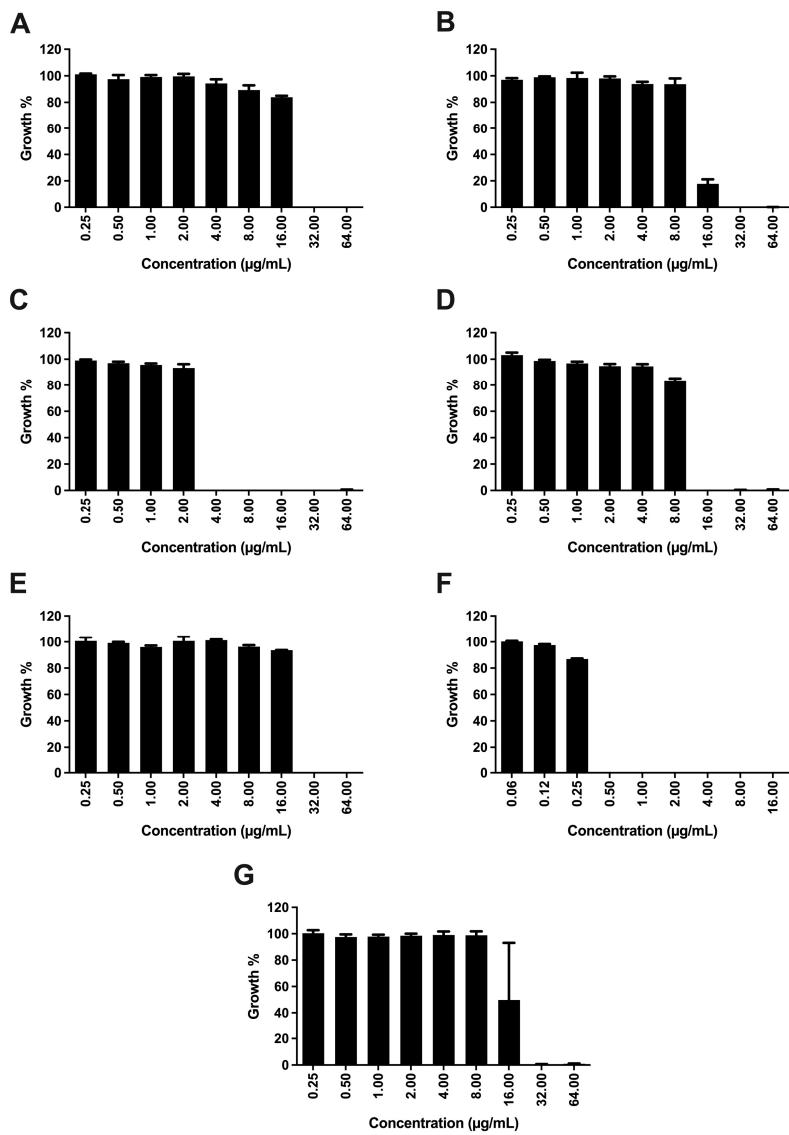
Supplemental materials for "Computationally Designed AMPs with Antibacterial and Antibiofilm Activity against MDR *Acinetobacter baumannii*" By Fahad M. Alsaab, Scott N. Dean, Shravani Bobde, Gabriel G. Ascoli and Monique L. van Hoek



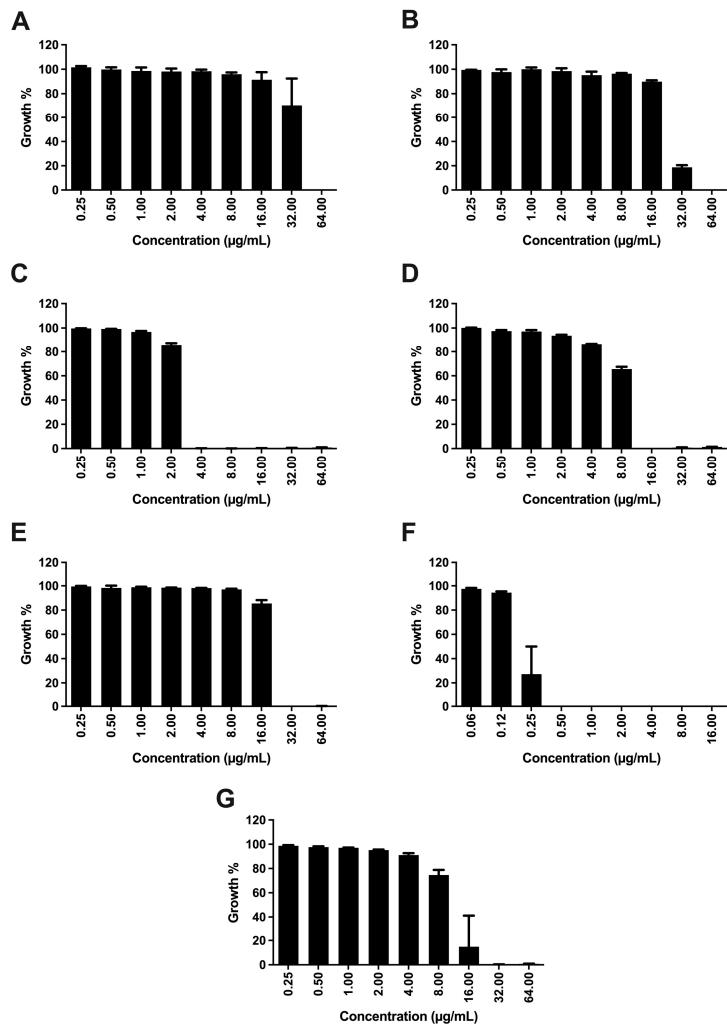
**Figure S1.** Flowchart of DFT plus positional analysis (PA) method used to design HRZN peptides.



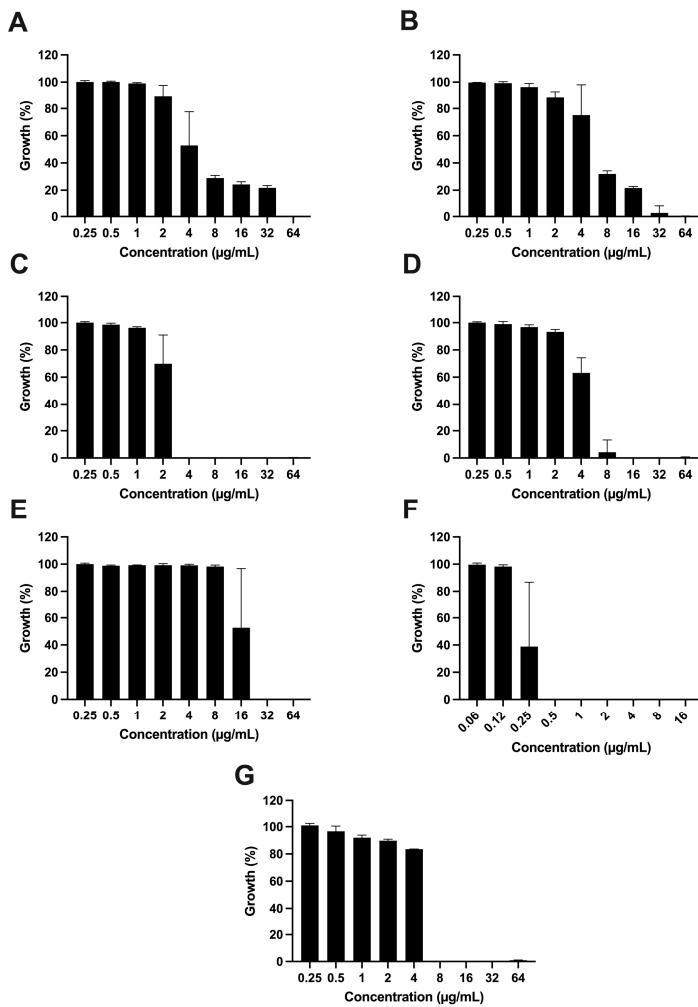
**Figure S2.** Minimum inhibitory concentration (MIC) of peptides against *A. baumannii* AB5075. (A) HRZN-13, (B) HRZN-14, (C) HRZN-15, (D) HRZN-16, (E) HRZN-17, (F) polymyxin B and (G) LL-37 resulted in MIC of 32, 32, 4, 16, 32, 0.5 and 8  $\mu\text{g/mL}$ , respectively.



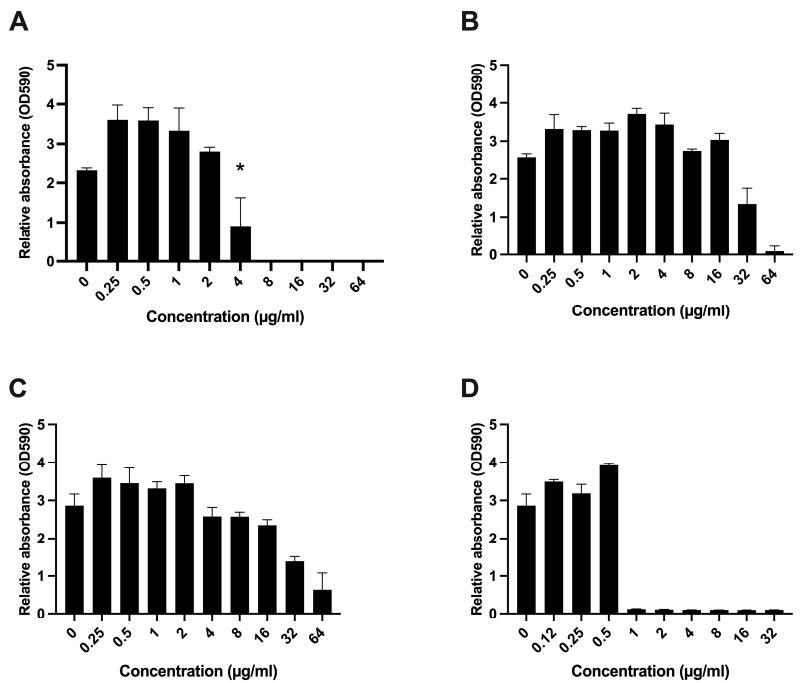
**Figure S3.** Minimum inhibitory concentration of peptides against *A. baumannii* BAA-1710. (A) HRZN-13, (B) HRZN-14, (C) HRZN-15, (D) HRZN-16, (E) HRZN-17, (F) polymyxin B and (G) LL-37 resulted in MIC of 32, 32, 4, 16, 32, 0.5 and 32  $\mu\text{g/mL}$ , respectively.



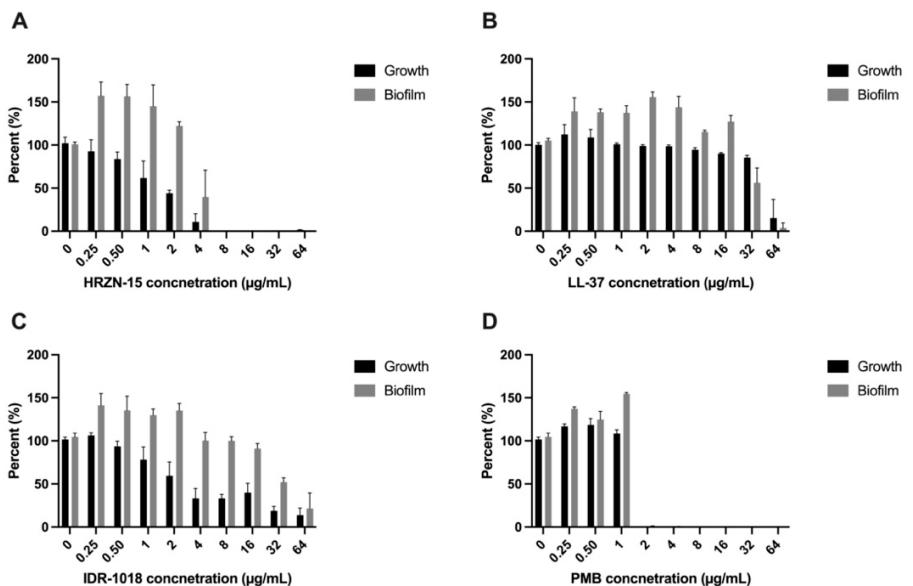
**Figure S4.** Minimum inhibitory concentration of peptides against *A. baumannii* BAA-1794. (A) HRZN-13, (B) HRZN-14, (C) HRZN-15, (D) HRZN-16, (E) HRZN-17, (F) polymyxin B and (G) LL-37 resulted in MIC of 64, 64, 4, 16, 32, 0.5 and 32  $\mu\text{g/mL}$ , respectively.



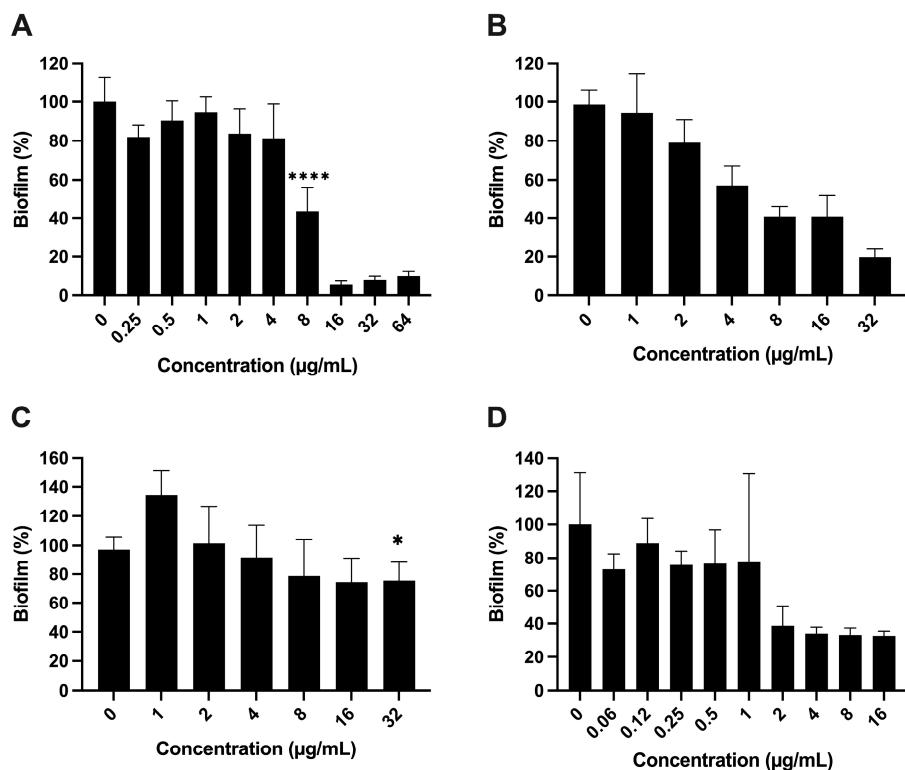
**Figure S5.** Minimum inhibitory concentration of peptides against *A. baumannii* BAA-1800. (A) HRZN-13, (B) HRZN-14, (C) HRZN-15, (D) HRZN-16, (E) HRZN-17, (F) polymyxin B and (G) LL-37 resulted in MIC of 64, 64, 4, 16, 32, 0.5 and 8  $\mu\text{g/mL}$ , respectively.



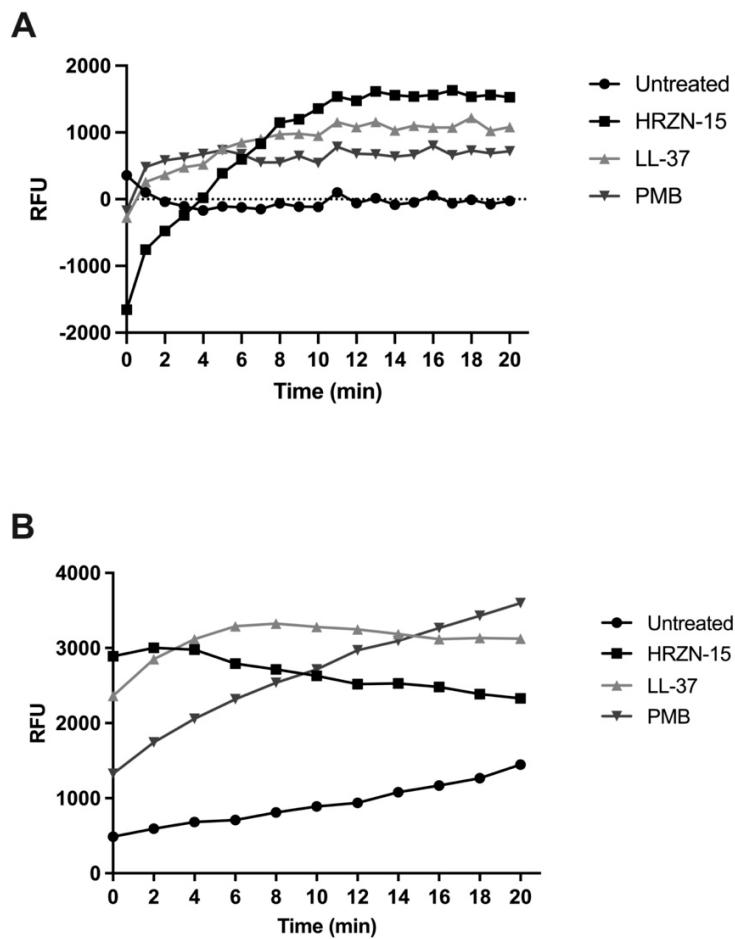
**Figure S6.** Minimum biofilm inhibition concentration (MBIC) of (A) HRZN-15, (B) LL-37, (C) IDR-1018 and (D) polymyxin B against *A. baumannii* BAA-1800. Biofilm detection on a polystyrene 96-well plate at 37°C after 24 h of growth in TSB was detected as the absorbance of crystal violet stain (590 nm). Percent biofilm production is indicated ( $n=3$ ), relative to “0 peptide/antibiotic” control. Asterisk \* indicates  $P < 0.05$  (unpaired t-test).



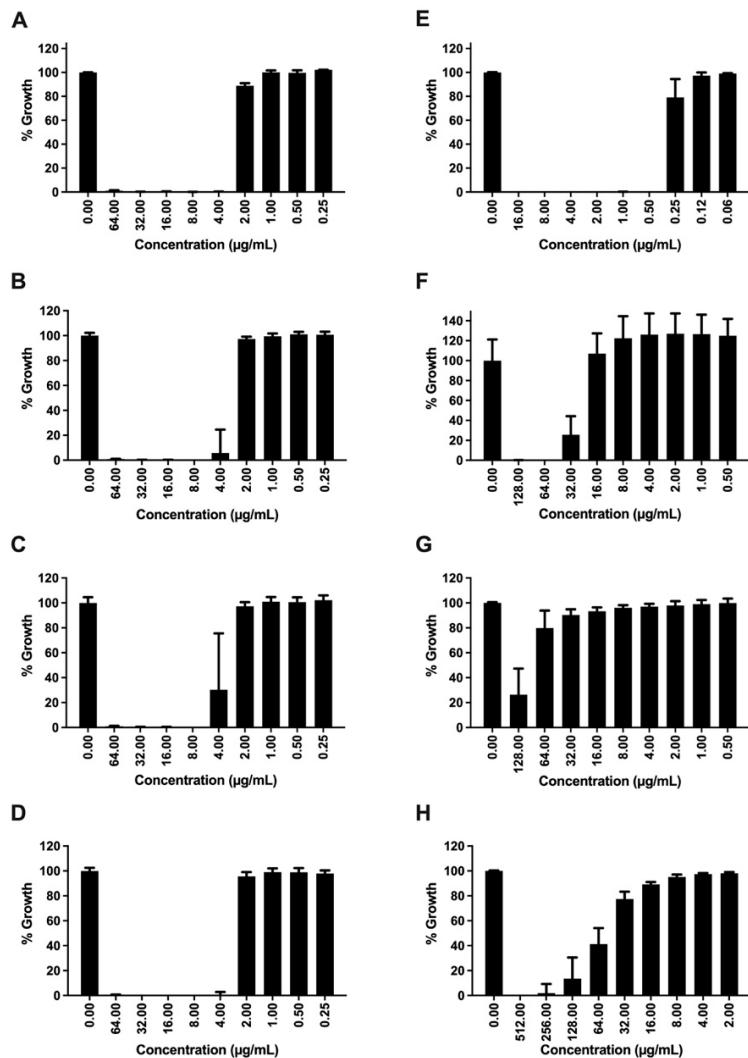
**Figure S7.** Minimum biofilm inhibition concentration (MBIC) of (A) HRZN-15, (B) LL-37, (C) IDR-1018 and (D) polymyxin B against *A. baumannii* BAA-1800. Panels indicate bacterial growth (absorbance at 600 nm) represented in black bars with “0 peptide/antibiotic” control set to 100%. Biofilm detection on a polystyrene 96-well plate at 37°C after 24 h of growth in TSB was detected as the absorbance of crystal violet stain (590 nm). Percent biofilm production is indicated by gray bars ( $n=3$ ), relative to “0 peptide/antibiotic” control.



**Figure S8.** Minimum biofilm eradication concentration (MBEC) of (A) HRZN-15, (B) LL-37, (C) IDR-1018 and (D) polymyxin B against AB5075 ( $n = 6$ ). Biofilm mass on pegs was detected at the absorbance of crystal violet stain (590 nm). Percentage biofilm mass is calculated relative to “0 peptide/antibiotic” control. The experiment was performed twice. (\*  $P < 0.05$  and \*\*\*\*  $P < 0.0001$ ).



**Figure S9.** Kinetics of (A) membrane depolarization ( $\text{DiSC}_3(5)$ ) and (B) disruption (EtBr) of HRZN-15, LL-37 and polymyxin B (PMB) against AB5075 upon exposure of 50  $\mu\text{g/mL}$  of each compound.



**Figure S10.** *In vitro* resistance acquisition induction of AB5075 upon exposure of HRZN-15 and colistin for 15 days. (A – D) shows consistent MIC values of AB5075 exposed to HRZN-15 on passage 0, 5, 10 and 15 (from top to bottom). (E – H) represents MIC of colistin against colistin-exposed bacteria performed on passage 0, 5, 10 and 15.

**Table S1.** *A. baumannii*-active peptides from GRAMPA database [43].

Strain	Sequence	µM	µg/mL
ATCC 19606	AAYLLAKINLKALAALAKKIL	3.6	8.0
NA	AAYLLAKINLKALAALAKKIL	7.2	16.0
CCARM 12036	AFHHIFRGIVHVGKTIHRLVTG	2.0	5.0
CCARM 12005	AFHHIFRGIVHVGKTIHRLVTG	2.0	5.0
CCARM 12035	AFHHIFRGIVHVGKTIHRLVTG	2.0	5.0
CCARM 12037	AFHHIFRGIVHVGKTIHRLVTG	2.0	5.0
ATCC 19606	AGR GKQGGKVRAKTRSSRAGLQFPVGRVHRLLRKGNY	60.1	256.0

ATCC 19606	AGYLLGKINLKALAALAKKIL	3.7	8.0
NA	AGYLLGKINLKALAALAKKIL	3.7	8.0
ATCC 19606	AGYLLGKINLKPLAALAKKIL	3.6	8.0
NA	AGYLLGKINLKPLAALAKKIL	3.6	8.0
ATCC 19606	AGYLLPKINLKPLAKLPKKIL	54.9	128.0
NA	AGYLLPKINLKPLAKLPKKIL	54.9	128.0
NA	AKKVFKRLGIGKFLHSACKF	3.1	7.2
KCTC 2508	AKKVFKRLGIGKFLHSACKF	6.3	14.4
NA	AKRHHGYKRKFH	81.8	128.0
NA	ALASLLKTLSKAACKKALKTLLKALSA	1.4	3.7
ATCC 19606	ALASLLKTLSKAACKKALKTLLKALSA	2.9	7.7
M89952	ALASLLKTLSKAACKKALKTLLKALSA	2.9	7.7
ATCC 17978	ALASLLKTLSKAACKKALKTLLKALSA	5.8	15.4
M89941	ALASLLKTLSKAACKKALKTLLKALSA	5.8	15.4
ATCC 19606	ALASLLKTLSKAKKKKLKTLKALSA	0.4	1.1
ATCC 17978	ALASLLKTLSKAKKKKLKTLKALSA	0.4	1.1
M89941	ALASLLKTLSKAKKKKLKTLKALSA	0.4	1.1
M89952	ALASLLKTLSKAKKKKLKTLKALSA	0.7	1.9
NA	ALASLLKTLSKAKKKKLKTLKALSA	0.7	1.9
M89955	ALKSLLLATLSKAACKKALKTLLAALSK	0.7	1.9
NA	ALKSLLLATLSKAACKKALKTLLAALSK	0.7	1.9
M89953	ALKSLLLATLSKAACKKALKTLLAALSK	1.4	3.7
ATCC 19606	ALKSLLLATLSKAACKKALKTLLAALSK	2.9	7.7
ATCC 17978	ALKSLLLATLSKAACKKALKTLLAALSK	2.9	7.7
M89941	ALKSLLLATLSKAACKKALKTLLAALSK	2.9	7.7
ATCC 19606	ALKSLLLATLSKAKKKKLKTLKALSA	0.4	1.1
ATCC 17978	ALKSLLLATLSKAKKKKLKTLKALSA	0.4	1.1
M89941	ALKSLLLATLSKAKKKKLKTLKALSA	0.4	1.1
M89952	ALKSLLLATLSKAKKKKLKTLKALSA	0.7	1.9
NA	ALKSLLLATLSKAKKKKLKTLKALSA	1.4	3.9
M89955	ALKSLLKTLSSAAAKKALATLLKALSK	0.4	1.1
M89953	ALKSLLKTLSSAAAKKALATLLKALSK	0.7	1.9
NA	ALKSLLKTLSSAAAKKALATLLKALSK	1.0	2.7
ATCC 19606	ALKSLLKTLSSAAAKKALATLLKALSK	1.4	3.7
ATCC 17978	ALKSLLKTLSSAAAKKALATLLKALSK	1.4	3.7
M89941	ALKSLLKTLSSAAAKKALATLLKALSK	1.4	3.7
M89963	ALKSLLKTLSSAAAKKALATLLKALSK	2.9	7.7
ATCC 17978	ALKSLLKTLSSAAAKKKLATLLKALSK	0.2	0.6
ATCC 19606	ALKSLLKTLSSAAAKKKLATLLKALSK	0.4	1.1

M89941	ALKSLLKTLSAAKKKLATLLKALSK	0.4	1.1
NA	ALKSLLKTLSAAKKKLATLLKALSK	1.4	3.9
ATCC 17978	ALKSLLKTLSKAAAALKTLKALSK	2.9	7.7
M89941	ALKSLLKTLSKAAAALKTLKALSK	2.9	7.7
ATCC 19606	ALKSLLKTLSKAAAALKTLKALSK	5.8	15.4
M89963	ALKSLLKTLSKAAAALKTLKALSK	5.8	15.4
NA	ALKSLLKTLSKAAAALKTLKALSK	92.8	246.2
ATCC 19606	ALWHHLLLHLLHSAAHHLG	15.0	31.9
ATCC 19606	ALWKKKKKLKSACKLG	1.9	3.9
ATCC 19606	ALWMTLKKVLKAAAKALNAVLVGANA	0.4	1.1
ATCC 17978	ALWMTLKKVLKAAAKALNAVLVGANA	0.7	2.0
NA	ALWMTLKKVLKAAAKALNAVLVGANA	1.4	3.9
NA	ALWMTLKKVLKAAAKALNAVLVGANA	0.7	1.9
ATCC 19606	ALWMTLKKVLKAAAKALNAVLVGANA	2.8	7.8
ATCC 17978	ALWMTLKKVLKAAAKALNAVLVGANA	2.8	7.8
ATCC 19606	ALWRRLRRLRSARRLG	3.8	8.5
NA	AMVGT	17.1	8.2
NA	AMVSS	15.2	7.5
ATCC 15308	AQWFAIQHISLNPPRSTIAMRAINNYRWR	1.5	5.3
ATCC 15308	AQWFAIQHISLNPPRSTIAMRAINNYRWRSKNQNTFLR	0.9	4.0
ATCC 19606	AVAGEKLWLLPHLLKMLLTPP	163.8	400.0
Q12	AWRWKAFRNCWRVRSSSL	13.9	32.0
Q13	AWRWKAFRNCWRVRSSSL	27.7	64.0
NA	CLRKLKRLLC	22.8	32.0
NA	CYCRIPACIAGERRYGTCIYQGRLWAFCC	0.3	1.0
CIP 70	CYCRIPACIAGERRYGTCIYQGRLWAFCC	1.2	4.0
NA	DCYCRIPACIAGERRYGTCIYQGRLWAFCC	0.3	1.0
CIP 70	DCYCRIPACIAGERRYGTCIYQGRLWAFCC	1.1	4.0
ATCC 19606	DDALHHLLHHLLHHL	100.0	182.1
ATCC 19606	DDALKHLLKHLLKHL	50.0	89.7
ATCC 19606	DDALKKKKKLKKL	25.0	44.2
ATCC 19606	DDALRHLLRHLLRHL	100.0	187.8
ATCC 19606	DDALRRRLRRLRRL	100.0	193.5
ATCC 19606	DHYNCVSSGGQCLYSACPIFTKIQGTCYRGKAKCCK	65.1	256.0
NA	DSHAKRHHGYKRKFHEKHHSHRGY	0.2	0.5
ATCC 19606	EKALEKLIAIQKAIKGMLNGWFTGVGVGFFRK	8.0	28.5
M3237	EKALEKLIAIQKAIKGMLNGWFTGVGVGFFRK	8.0	28.5
ATCC 17978	EKALEKLIAIQKAIKGMLNGWFTGVGVGFFRK	8.0	28.5
CCARM 12036	FAHHIFRGIVHVGKTIHRLVTG	4.0	10.0

CCARM 12005	FAHHIFRGIVHVGKTIHRLVTG	4.0	10.0
CCARM 12035	FAHHIFRGIVHVGKTIHRLVTG	4.0	10.0
CCARM 12037	FAHHIFRGIVHVGKTIHRLVTG	4.0	10.0
ATCC 19606	FAKGIAAGMAGKLF	200.0	262.1
NA	FALGAVTKRLPSLFCCLTRKC	4.0	9.4
ATCC 19606	FASGIAAGMAGKLF	200.0	253.9
ATCC 19606	FFFLRRIF	100.0	114.5
ATCC 19606	FFFLSRIF	100.0	107.6
ATCC 19606	FFGRLKSVWSAVKHGWKAAKSR	4.2	10.8
CCARM 12036	FFHHIARGIVHVGKTIHRLVTG	4.0	10.0
CCARM 12005	FFHHIARGIVHVGKTIHRLVTG	4.0	10.0
CCARM 12035	FFHHIARGIVHVGKTIHRLVTG	4.0	10.0
CCARM 12037	FFHHIARGIVHVGKTIHRLVTG	4.0	10.0
CCARM 12036	FFHHIFRGIKHVGKTIHRLVTG	2.0	5.2
CCARM 12005	FFHHIFRGIKHVGKTIHRLVTG	2.0	5.2
CCARM 12035	FFHHIFRGIKHVGKTIHRLVTG	2.0	5.2
CCARM 12037	FFHHIFRGIKHVGKTIHRLVTG	2.0	5.2
NA	FFHHIFRGIVHKGKTIHRLVTG	1.5	3.9
ATCC 19606	FFHHIFRGIVHKGKTIHRLVTG	3.0	7.8
ATCC 17978	FFHHIFRGIVHKGKTIHRLVTG	3.0	7.8
ATCC 19606	FFHHIFRGKVHVGKTIHRLVTG	1.5	3.9
ATCC 17978	FFHHIFRGKVHVGKTIHRLVTG	3.0	7.8
NA	FFHHIFRGKVHVGKTIHRLVTG	6.0	15.5
ATCC 19606	FFHHIFRPIVHVGKTIHRLVTG	5.9	15.4
ATCC 17978	FFHHIFRPIVHVGKTIHRLVTG	5.9	15.4
NA	FFHHIFRPIVHVGKTIHRLVTG	5.9	15.4
CCARM 12036	FFHHIKRGIKHVGKTIHRLVTG	4.0	10.3
CCARM 12005	FFHHIKRGIKHVGKTIHRLVTG	4.0	10.3
CCARM 12035	FFHHIKRGIKHVGKTIHRLVTG	4.0	10.3
CCARM 12037	FFHHIKRGIKHVGKTIHRLVTG	4.0	10.3
CCARM 12036	FFHHIKRGIVHVGKTIHRLVTG	4.0	10.2
CCARM 12005	FFHHIKRGIVHVGKTIHRLVTG	4.0	10.2
CCARM 12035	FFHHIKRGIVHVGKTIHRLVTG	4.0	10.2
CCARM 12037	FFHHIKRGIVHVGKTIHRLVTG	4.0	10.2
NA	FFPVIGRILNGIL	6.0	8.8
CCARM 12036	FKHHIFRGIKHVGKTIHRLVTG	2.0	5.2
CCARM 12005	FKHHIFRGIKHVGKTIHRLVTG	2.0	5.2
CCARM 12035	FKHHIFRGIKHVGKTIHRLVTG	2.0	5.2
CCARM 12037	FKHHIFRGIKHVGKTIHRLVTG	2.0	5.2

CCARM 12036	FKHHIFRGIVHVGKTIHRLVTG	2.0	5.1
CCARM 12005	FKHHIFRGIVHVGKTIHRLVTG	2.0	5.1
CCARM 12035	FKHHIFRGIVHVGKTIHRLVTG	2.0	5.1
CCARM 12037	FKHHIFRGIVHVGKTIHRLVTG	2.0	5.1
ATCC 19606	FLFSLIPSAIGGLISAFK	20.0	37.6
ATCC 15308	FLGGLIKIVPAMICAVRKKC	115.7	250.0
SR 201346	FLGGLIKIVPAMICAVTKKCHHHHHH	10.9	32.0
NA	FLGGLIKIVPAMICAVTKKCHHHHHH	21.9	64.0
ATCC 15308	FLGGLIKPVPAVICAVRKKC	116.6	250.0
ATCC 15308	FLGGLIKPPWPKWRR	69.0	125.0
ATCC 15308	FLGGLIKRPAPAMICAVRKKC	113.5	250.0
ATCC 15308	FLGGLIKRVPAVICAVRKKC	113.4	250.0
ATCC 15308	FLGGLIKWKWPWWPWRR	13.5	31.3
ATCC 15308	FLGGLIKWPWWPWRR	31.3	62.5
ATCC 15308	FLGGLIKWWPWRR	18.2	31.3
ATCC 19606	FLKGICKGMLGKLF	25.0	36.3
ATCC 19606	FLKGICKGMLGKLL	25.0	35.4
ATCC 19606	FLKGIVGKLGKLF	25.0	35.5
ATCC 19606	FLKGIVGMLGKLF	3.0	4.3
ATCC 19606	FLKGIVGMLGKLL	6.0	8.3
ATCC 19606	FLKGIVGMLGKLW	6.0	8.8
NA	FLPAALAGIGGILGKLF	15.8	26.2
ATCC 19606	FLPAALAGIGGILGKLF	25.0	41.5
NA	FLPLIGRVLSGIL	24.0	33.5
ATCC 19606	FLPWFSKFLGRIL	12.0	19.5
ATCC 19606	FLSGIVGMLGKLF	6.0	8.3
ATCC 19606	FLSLIPHIVSGVASIAKHF	6.3	12.7
ATCC 19606	FLSLIPHIVSGVASLAIHF	200.0	404.3
ATCC 19606	FLSLIPHIVSGVASLAKHF	6.3	12.7
ATCC 19606	FLSMIPHIVSGVAALAKHL	6.3	12.5
ATCC 19606	FSFLSRIF	100.0	101.6
NA	FSTKTRNWFSEHFKVKEKLKDTFA	80.6	250.0
ATCC 19606	FVPWFPSKFLGRIL	12.5	20.1
ATCC 19606	FVPWFPSKFLKRIL	3.1	5.3
ATCC 19606	FVPWFPSKFLPRIL	50.0	82.5
ATCC 19606	FVPWFPSKFLWRIL	3.1	5.4
ATCC 19606	FVQWFPSKFLGKIL	6.0	9.7
ATCC 19606	FVQWFPSKFLGRIL	6.0	9.8
ATCC 19606	FVQWFPSKFLLRIL	48.0	81.5

ATCC 19606	FVQWFSRFLGRIL	6.0	10.0
ATCC 19606	FVRWFSKFLGRIL	6.0	10.0
ATCC 19606	FVRWFSRFLGRIL	6.0	10.2
NA	FWGKLWEGVKNAI	38.0	58.8
ATCC 19606	GCKKYRRFRWKFKGKFWF	24.1	64.0
ATCC 19606	GCKKYRRFRWKFKGKFWFWG	23.1	64.0
ATCC 19606	GCRALCYKQRCVTYCRGA	8.0	16.4
ATCC 19606	GCRRFKFKKKWRYRGRFWF	20.3	64.0
ATCC 19606	GCRRLCYKQRCVTYCRGPPR	1.0	2.4
ATCC 19606	GCRRLCYKQRCVTYCRGR	1.0	2.2
ATCC 19606	GCRRWKKFRWRYRGKF	22.0	64.0
ATCC 19606	GFCWYVCVYRNGVRVCYRCN	0.2	0.5
NM8	GFGSLLGKALRLGANVL	3.0	5.1
NA	GFGSLLGKALRLGANVL	3.1	5.2
ATCC 19606	GFGSLLGKALRLGANVL	4.7	8.0
NA	GFLGPLLKLGLKGVAKVLP	12.5	36.0
NM8	GFLGPLLKLGLKGVAKVLP	12.5	36.0
NM8	GFLGSLLKTGLKVGSNL	6.0	10.9
NM8	GFSSIFRGVAKFASKGLGKD	50.0	152.6
NM8	GFSSIFRGVAKFASKGLGKD	6.0	23.1
NM8	GFSSIFRGVAKFASKGLGKD	12.5	47.6
NM35	GFSSIFRGVAKFASKGLGKK	1.5	5.8
NM8	GFSSIFRGVAKFASKGLGKK	3.0	11.6
NA	GFWGKLWEGVKNAI	7.0	11.2
NA	GFWSSALEGLKKFAKG	12.5	33.1
NM8	GFWSSALEGLKKFAKG	12.5	33.1
AB3	GGLKLGKKLEGAGKRVFK	0.3	1.0
AB1	GGLKLGKKLEGAGKRVFK	0.5	2.0
ATCC 17978	GGLKLGKKLEGAGKRVFK	0.5	2.0
ATCC 17978	GGLKLGKKLEGAGKRVFNAAE	0.5	2.0
NM35	GIFPIFAKLLGKVIKVASSL	10.0	28.7
NA	GIFPIFAKLLGKVIKVASSL	20.0	57.5
NM8	GIFPIFAKLLGKVIKVASSL	20.0	57.5
NA	GIGAVLKVLTTGLPALISWIKRKRQQ	4.2	12.1
NA	GIGDPVTCLKSGAICH	29.5	128.0
ATCC 19606	GIGK	100.0	37.3
ATCC 19606	GIGKFLHSAGKFGKAFVG	26.6	64.0
ATCC 19606	GIGKFLHSACKFGKAFVG	20.0	49.3
NA	GILKTIKSIASKLKRKAK	1.6	3.1

NA	GILKTIKSIASKVANTVQKLKRKAKNAV	3.1	9.3
NA	GILKTIKSIASKVANTVQKLKRKAKNAVA	3.1	9.5
NA	GILNTIKSIASKLKRKAK	1.6	3.1
NA	GIWDTIKSMGKVFAGAILQNL	12.5	28.3
NA	GIWDTIKSMGKVFAGLILQNL	25.0	57.6
NM109	GIWKTIKSMGKVFAGAIKQNL	3.0	6.9
NM8	GIWKTIKSMGKVFAGAIKQNL	3.0	6.9
NM75	GIWKTIKSMGKVFAGAIKQNL	3.0	6.9
NM35	GIWKTIKSMGKVFAGAIKQNL	3.0	6.9
NM124	GIWKTIKSMGKVFAGAIKQNL	3.0	6.9
NA	GIWKTIKSMGKVFAGAIKQNL	6.3	14.3
NA	GIWKTIKSMGKVFAGAILQNL	12.5	28.4
NM75	GIWKTIKSMGKVFAGKIKQNL	3.0	7.0
NM109	GIWKTIKSMGKVFAGKIKQNL	6.0	14.1
NM8	GIWKTIKSMGKVFAGKIKQNL	6.0	14.1
NM35	GIWKTIKSMGKVFAGKIKQNL	6.0	14.1
NM124	GIWKTIKSMGKVFAGKIKQNL	6.0	14.1
NA	GIWKTIKSMGKVFAGKIKQNL	6.3	14.7
NM109	GIWKTIKSMGKVFAGKILQNL	1.5	3.5
NM124	GIWKTIKSMGKVFAGKILQNL	1.5	3.5
NM8	GIWKTIKSMGKVFAGKILQNL	3.0	7.0
NM75	GIWKTIKSMGKVFAGKILQNL	3.0	7.0
NM35	GIWKTIKSMGKVFAGKILQNL	3.0	7.0
NA	GIWKTIKSMGKVFAGKILQNL	6.9	16.0
NA	GIWSSIKNLASKAWNNSDIGQSLRNKAAGAINKFVADKIGVT SQAAS	5.0	24.4
ATCC 19606	GKKYRRFRWKFKGKWFWFG	6.1	16.0
ATCC 19606	GKKYRRFRWKFRKGRFWFWG	5.7	16.0
ATCC 19606	GKKYRRFWFKFKGKWFWFWG	6.1	16.0
ATCC 17978	GKLTKDKLKRGAKKALNVASKVAPIVAAGASIAR	0.9	3.0
NA	GLASTIGSLLGKFAKGGAQAFQPK	25.0	61.5
NM8	GLASTIGSLLGKFAKGGAQAFQPK	25.0	61.5
ATCC 15308	GLFDIWAWWRWRR	16.9	31.3
ATCC 15308	GLFDIWKKLRWRR	17.6	31.3
ATCC 15308	GLFDIWKKWRWRR	16.9	31.3
ATCC 15308	GLFDIWKKWRWRR	8.2	15.6
ATCC 15308	GLFDKWAwwRWRR	33.5	62.5
NA	GLFKKLRRKIKKGFKKIFKRL	3.8	10.0
ATCC 9955	GLFKKLRRKIKKGFKKIFKRL	15.9	42.0

ATCC 9955	GLFKKLRRKIKKGFKKIFKRLPPIGVGVSIPLAGKR	1.3	5.2
NA	GLFKKLRRKIKKGFKKIFKRLPPIGVGVSIPLAGKR	1.3	5.2
NM8	GLGKDLAKLGVDLVACKISKQC	200.0	452.0
NM35	GLGKDLAKLGVDLVACKISKQC	200.0	452.0
NA	GLGSLLGKAFKIGLKTVGKMMGGAPREQ	4.0	11.4
NA	GLGSVLGKALKIGANLL	4.0	6.5
NM8	GLGSVLGKALKIGANLL	6.0	9.7
NM8	GLKEIFKAGL GSLVKGIAAHVAS	5.0	11.3
NM35	GLKEIFKAGL GSLVKGIAAHVAS	10.0	22.7
NM8	GLKKIFKAGL GSLKKGIAAHVAS	20.0	45.9
NM35	GLKKIFKAGL GSLKKGIAAHVAS	20.0	45.9
NM75	GLKKIFKAGL GSLVKGIAAHVAS	2.5	5.7
NM35	GLKKIFKAGL GSLVKGIAAHVAS	20.0	45.3
NM8	GLKKIFKAGL GSLVKGIAAHVAS	40.0	90.6
NM75	GLKKIFKAGL GSLVKG IKAHVAS	5.0	11.6
NM8	GLKKIFKAGL GSLVKG IKAHVAS	10.0	23.2
NM124	GLKKIFKAGL GSLVKG IKAHVAS	20.0	46.5
NM75	GLKKIFKAGL GSLVKGIAAHVAS	2.5	5.8
NM8	GLKKIFKAGL GSLVKGIAAHVAS	5.0	11.6
NM35	GLKKIFKAGL GSLVKGIAAHVAS	10.0	23.2
NA	GLLKPLLKIAAKVGSNLL	1.6	3.0
KCTC 2508	GLNALKKVFQGIHEAIKKINNHVQ	2.0	5.4
CCARM 12036	GLNALKKVFQGIHEAIKKINNHVQ	4.0	10.8
CCARM 12035	GLNALKKVFQGIHEAIKKINNHVQ	4.0	10.8
CCARM 12036	GLNALKKVFQGIHKAIKKINNHVQ	2.0	5.4
CCARM 12035	GLNALKKVFQGIHKAIKKINNHVQ	2.0	5.4
KCTC 2508	GLNALKKVFQGIHKAIKKINNHVQ	2.0	5.4
CCARM 12036	GLNALKKVFQPIHEAIKKINNHVQ	16.0	43.8
CCARM 12035	GLNALKKVFQPIHEAIKKINNHVQ	16.0	43.8
KCTC 2508	GLNALKKVFQPIHEAIKKINNHVQ	16.0	43.8
CCARM 12036	GLNALKKVFQPIHEAIKLINNHVQ	8.0	21.8
CCARM 12035	GLNALKKVFQPIHEAIKLINNHVQ	8.0	21.8
KCTC 2508	GLNALKKVFQPIHEAIKLINNHVQ	8.0	21.8
CCARM 12036	GLNALKKVFQPIHKAIKKINNHVQ	8.0	21.9
KCTC 2508	GLNALKKVFQPIHKAIKKINNHVQ	8.0	21.9
CCARM 12035	GLNALKKVFQPIHKAIKKINNHVQ	16.0	43.8
NA	GLVGTLLGHIGKAILG	62.5	94.9
NM124	GLVGTLLGHIGKAILG	250.0	379.7
NM75	GLVGTLLGHIGKAILG	250.0	379.7

NM8	GLVGTLGHIGKAILG	250.0	379.7
NM35	GLVGTLGHIGKAILG	250.0	379.7
NM109	GLVGTLGHIGKAILG	250.0	379.7
NA	GLVGTLGHIGKAILS	62.5	96.8
NM75	GLVGTLGHIGKAILS	62.5	96.8
NM124	GLVGTLGHIGKAILS	125.0	193.6
NM8	GLVGTLGHIGKAILS	125.0	193.6
NM35	GLVGTLGHIGKAILS	125.0	193.6
NM109	GLVGTLGHIGKAILS	125.0	193.6
NA	GMASKAGSVLGKVAKVALKAAL	4.0	8.3
NM8	GMATKAGTALGKVAKAVIGAAL	25.0	50.0
ATCC 19606	GRKKRQRGGWMVVTNLRTD	2.8	8.0
NA	GRKKRQRGGWMVVTNLRTD	5.7	16.0
NA	GRLRNLEKAGQNIRGKIQGIGRRIKDILKNLQPRPQV	1.1	4.7
ATCC 19606	GRRYKKFRWKFKGRWFWFG	6.1	16.0
Q13	GTAWRWHYRARS	82.8	128.0
Q12	GTAWRWHYRARS	82.8	128.0
NM8	GVIKSVLKGVAKTVALGML	6.0	11.3
NM35	GVIKSVLKGVAKTVALGML	6.0	11.3
NM109	GVIKSVLKGVAKTVALGML	12.5	23.6
NM75	GVIKSVLKGVAKTVALGML	12.5	23.6
NM124	GVIKSVLKGVAKTVALGML	12.5	23.6
NA	GWANTLKNVAGGLCKITGAA	19.3	37.5
NA	GWFKKAWRKVKNAAGRVLKGVGIGHYVGGLI	2.4	8.0
Q13	HLRRINKLLTRIGLYRHAFG	3.3	8.0
NA	HLRRINKLLTRIGLYRHAFG	26.3	64.0
NA	IASKVANTVQKLKRKAKNAV	50.0	108.4
NA	IASKVANTVQKLKRKAKNAVA	6.3	14.0
ATCC 19606	IDWKVWDKKVSKTCKVMLACKFLG	0.0	0.1
NM35	IKIPSFFRNILKKVGKEAVSLIAGALKQS	5.0	15.8
NM8	IKIPSFFRNILKKVGKEAVSLIAGALKQS	10.0	31.6
NA	IKLSKETKDNLKKVLGAIKGAIAVAKMV	6.3	19.3
NA	IKLSKETKKNLKKVLGAIKGAIAVAKMV	3.1	9.6
NA	IKLSKTKDNLKKVLGAIKGAIAVAKMV	3.1	9.6
NA	IKLSPETKDNLKKVLGAIKGAIAVAKMV	6.3	19.2
NA	IKLSPETKKNLKKVLGAIKGAIAVAKMV	3.1	9.5
NA	IKLSPKTKDNLKKVLGAIKGAIAVAKMV	3.1	9.5
NA	IKLSPKTKNLKKVLGAIKGAIAVAKMV	3.1	9.5
NA	IKSIAKSVANTVQKLKRKAKNAV	6.3	15.6

NA	IKSIASKVANTVQKLKRKAKNAVA	3.1	8.0
NM8	ILGAILPLVSGLLSNKL	128.0	220.3
NM8	ILGKLLKTAAGLLSNL	64.0	104.0
NM8	ILGKLLKTAAKLLSNL	4.0	6.8
NM8	ILGKLLSTAAGLLKNL	32.0	52.0
NM8	ILGKLLSTAAGLLSKL	128.0	204.5
NM8	ILGKLLSTAAGLLSNL	64.0	101.4
NM8	ILGKLLSTAAKLLSNL	8.0	13.2
NA	IWSAIWSGIKSLF	10.0	14.3
NA	INLKAIAAALAKKLF	3.7	5.7
ATCC 19606	ISKRILTGKK	223.9	256.0
ATCC 15308	ISLNPPRSTIAMRAINNYRWRSKNQNTFLR	3.5	12.7
NA	IWSAIWSGIKGLL	14.0	20.2
ATCC 19606	KAAAKWAAKAAK	100.0	121.4
ATCC 19606	KAK	100.0	34.5
ATCC 19606	KCRRRLCYRQRCVTYCRGR	1.0	2.3
ATCC 19606	KCRRRYCYRQRCVTYCRGR	1.0	2.4
ATCC 15308	KESRAKFQRQHMDSDSPSSSTYSNQMMRRRNMTQGRSK PVNTFVH	9.0	50.7
NM124	KFASKGLGKDLAKLGVDLVACKISKQC	100.0	282.1
NM8	KFASKGLGKDLAKLGVDLVACKISKQC	200.0	564.3
NA	KFFKRLLKSVRRAVKKFRKKPRLIGLSTLL	55.1	200.0
ATCC 19606	KFHEKHHSHRGY	20.5	32.0
CCARM 12036	KFHHIFRGIKHVGKTIHRLVTG	2.0	5.2
CCARM 12005	KFHHIFRGIKHVGKTIHRLVTG	2.0	5.2
CCARM 12035	KFHHIFRGIKHVGKTIHRLVTG	2.0	5.2
CCARM 12037	KFHHIFRGIKHVGKTIHRLVTG	2.0	5.2
CCARM 12036	KFHHIFRGIVHVGKTIHRLVTG	2.0	5.1
CCARM 12005	KFHHIFRGIVHVGKTIHRLVTG	2.0	5.1
CCARM 12035	KFHHIFRGIVHVGKTIHRLVTG	2.0	5.1
CCARM 12037	KFHHIFRGIVHVGKTIHRLVTG	2.0	5.1
Q12	KFVRLKIYCRDKNKGRGISF	26.3	64.0
Q13	KFVRLKIYCRDKNKGRGISF	52.7	128.0
ATCC 19606	KFWKLLKKALRLWAKVL	3.7	8.0
NA	KFWKLLKKALRLWAKVL	7.5	16.0
ATCC 19606	KFWKLLKKALRLWKKVL	3.6	8.0
NA	KFWKLLKKALRLWKKVL	3.6	8.0
ATCC 19606	KFWSLLKKALRLWANVL	3.8	8.0
NA	KFWSLLKKALRLWANVL	3.8	8.0

ATCC 19606	KGGGKWGGKGKK	25.0	27.9
ATCC 19606	KGGK	12.5	4.9
ATCC 19606	KGIVGMLGKLF	50.0	58.1
NM8	KGLGKD LA LGV DL VACK IS KQC	200.0	477.6
ATCC 19606	KIAKVAL KALKIA KGALKAL	1.5	3.1
NA	KIAKVAL KALKIA KGALKAL	1.5	3.1
ATCC 19606	KIAKVAL KALKIA KVAL KAL	1.5	3.1
NA	KIAKVAL KALKIA KVAL KAL	1.5	3.1
NA	KIKKGFKKIFKRLPPIGVGVSIPLAGKR	3.3	10.0
ATCC 9955	KIKKGFKKIFKRLPPIGVGVSIPLAGKR	9.1	28.0
ATCC 19606	KILGVSKKIMRRISKDILTGKK	6.4	16.0
ATCC 19606	KILRGVSKKIMRRIRLTGKK	0.9	2.0
ATCC 19606	KILRGVSKKIMRRISKDILTGKK	3.0	8.0
ATCC 19606	KILRGVSKKIMRTFLRR	3.8	8.0
ATCC 19606	KILRGVSKRIL TGKK	75.4	128.0
ATCC 19606	KISKKIMRTFLRR	152.6	256.0
ATCC 19606	KISKKIMRTFLRRIRLTGKK	1.7	4.0
ATCC 19606	KISKKIMRTFLRRISKDILTGKK	1.4	4.0
ATCC 19606	KK	75.0	20.6
NA	KKCGFFCKLKNKLKSTGSRSNIAAGTHGGTFRV	56.4	200.0
NA	KKCKFFCKVKKKIKSIGFQIPIVSIPFK	60.9	200.0
ATCC 19606	KKEK	37.0	19.7
ATCC 19606	KKIMRTFLRR	94.9	128.0
ATCC 19606	KKIMRTFLRRISKDILTGKK	3.3	8.0
ATCC 19606	KKIMRTFLRRISKKILTGKK	3.3	8.0
ATCC 19606	KKKK	12.5	6.6
ATCC 19606	KKKLKKLKKKKL	50.0	75.6
ATCC 19606	KKKLLLLL LKKKK	50.0	90.3
ATCC 19606	KKLLKKLKKLLL	19.0	28.1
ATCC 19606	KKLLKLLLKLL	4.5	6.5
NA	KKRLKKIFKKPMVIGVTIPF	1.7	4.0
NA	KKWRKLLKKLKKLL	0.5	1.0
NA	KKWRKLLKWLAKK	1.3	2.3
NA	KKWRWWLKALAKK	2.3	4.0
NA	KKWRWWLKALAKKL	0.2	0.4
ATCC 19606	KLA KLA KKLA KLAK	196.9	300.0
ATCC 19606	KLK	100.0	38.8
ATCC 19606	KLKLLKLLKLLKLL	15.0	27.1
ATCC 899	KLKSLLKTL SKAKKKKLKTL LKAL SK	0.3	0.9

ATCC 821	KLKSLLKTL SKAKKKKLKTL KALSK	0.3	0.9
ATCC 985	KLKSLLKTL SKAKKKKLKTL KALSK	0.3	0.9
ATCC 1012	KLKSLLKTL SKAKKKKLKTL KALSK	0.3	0.9
ATCC 884	KLKSLLKTL SKAKKKKLKTL KALSK	0.3	0.9
ATCC 689	KLKSLLKTL SKAKKKKLKTL KALSK	0.3	0.9
ATCC 649	KLKSLLKTL SKAKKKKLKTL KALSK	0.3	0.9
ATCC 19606	KLKSLLKTL SKAKKKKLKTL KALSK	0.7	2.1
ATCC 17978	KLKSLLKTL SKAKKKKLKTL KALSK	0.7	2.1
ATCC 964	KLKSLLKTL SKAKKKKLKTL KALSK	0.7	2.1
ATCC 759	KLKSLLKTL SKAKKKKLKTL KALSK	0.7	2.1
ATCC 821	KLKSLLKTL SKAKKKLLK TALK ALSK	0.3	0.9
ATCC 985	KLKSLLKTL SKAKKKLLK TALK ALSK	0.3	0.9
ATCC 759	KLKSLLKTL SKAKKKLLK TALK ALSK	0.3	0.9
ATCC 649	KLKSLLKTL SKAKKKLLK TALK ALSK	0.3	0.9
ATCC 19606	KLKSLLKTL SKAKKKLLK TALK ALSK	0.7	2.0
ATCC 17978	KLKSLLKTL SKAKKKLLK TALK ALSK	0.7	2.0
ATCC 964	KLKSLLKTL SKAKKKLLK TALK ALSK	0.7	2.0
ATCC 899	KLKSLLKTL SKAKKKLLK TALK ALSK	0.7	2.0
ATCC 1012	KLKSLLKTL SKAKKKLLK TALK ALSK	0.7	2.0
ATCC 884	KLKSLLKTL SKAKKKLLK TALK ALSK	0.7	2.0
ATCC 689	KLKSLLKTL SKAKKKLLK TALK ALSK	0.7	2.0
NA	KLLK	127.8	64.0
ATCC 19606	KLLLKWLLKLLK	100.0	150.9
ATCC 19606	KNLRRRIIRKIIHIKKYG	2.6	5.9
ATCC 15308	KPKDMTSSQWFKTQHVQPSPQASNSAMSIIINKYTERSKDLNT FLH	10.0	52.1
ATCC 15308	KPKGMTSSQWFKIQHMQPSPQASNSAMKNINKHTKRSKDL NTFLH	1.2	6.3
ATCC 15308	KPPQFTWAQWFETQHINMTSQQSTNAMQVINNYQRRSKNQ NTFLL	10.0	54.6
NA	KRFFKKKLNSVKRACKFFFKPRVIGVSIPF	3.9	16.0
NA	KRFFKKKLNSVKRVKFFRKPRVIGVTFPF	0.3	1.1
NA	KRFFKKFKVKVKKSV	71.2	128.0
NA	KRFFKKFKVKKSVKRKKIFKKPMVIGVTIPF	0.3	1.0
NA	KRGFGKKLRKRLKKFRNSIKKRLKNFNVVVIPLPG	1.9	8.1
ATCC 19606	KRGFGKKLRKRLKKFRNSIKKRLKNFNVVVIPLPG	3.8	16.3
NA	KRIVQRIKDFLRNLVPRTES	6.5	16.0
ATCC 19606	KRIVQRIKDFLRNLVPRTES	25.9	64.0
NA	KRRGGSVTTRYQFLMIHLLRPKKLFA	3.1	9.4
ATCC 17978	KRWWKWIRW	5.0	7.2

ATCC 17978	KRWWKWWRR	20.0	29.8
NA	KSKEKIGKEFKRIVQRIKDFRLRNLVPRTES	2.2	8.0
ATCC 19606	KSKEKIGKEFKRIVQRIKDFRLRNLVPRTES	4.4	16.0
NA	KTRNWFSEHFKKVKEKLKDFA	90.3	250.0
NA	KVANTVQKLKRKAKNAVA	50.0	98.4
ATCC 19606	KVVVKWVVVKVVK	100.0	141.1
NA	KWCFRVCYRGICYRKCR	7.1	16.0
ATCC 19606	KWCFRVCYRGICYRRCR	0.1	0.1
ATCC 19606	KWKIFKKIEKVGRNIRNGIIKAGPAVALGEAKAL	33.5	128.0
NA	KWKLFFKIGIGAVLKVLTTG	3.1	6.9
KCTC 2508	KWKLFFKIGIGAVLKVLTTG	3.1	6.9
NA	KWKLFFKIGIGKFLHSACKF	3.1	7.5
KCTC 2508	KWKLFFKIGIGKFLHSACKF	12.5	30.1
NA	KWKLFFKKIPKFLHLAKKF	5.4	12.5
NA	KWKSFIKKLTKKFLHSACKF	0.6	1.6
NA	KWKSFIKKLTSKFLHSACKF	1.3	3.1
ATCC 19606	KWKSFLKTFKSAVKTVLHTALKAISS	0.7	2.0
ATCC 17978	KWKSFLKTFKSAVKTVLHTALKAISS	0.7	2.0
ATCC 899	KWKSFLKTFKSAVKTVLHTALKAISS	0.7	2.0
ATCC 821	KWKSFLKTFKSAVKTVLHTALKAISS	0.7	2.0
ATCC 985	KWKSFLKTFKSAVKTVLHTALKAISS	0.7	2.0
ATCC 1012	KWKSFLKTFKSAVKTVLHTALKAISS	0.7	2.0
ATCC 759	KWKSFLKTFKSAVKTVLHTALKAISS	0.7	2.0
ATCC 884	KWKSFLKTFKSAVKTVLHTALKAISS	0.7	2.0
ATCC 689	KWKSFLKTFKSAVKTVLHTALKAISS	0.7	2.0
ATCC 649	KWKSFLKTFKSAVKTVLHTALKAISS	0.7	2.0
ATCC 964	KWKSFLKTFKSAVKTVLHTALKAISS	1.3	3.8
ATCC 17978	KWKSFLKTFSKAKKKALKTLKAISK	0.7	2.1
ATCC 964	KWKSFLKTFSKAKKKALKTLKAISK	0.7	2.1
ATCC 899	KWKSFLKTFSKAKKKALKTLKAISK	0.7	2.1
ATCC 821	KWKSFLKTFSKAKKKALKTLKAISK	0.7	2.1
ATCC 985	KWKSFLKTFSKAKKKALKTLKAISK	0.7	2.1
ATCC 1012	KWKSFLKTFSKAKKKALKTLKAISK	0.7	2.1
ATCC 759	KWKSFLKTFSKAKKKALKTLKAISK	0.7	2.1
ATCC 884	KWKSFLKTFSKAKKKALKTLKAISK	0.7	2.1
ATCC 19606	KWKSFLKTFSKAKKKALKTLKAISK	1.3	3.9
ATCC 689	KWKSFLKTFSKAKKKALKTLKAISK	1.3	3.9
ATCC 649	KWKSFLKTFSKAKKKALKTLKAISK	1.3	3.9
ATCC 19606	KWKSFLKTFSKAKKKKLKTLKAISK	0.6	1.8
ATCC 899	KWKSFLKTFSKAKKKKLKTLKAISK	0.6	1.8
ATCC 985	KWKSFLKTFSKAKKKKLKTLKAISK	0.6	1.8
ATCC 1012	KWKSFLKTFSKAKKKKLKTLKAISK	0.6	1.8
ATCC 759	KWKSFLKTFSKAKKKKLKTLKAISK	0.6	1.8
ATCC 884	KWKSFLKTFSKAKKKKLKTLKAISK	0.6	1.8
ATCC 649	KWKSFLKTFSKAKKKKLKTLKAISK	0.6	1.8
ATCC 17978	KWKSFLKTFSKAKKKKLKTLKAISK	1.2	3.7
ATCC 964	KWKSFLKTFSKAKKKKLKTLKAISK	1.2	3.7
ATCC 821	KWKSFLKTFSKAKKKKLKTLKAISK	1.2	3.7
ATCC 689	KWKSFLKTFSKAKKKKLKTLKAISK	1.2	3.7
ATCC 899	KWKSFLKTFSKAKKKVLKTALKAISS	0.3	0.9

ATCC 759	KWKSFLKTFSKAKKKVLKTALKAIISK	0.3	0.9
ATCC 884	KWKSFLKTFSKAKKKVLKTALKAIISK	0.3	0.9
ATCC 649	KWKSFLKTFSKAKKKVLKTALKAIISK	0.3	0.9
ATCC 19606	KWKSFLKTFSKAKKKVLKTALKAIISK	0.7	2.1
ATCC 17978	KWKSFLKTFSKAKKKVLKTALKAIISK	0.7	2.1
ATCC 821	KWKSFLKTFSKAKKKVLKTALKAIISK	0.7	2.1
ATCC 985	KWKSFLKTFSKAKKKVLKTALKAIISK	0.7	2.1
ATCC 689	KWKSFLKTFSKAKKKVLKTALKAIISK	0.7	2.1
ATCC 964	KWKSFLKTFSKAKKKVLKTALKAIISK	1.3	3.9
ATCC 1012	KWKSFLKTFSKAKKKVLKTALKAIISK	1.3	3.9
ATCC 19606	KWLKKWLKWLLKK	4.7	8.0
NA	KWWKWWKKWWKK	3.3	6.3
ATCC 19606	LFWKLLLKALRLWAKVL	3.8	8.0
NA	LFWKLLLKALRLWAKVL	3.8	8.0
NA	LGAWLAGKVAGTVATYAWNRYV	25.0	59.2
ATCC 19606	LIRGLFKSFWQVF	6.0	9.8
NA	LKAAAAAAKLAAKAAKAALKAAAAAAKL	3.2	8.1
NA	LKFLKFG	128.0	109.1
NA	LKLKAIAALAKKKW	5.1	8.0
NA	LKLKSIVSWAKKVL	1.2	2.0
NA	LKLLKKLLKKLLKLL	3.1	5.6
ATCC 19606	LKLLKKLLKKLLKLL	13.0	23.5
NA	LKLSPKTKDTLKKVLGAIKGAIASMA	0.6	1.8
NA	LKWLKWG	128.0	119.1
NA	LLKKALRLWKKVL	19.9	32.0
ATCC 19606	LLKKALRLWKKVL	79.5	128.0
NA	LLKKLLKKC	18.4	20.0
ATCC 19606	LLKKLLKLLKLLKK	11.0	19.9
ATCC 19606	LLKLLKKLLKLLKL	10.0	18.1
ATCC 19606	LLLLLKKKKKKLLLL	50.0	90.3
ATCC 15308	LLPWKPWWPKWRR	129.0	250.0
ATCC 19606	LLQWLSKLLGRLL	12.0	18.6
ATCC 19606	LLQWLSKLLGRWL	6.0	9.8
ATCC 19606	LLWKALRLWWKVL	9.3	16.0
NA	LLWKALRLWWKVL	9.3	16.0
Q13	LPRRNRWSKIWKKVVTVFS	1.7	4.0
NA	LPRRNRWSKIWKKVVTVFS	9.4	22.6
NA	LRDLVCYCRTGCKRRERMNGTCRKGHLMYTLCCR	30.1	128.0
NA	LRKLRKRLLRKLRKLL	13.5	32.0
NA	LRKLRKRLVRLASHLRKLRKLL	2.1	6.0
NA	LRWLRWG	128.0	126.2
ATCC 19606	LRWTPTPSYPRYPTRSRGSRWSR	8.0	22.9
NA	LVQRGRFGRFLKKVRRFIPKVIIAQIGSRFG	1.3	4.8
ATCC 17978	NPEKALEKLIAIQKAIKGMLNGWFTGVGFRRKR	4.0	15.1
M6337	NPEKALEKLIAIQKAIKGMLNGWFTGVGFRRKR	4.0	15.1
ATCC 19606	NPEKALEKLIAIQKAIKGMLNGWFTGVGFRRKR	8.0	30.2
M105656	NPEKALEKLIAIQKAIKGMLNGWFTGVGFRRKR	8.0	30.2
M2925	NPEKALEKLIAIQKAIKGMLNGWFTGVGFRRKR	8.0	30.2
M3237	NPEKALEKLIAIQKAIKGMLNGWFTGVGFRRKR	16.0	60.3
ATCC 19606	NPEKALEPLIAIQIAIKGMLNGWFTGVGFRRKR	64.0	238.4
M3237	NPEKALEPLIAIQIAIKGMLNGWFTGVGFRRKR	64.0	238.4

ATCC 17978	NPEKALEPLIAIQIAIKGMLNGWFTGVGFRRKR	64.0	238.4
Q12	NRFTARFRRTPWRLCLQFRQ	3.0	8.0
Q13	NRFTARFRRTPWRLCLQFRQ	12.1	32.0
NA	NRFTARFRRTPWRLCLQFRQ	17.1	45.3
NA	PPPVIKFNPFLMWIVERDTRSILFMGKIVNPKAP	60.8	250.0
ICU 63169	PRPGPRP	165.0	128.0
ICU 63169	PRPLPRP	153.8	128.0
ICU 63169	PRPRPRP	146.3	128.0
ICU 63169	PRPWPRP	141.4	128.0
ATCC 15308	QDGMYQRFLRQHVHPEETGGSDRYSNLMMQRRKMTLYHSK RFNTFIH	0.5	2.9
ATCC 15308	QDNSRYTHFLTQHYDAKPQGRDDRYSESIMRRRGLTSPSKDI NTFIH	10.0	56.4
AB1	QKKIRVRLSA	13.4	16.0
AB7	QKKIRVRLSA	26.7	32.0
Q12	QVRWWGRYWRRKWATCR	6.7	16.0
Q13	QVRWWGRYWRRKWATCR	26.7	64.0
NA	RGGLCYCRGRFCVCVGR	2.1	4.0
NM124	RGVAKFASKGLGKDLAKLGVDLVACKISKQC	50.0	160.2
NM8	RGVAKFASKGLGKDLAKLGVDLVACKISKQC	100.0	320.5
NM35	RGVAKFASKGLGKDLAKLGVDLVACKISKQC	200.0	641.0
NA	RIKRFWPVVIRTVVAGYNLYRAIKKK	0.7	2.4
ATCC 19606	RILRGVSRRIMRRILTGRR	3.4	8.0
ATCC 17978	RKWWWRWIKW	5.0	7.2
ATCC 15308	RLPWRWPWRPWRR	130.3	250.0
AB5075	RLVRILVSKRPVAIKPYFRL	2.0	4.9
ATCC 15308	RPPQFTRAQWFAIQHISLN	10.0	23.1
ATCC 15308	RPPQFTRAQWFAIQHISLNPPRCTIAMRAINNYRWCKKNQN TFLRTTFANVVNVCGNQSIRCPhNRTLNNCHRSRFRVPLLHC DLINPGAQNISNCTYADRPGRRFYVVACDNRDPRDPRSPYPVV PVHLDTTI	0.3	4.8
ATCC 15308	RPPQFTRAQWFAIQHISLNPPRCTIAMRAINNYRWRSKNQNT FL	0.3	1.6
ATCC 15308	RPPQFTRAQWFAIQHISLNPPRCTIAMRAINNYRWRSKNQNT FLR	0.6	3.3
NA	RRGLFKLRRKIKKGFKKIFKRLPPVGVGSIPLAGR	1.1	4.7
NA	RRIRPRPPLRPRPRPLFPGRPPIPRLPFP	0.5	2.1
ATCC 15308	RRPWRWPWRPWRR	125.5	250.0
ATCC 15308	RRPWRWPWWPWRR	123.7	250.0
ATCC 19606	RRRRRFRRVIRRILPKYLTINTE	2.0	6.5
ATCC 19606	RRRRRYRYWRRGLTIQGRPKSLPLNTGD	2.0	7.1
NA	RRSKARGGSRGSKMGRKDSKGGSRGPGSGSRPGGGSSIAGA SRGDRGTRNA	4.7	24.4
AB1	RRWVRRVRRWVRRVVRVWRVRR	1.5	5.0
AB3	RRWVRRVRRWVRRVVRVWRVRR	1.8	6.0
AB2	RRWVRRVRRWVRRVVRVWRVRR	3.2	11.0
Q13	RSITRPVLVRRWRVRPVF	52.2	128.0
Q12	RSITRPVLVRRWRVRPVF	52.2	128.0
NA	RVRRFWPLVPVAINTVAAGINLYKAIRRK	2.8	9.5
NA	RWKIFKKIEKMGRNIIRDGIVKAGPAIEVLGSAKAIGK	1.4	5.7
CCARM 12035	RWKIFKKIEKVGRNVRDGIKAGPAVAVVGQAATVVK	1.0	4.0

CCARM 12037	RWKIFKKIEKVGRNVRDGIIKAGPAVAVVGQAATVVK	1.0	4.0
CCARM 12036	RWKIFKKIEKVGRNVRDGIIKAGPAVAVVGQAATVVK	1.0	4.0
CCARM 12005	RWKIFKKIEKVGRNVRDGIIKAGPAVAVVGQAATVVK	2.0	8.0
CCARM 12035	RWKIFKKIPKFLHSACKF	2.0	4.6
CCARM 12037	RWKIFKKIPKFLHSACKF	2.0	4.6
CCARM 12036	RWKIFKKIPKFLHSACKF	2.0	4.6
CCARM 12005	RWKIFKKIPKFLHSACKF	2.0	4.6
DSM 30007	RWRWRW	85.0	88.8
AB2	RWWRWWRRWWRR	1.4	3.0
AB1	RWWRWWRRWWRR	2.4	5.0
NA	RWWRWWRRWWRR	2.7	5.6
AB3	RWWRWWRRWWRR	5.3	11.0
NA	SAVGRHRRFGLRKHRKH	50.0	107.8
CICC 22934	SAVGRHRRFGLRKHRKH	100.0	215.6
CICC 22934	SAVGRHLRRFGLRKHRKH	100.0	221.2
CICC 22934	SAVGRHLRRFLLRKHRKH	100.0	226.8
CICC 22934	SAVLRHLLRFLLRKHRKH	100.0	232.4
Q12	SIKILKIYFIQGKRHWSF	14.1	32.0
Q13	SIKILKIYFIQGKRHWSF	28.3	64.0
CICC 22934	SKVGRHRRFGHRAHRKL	100.0	215.6
CICC 22934	SKVGRHLRRFGHRAHRKL	100.0	221.2
CICC 22934	SKVGRHLRRFLHRAHRKL	100.0	226.8
CICC 22934	SKVLRHLRRFLHRAHRKL	100.0	232.4
CICC 22934	SKVWRHWRRFWHRAHRKK	7.8	20.0
NA	SKVWRHWRRFWHRAHRLH	25.0	63.8
ATCC 19606	SMATPHVAGAAALILSKHPTWTNAQVRDRLESTATYLGNSF YYGK	26.1	128.0
SRAC2	SMATPHVAGAAALILSKHPTWTNAQVRDRLESTATYLGNSF YYGK	26.1	128.0
ATCC 15308	TIAMRAINNYRWRSKNQNTFLR	1.1	3.0
Q12	TMSLRFWRWKVR	9.6	16.0
Q13	TMSLRFWRWKVR	19.2	32.0
NA	TMSLRFWRWKVR	76.8	128.0
NA	TRWLWLLRGGLKAAGWGIRAHLNRNQ	65.7	200.0
AB5075	TTSIRRYYQVSLIRRHRGKR	1.0	2.5
DSM 3008	TWLKKRWRKKVKPP	34.6	64.0
AB1	VAKGLIKGVAKGELPAKGVFKGLKESIGKRAVLKG	8.7	32.0
ATCC 17978	VAKGLIKGVAKGELPAKGVFKGLKESIGKRAVLKG	8.7	32.0
DSM 30008	VDKPPYLPRPRPPRRIYNR	6.7	16.0
ATCC 19606	VKGWSKKFEVIA	1.6	2.3
NA	VKGWSKKFEVIA	3.1	4.6
Q12	VLHTGYRKFLHRSKRFHHLR	24.6	64.0
Q13	VLHTGYRKFLHRSKRFHHLR	49.2	128.0
NA	VQLRIRVAVIRA	23.0	32.0
NA	VQLRIRVCVIRK	10.8	16.0
NA	VQLRIRVCVIRR	21.2	32.0
NA	VQWRIRIAVIRA	10.8	16.0
NA	VQWRIRVAVIRK	5.2	8.0
NA	VWLSALKFIGKHLAKHQLSKL	3.1	7.5
ATCC 19606	WFKKLLKKALRLWKKVL	3.6	8.0
NA	WFKKLLKKALRLWKKVL	7.3	16.0

ATCC 19606	WFWKLLWKALRLWWKVL	6.7	16.0
NA	WFWKLLWKALRLWWKVL	6.7	16.0
ATCC 19606	WGRRWRIRIPRLPRPWPPRKWPRSATINTDQ	2.0	8.1
ATCC 19606	WKRRRIKIWKKIR	256.0	438.1
NA	WKRRRIKIWKKIR	256.0	438.1
ATCC 19606	WLRRRIKAWLRR	16.0	24.9
NA	WLRRRIKAWLRR	64.0	99.5
ATCC 19606	WLRRRIKAWLRRKA	2.0	3.7
NA	WLRRRIKAWLRRKA	2.0	3.7
NA	WLRRRIKAWLRRKRK	4.0	7.9
ATCC 19606	WLRRRIKAWLRRKRK	16.0	31.5
ATCC 15308	WPKRRLTKAHWFIEIQHIQPSPLQCNCNRAMSGINNYTQHCKHQ NTFLH	0.9	5.1
ATCC 15308	WPKRRLTKAHWFIEIQHIQPSPLQCNCNRAMSGINNYTQHCKHQ NTFLHDSFQNVAAVCDLLSIVCKNRRHNCHQSSKPVNMTD CRLTSGKYPQCRYSAAAQYKFFIVACDPPQKSDPPYKLVPVH LDSIL	0.6	9.1
ATCC 15308	WPKRRLTKAHWFIEIQHIQPSPLQSNRAMSGINNYTQHSKHQN TFLH	1.2	6.5
ATCC 19606	WPRFPKPRKPTYPGPTYPGPTWPRPTWRRSATIDTEH	32.0	141.8
ATCC 19606	WW	145.5	56.8
ATCC 19606	YSWPRMPRIPRLPRYPRYPRYPRWPRHPTIYA	1.0	4.2
ATCC 19606	YSWPRMPRIPRLPRYPRYPRYPRWPRWPRQPTIYA	4.0	18.5

**Table S2:** Dataset 1 containing unique antimicrobial peptides with activity against *A. baumannii*. By removing duplicate sequences from the Table S1 peptide list, we generated **Dataset 1** (374 sequences), and this dataset was used for designing novel HRZN peptides using our “DFT+PA” method.

Strain	Sequence	μM	μg/mL
ATCC 19606	IDWKKVDWKKVSKTCKVMLKACKFLG	0.0	0.1
ATCC 19606	KWCFRVCYRGICYRRCR	0.1	0.1
NA	KKWRWWLKALAKLLL	0.2	0.4
ATCC 19606	GFCWYVCVYRNGVRVCYRRCN	0.2	0.5
NA	DSHAKRHGYKRKFHEKHHSHRGY	0.2	0.5
ATCC 17978	ALKSLLKTLSAAKKKKLATLLKALSK	0.2	0.6
ATCC 821	KLKSLLKTLSKAKKKLLKTALKALSK	0.3	0.9
ATCC 899	KLKSLLKTLSKAKKKKKLKTLLKALSK	0.3	0.9
ATCC 899	KWKSFLKTFSKAKKKVLKTALKAIISK	0.3	0.9
NA	CYCRIPTACIAGERRYGTCIYQGRLWAFCC	0.3	1.0
NA	DCYCRIPACIAGERRYGTCIYQGRLWAFCC	0.3	1.0
AB3	GGLKKLGKKLEGAGKRVFKASEKALPVVVVGIAIGK	0.3	1.0
NA	KKWRKLLKKLKLL	0.5	1.0
NA	KRFKKFFKKVKKSVKKRLKKIFKKPMVIGVTIPF	0.3	1.0
M89955	ALKSLLKTLAAKKALATLLKALSK	0.4	1.1
NA	KRFKKFFKKLKNSVKKRVKKFFRKPRVIGVTFPF	0.3	1.1
ATCC 19606	ALKSLLATLSKAKKKKKLKTLLAALSK	0.4	1.1
ATCC 19606	ALWMTLKKVLKAAAKALNAVLVGANA	0.4	1.1
ATCC 15308	RPPQFTRAQWFAIQHISLNPPRSTIAMRAINNYRWRSKNQNT FL	0.3	1.6
NA	KWKSFIKKLTKKFLHSAKKF	0.6	1.6

NA	LKLSPKTKDTLKKVLGAIKGAIASMA	0.6	1.8
ATCC 19606	KWKSFLKTFSKAKKKLKTLKAISK	0.6	1.8
M89955	ALKSLLATLSKAACKALKTLLAALSK	0.7	1.9
ATCC 19606	KILRGVSKKIMRRILTGKK	0.9	2.0
ATCC 17978	GGLKKLGKKLEGAGKRVFNAAEKALPVVAGAKALRK	0.5	2.0
NA	LKLKSIVSWAKKVL	1.2	2.0
ATCC 19606	KWKSFLKTFSAVKTVLHTALKAISS	0.7	2.0
NA	RRIRPRPPRLPRLPRLPFPRLPGRPIPRPLPFP	0.5	2.1
ATCC 17978	KWKSFLKTFSKAKKKALKTLLKAISK	0.7	2.1
ATCC 19606	GCRRLCYKQRCVTYCRGR	1.0	2.2
NA	KKWRKLLKWLAKK	1.3	2.3
ATCC 19606	VKGWSKKFEVIA	1.6	2.3
ATCC 19606	KCRRLCYRQRCVTYCRGR	1.0	2.3
NA	RIKRFWPVVIRTVVAGYNLYRAIKKK	0.7	2.4
ATCC 19606	KCRRYCYRQRCVTYCRGR	1.0	2.4
ATCC 19606	GCRRLCYKQRCVTYCRGPPR	1.0	2.4
AB5075	TTSIRRYYQVSLIRRHRGKR	1.0	2.5
ATCC 15308	QDGMYQRFLRQHVHPEETGGSDRYSNLMMQRRKMTLYHSK RFNTFIH	0.5	2.9
NA	GLLKPLLKIAAKVGSNLL	1.6	3.0
ATCC 17978	GKLTKDKLKRGAKKALNVASKVAPIVAAGASIAR	0.9	3.0
AB2	RWWRWWRWWRR	1.4	3.0
ATCC 15308	TIAMRAINNYRWRSKNQNQNTFLR	1.1	3.0
NA	GILNTIKSIASKLKRKAK	1.6	3.1
ATCC 19606	KIAKVALKALKIAGGALKAL	1.5	3.1
NA	GILNTIKSIASKLKRKAK	1.6	3.1
NA	KWKSFIKKLTSKFLHSACKF	1.3	3.1
ATCC 19606	KIAKVALKALKIAKVALKAL	1.5	3.1
ATCC 15308	RPPQFTRAQWFAIQHISLNPPRSTIAMRAINNYRWRSKNQNT FLR	0.6	3.3
NM109	GIWKTIKSMGKVAGKILQNL	1.5	3.5
NA	ALASLLKTLKSAACKALKTLLKALSA	1.4	3.7
ATCC 19606	WLRRRIKAWLRRRIKA	2.0	3.7
ATCC 19606	ALWKKLLKKLLKSAKKLG	1.9	3.9
ATCC 19606	FFHHIFRGKVHVVGKTIHRLVTG	1.5	3.9
NA	RGGLCYCRGRFCVCVGR	2.1	4.0
ATCC 19606	KISKKIMRTFLRRILTGKK	1.7	4.0
ATCC 19606	KISKKIMRTFLRRISKDILTGKK	1.4	4.0
NA	KKRLKKIFKKPMVIGVTIPF	1.7	4.0
Q13	LPRRNWRWSKIWKVVTVFS	1.7	4.0
NA	KKWRWWLKLAKK	2.3	4.0
CCARM 12035	RWKIFKKIEKVGRNRDGIKAGPAVAVVGQAATVVK	1.0	4.0
ATCC 15308	AQWFAIQHISLNPPRSTIAMRAINNYRWRSKNQNQNTFLR	0.9	4.0
ATCC 19606	YSWPRMPRIPLPRYPRYPRYPRWPRHPTIYA	1.0	4.2
ATCC 19606	FLKGIVGMLGKF	3.0	4.3
CCARM 12035	RWKIFKKIPKFLHSACKF	2.0	4.6
NA	RRGLFKKLRRKIKKGFKKIFKRLPPVGVGSIPLAGR	1.1	4.7
NA	GRLRNLIKEAGQNIRGKIQGIGRIKDIKLKNLQPRPQV	1.1	4.7

	RPPQFTRAQWFAIQHISLNPPRCIAMRAINNYRWRCKNQN			
ATCC 15308	TFLRTTFANVVNVCGNQSIRCPhNRTLNNCHRShFRVPLLHC	0.3	4.8	
	DLINPGAQNISNCTYADRPGRFYVVACDNRDPRDSPRYPVV			
	PVHLDTTI			
NA	LVQRGRFGRFLKKVRRFIPKVIIAQIGSRFG	1.3	4.8	
AB5075	RLVRILVSKRPVAIKPYFRL	2.0	4.9	
ATCC 19606	KGGK	12.5	4.9	
CCARM 12036	AFHHIFRGIVHVGKTIHRLVTG	2.0	5.0	
AB1	RRWVRRVRRWVRRVVVRRWVRR	1.5	5.0	
NM8	GFGSLLGKALRLGANVL	3.0	5.1	
ATCC 15308	WPKRlTKAHWFElQHlQPSPLQCNRAMSGINNYTQHCKHQ NTFLH	0.9	5.1	
CCARM 12036	FKHHIFRGIVHVGKTIHRLVTG	2.0	5.1	
CCARM 12005	KFHHIFRGIVHVGKTIHRLVTG	2.0	5.1	
CCARM 12036	FKHHIFRGIKHVGKTIHRLVTG	2.0	5.2	
CCARM 12036	KFHHIFRGIKHVGKTIHRLVTG	2.0	5.2	
ATCC 9955	GLFKKKRKKIKKGFKKFKRLPPIGVGVSILAGKR	1.3	5.2	
CCARM 12036	FFHHIFRGIKHVGKTIHRLVTG	2.0	5.2	
ATCC 19606	FVPWFSKFLKRIL	3.1	5.3	
ATCC 15308	AQWFAIQHISLNPPRCIAMRAINNYRWR	1.5	5.3	
CCARM 12036	GLNALKKVFQGIHKAIKKINNHVQ	2.0	5.4	
KCTC 2508	GLNALKKVFQGIHEAIKKINNHVQ	2.0	5.4	
ATCC 19606	FVPWFSKFLWRIL	3.1	5.4	
NA	LKLLKKLLKKLLKLL	3.1	5.6	
NA	INLKAIAALAKKL	3.7	5.7	
NM75	GLKKIKAGLGSVLVKGIAAHVAS	2.5	5.7	
NA	RWKIKKIEKMGRNIRDGIVKAGPAIEVLGSAKAIKG	1.4	5.7	
NM35	GFSSIFRGVAKFASKGLGKKLAkLGVKLVACKISKQC	1.5	5.8	
ATCC 19606	KNLRRRIRKIIHIKKY	2.6	5.9	
NA	LRKLRKRLVRLASHLRKLRKRL	2.1	6.0	
ATCC 15308	KPKGMTSSQWFKIQHMQPSPQASNSAMKNINKHTKRSKDL NTFLH	1.2	6.3	
NA	KWWKWWKKWWKK	3.3	6.3	
ATCC 19606	RRRRRFRRVIRRIRLPKYLTINTE	2.0	6.5	
ATCC 15308	WPKRlTKAHWFElQHlQPSPLQSNRAMSGINNYTQHSKHQN TFLH	1.2	6.5	
NA	GLGSVLGKALKIGANLL	4.0	6.5	
ATCC 19606	KKLLKLLKLLK	4.5	6.5	
ATCC 19606	KKKK	12.5	6.6	
NM8	ILGKLLKTAAKLLSNL	4.0	6.8	
NA	KWKLFKKIGIGAVLKVLTTG	3.1	6.9	
NM109	GIWKTlKSMGKVFAGAIKQNL	3.0	6.9	
NM75	GIWKTlKSMGKVFAGKIKQNL	3.0	7.0	
ATCC 19606	RRRRRYRYWRRGLTIQGRPSSLPLNTGD	2.0	7.1	
NA	AKKVFKRLGIGKFLHSACKF	3.1	7.2	
ATCC 17978	KRWWKWIRW	5.0	7.2	
ATCC 17978	RKWWRWIKW	5.0	7.2	
NA	VWLSALKFIGKHLAKHQLSKL	3.1	7.5	
NA	AMVSS	15.2	7.5	

NA	KWKLFKKIGIGKFLHSAKF	3.1	7.5
ATCC 17978	ALKSLLKTSKAAAALKTLLKALSK	2.9	7.7
NA	WLRRIKAWLRRKRK	4.0	7.9
ATCC 19606	RILRGVSRRIMRRILTGR	3.4	8.0
ATCC 19606	GRKKRRQRRGGWMWVTNLRTD	2.8	8.0
ATCC 19606	KILRGVSKKIMRTFLRR	3.8	8.0
ATCC 19606	KILRGVSKKIMRRISKDILTGKK	3.0	8.0
ATCC 19606	KKIMRTFLRRISKDILTGKK	3.3	8.0
ATCC 19606	KKIMRTFLRRISKKILTGKK	3.3	8.0
Q12	NRFTARFR RTPWRLCLQFRQ	3.0	8.0
NA	KSKEKIGKEFKRIVQRIKDFLRNLPRTES	2.2	8.0
Q13	HLRRINKLLTRIGLYRHAFG	3.3	8.0
NA	VQWRIRVAVIRK	5.2	8.0
NA	GWFKKAWRKVKNAGRRVLKGVGVIHYGVGLI	2.4	8.0
ATCC 19606	AGYLLGKINLKALAALAKKIL	3.7	8.0
ATCC 19606	AAYLLAKINLKALAALAKKIL	3.6	8.0
NA	LKLKAIAALAKKKW	5.1	8.0
ATCC 19606	KFWSSLKKALRLWANVL	3.8	8.0
ATCC 19606	KFWKLLKKALRLWAKVL	3.7	8.0
ATCC 19606	KFWKLLKKALRLWKKVL	3.6	8.0
ATCC 19606	WFKKLLKKALRLWKKVL	3.6	8.0
ATCC 19606	LFWKLLLKALRLWAKVL	3.8	8.0
ATCC 19606	KWLKKWLKWLLKK	4.7	8.0
NA	IKSIASKVANTVQKLKRKAKNAVA	3.1	8.0
NA	LKAAAAAAKLAAKAAKAALKAAAAAAKL	3.2	8.1
ATCC 19606	WGRRWRIRIPRLPRPWPPRPKWPRSATINTDQ	2.0	8.1
NA	KRGFGKKLRKRLKKFRNSIKKRLKNFNVVIPILPG	1.9	8.1
NA	AMVGT	17.1	8.2
NA	GMASKAGSVLGKVAKVALKAAL	4.0	8.3
ATCC 19606	FLSGIVGMLGKLF	6.0	8.3
ATCC 19606	FLKGIVGMLGKLL	6.0	8.3
ATCC 19606	ALWRRRLRRLRSARRLG	3.8	8.5
NA	FFPVIGRILNGIL	6.0	8.8
ATCC 19606	FLKGIVGMLGKLW	6.0	8.8
ATCC 15308	WPKR LTKAHWFEIQHQPSPLQCNRAMSGINNYTQHCKHQ NTFLHDSFQNVAAVCDLLSIVCKNRRHNCHQSSKPVNMTD CRLTSGKYPQCRYSAAQYKFFIVACDPPQKSDPPYKLPVH LDSIL	0.6	9.1
NA	GILKTIKSIASKVANTVQKLKRKAKNAV	3.1	9.3
NA	FALGAVTKRLPSLFLCLITRK	4.0	9.4
NA	KRRGSVTTRYQFLMIHLLRPKKLFA	3.1	9.4
NA	RVRRFWPLPVAINTVAAGINLYKAIRRK	2.8	9.5
NA	IKLSPKTKDNLKKVLKGAIKGAIAVAKMV	3.1	9.5
NA	IKLSPKTKKNLKKVLKGAIKGAIAVAKMV	3.1	9.5
NA	IKLSPETKKNLKKVLKGAIKGAIAVAKMV	3.1	9.5
NA	GILKTIKSIASKVANTVQKLKRKAKNAVA	3.1	9.5
NA	IKLSKKTKDNLKKVLKGAIKGAIAVAKMV	3.1	9.6
NA	IKLSKETKKNLKKVLKGAIKGAIAVAKMV	3.1	9.6
ATCC 19606	FVQWFSKFLGKIL	6.0	9.7

ATCC 19606	LLQWLSKLLGRWL	6.0	9.8
ATCC 19606	FVQWFSKFLGRIL	6.0	9.8
ATCC 19606	LIRGLFKSFWQVF	6.0	9.8
CCARM 12036	FAHHIFRGIVHVGKTIHRLVTG	4.0	10.0
CCARM 12036	FFHHIARGIVHVGKTIHRLVTG	4.0	10.0
NA	KIKKGFKKIFKRLPIVGVSIPLAGKR	3.3	10.0
NA	GLFKKLRRKIKKGFKKIFKRL	3.8	10.0
ATCC 19606	FVQWFSRFLGRIL	6.0	10.0
ATCC 19606	FVRWFSKFLGRIL	6.0	10.0
ATCC 19606	FVRWFSRFLGRIL	6.0	10.2
CCARM 12036	FFHHIKRGIVHVGKTIHRLVTG	4.0	10.2
CCARM 12036	FFHHIKRGIKHVGKTIHRLVTG	4.0	10.3
ATCC 19606	FFGRLKSVWSAVKHGWKAAKSR	4.2	10.8
NM8	GFLGSLLKTGLKVGSNLL	6.0	10.9
NA	GFWGKLWEGVKNAI	7.0	11.2
NM8	GVIKSVLKGVAKTVALGML	6.0	11.3
NM8	GLKEIFKAGLGSVLVKGIAAHVAS	5.0	11.3
NA	GLGSLLGKAFKIGLKTVGKMMGGAPREQ	4.0	11.4
NM75	GLKKIFKAGLGSVLVKGIAHVAS	5.0	11.6
NA	GIGAVLKVLTTGLPALISWIKRKRRQQ	4.2	12.1
NA	KWKLFKKIPKFLHLAKKF	5.4	12.5
ATCC 19606	FLSMIPHIVSGVAALAKHL	6.3	12.5
ATCC 15308	ISLNPPRSTIAMRAINNYWRWSKNQNTFLR	3.5	12.7
ATCC 19606	FLSLIPHIVSGVASIAKHF	6.3	12.7
ATCC 19606	FLSLIPHIVSGVASLAKHF	6.3	12.7
NM8	ILGKLLSTAALKLNSL	8.0	13.2
NA	IASKVANTVQKLKRKAKNAVA	6.3	14.0
NA	ILSAIWSGIKSLF	10.0	14.3
ATCC 17978	NPEKALEKLIAIQKAIKGMLNGWFTGVGFRRKR	4.0	15.1
ATCC 19606	FFHHIFRPIVHVGKTIHRLVTG	5.9	15.4
NA	IKSIASKVANTVQKLKRKAKNAV	6.3	15.6
ATCC 15308	GLFDIWKWWRWRR	8.2	15.6
NM35	IKIPSFRNILKKVGKEAVSILIAGALKQS	5.0	15.8
NA	KWCFRVCYRGICYRKCR	7.1	16.0
NA	VQLRIRVCVIRK	10.8	16.0
Q12	TMSLRFWRWKVR	9.6	16.0
ATCC 19606	KILGVSKKIMRRISKDILTGKK	6.4	16.0
Q12	QVRWWGRYWRRKWATCR	6.7	16.0
AB1	QKKIRVRLSA	13.4	16.0
NA	KRIVQRIKDFLRNLVPRTES	6.5	16.0
DSM 30008	VDKPPYLPRPRPPRRIYNR	6.7	16.0
NA	VQWRIRIAVIRA	10.8	16.0
NA	KRFKKFFKKLKNSVKRAKKFFKKPRVIGVSIPF	3.9	16.0
ATCC 19606	GKKYRRFRWKFRKGRFWFWG	5.7	16.0
ATCC 19606	GRRYKKFRWKFKGRFWFWFG	6.1	16.0
ATCC 19606	GKKYRRFRWKFKGKWFWFWG	6.1	16.0
ATCC 19606	LLWKALRLWWKVL	9.3	16.0
ATCC 19606	GKKYRRFWKFKGKWFWFWG	6.1	16.0
ATCC 19606	WFWKLLWKALRLWWKVL	6.7	16.0

ATCC 19606	GCRALCYKQRCVTYCRGA	8.0	16.4
ATCC 19606	LLKLLKKLLKKLLKL	10.0	18.1
ATCC 19606	YSWPRMPRIPRLPYPRYPRYPRWPRWPRQPTIYA	4.0	18.5
ATCC 19606	LLQWLSKLLGRLL	12.0	18.6
NA	IKLSPETKDNLKKVLKGAIKGAIAVAKMV	6.3	19.2
NA	IKLSKETKDNLKKVLKGAIKGAIAVAKMV	6.3	19.3
ATCC 19606	FLPWFSKFLGRIL	12.0	19.5
ATCC 19606	KKEK	37.0	19.7
ATCC 19606	LLKKLLKLLKKLLKK	11.0	19.9
CICC 22934	SKVWRHWRRFWHRAHRKK	7.8	20.0
NA	LLKKLLKKC	18.4	20.0
ATCC 19606	FVPWFSKFLGRIL	12.5	20.1
NA	IWSAIWSGIKGLL	14.0	20.2
ATCC 19606	KK	75.0	20.6
CCARM 12036	GLNALKKVFQPIHEAIKLIINNHVQ	8.0	21.8
CCARM 12036	GLNALKKVFQPIHKAIKKINNHVQ	8.0	21.9
ATCC 19606	LRWTPTPSYPRYPTRSRGSRWSR	8.0	22.9
NM8	GFSSIFRGVAKFASKGLKDLAKLGVDLVACKISKQC	6.0	23.1
ATCC 15308	RPPQFTRAQWFAIQHISLN	10.0	23.1
NA	GIWSSIKNLASKAWNDSIGQSLRNKAAGAINKFVADKIGVTP SQAAS	5.0	24.4
NA	RRSKARGGSRGSKMGRKDSKGGSRGRPCSGSRPGGGSSIAGA SRGDRGGTRNA	4.7	24.4
ATCC 19606	WLRRRIKAWLRR	16.0	24.9
NA	FLPAALAGIGGILGKLF	15.8	26.2
ATCC 19606	KLKLLKKLLKKLLKL	15.0	27.1
ATCC 19606	KGGGKWGGKGGK	25.0	27.9
ATCC 19606	KKLLKKLKLLKL	19.0	28.1
NA	GIWDTIKSMGVFAGAILQNL	12.5	28.3
NA	GIWKTIKSMGVFAGAILQNL	12.5	28.4
ATCC 19606	EKALEKLIAIQKAIGMLNGWFTGVGFRRKR	8.0	28.5
NM35	GIFPIFAKLLGKVIKVASSLISKGRTE	10.0	28.7
ATCC 17978	KRWWKWWRR	20.0	29.8
ATCC 15308	FLGGLIKWWPWWR	18.2	31.3
ATCC 15308	FLGGLIKWKWPWWPWWR	13.5	31.3
ATCC 15308	GLFDIWKKLRWRR	17.6	31.3
ATCC 15308	GLFDIWKKWRWRR	16.9	31.3
ATCC 15308	GLFDIWAWRWR	16.9	31.3
ATCC 19606	ALWHHLLHHLLHSAAHHLG	15.0	31.9
NA	CLRKLRLKRLLC	22.8	32.0
SR 201346	FLGGLIKIVPAMICAVTKCHHHHH	10.9	32.0
NA	VQLRIRVCVIRR	21.2	32.0
Q12	AWRWKAFRNCWRVRSSL	13.9	32.0
NA	VQLRIRVAVIRA	23.0	32.0
ATCC 19606	KFHEKHSHRGY	20.5	32.0
NA	LRKLRKRLLRKLRKRL	13.5	32.0
AB1	VAKGLIKGVKAKGELPAKGVFKGLKESIGKRAVLKG	8.7	32.0
NA	LLKKALRLWKKVL	19.9	32.0
Q12	SIKILKIYFIQGKRHWSF	14.1	32.0

NA	GFWSSALEGLKKFAKGGLEALTNPK	12.5	33.1
NA	FLPLIGRVLSGIL	24.0	33.5
ATCC 19606	KAK	100.0	34.5
ATCC 19606	FLKGKIKGMLGKLL	25.0	35.4
ATCC 19606	FLKGIVGKLGKLF	25.0	35.5
NA	GFLGPLLKLGLKGVAKVLPHLIPSRQQ	12.5	36.0
ATCC 19606	FLKGKIKGMLGKLF	25.0	36.3
ATCC 19606	GIGK	100.0	37.3
NA	GWANTLKNVAGGLCKITGAA	19.3	37.5
ATCC 19606	FLFSLIPSAIGGLISAFK	20.0	37.6
ATCC 19606	KLK	100.0	38.8
CCARM 12036	GLNALKKVFQPIHEAIKKINNHVQ	16.0	43.8
ATCC 19606	DDALKKLLKKLLKLL	25.0	44.2
NM8	GLKKIFKAGL GSLKKGIAAHVAS	20.0	45.9
NM8	GFSSIFRGVAKFASKGLKDLAKLGVDLVASKISKQS	12.5	47.6
ATCC 19606	GIGKFLHSACKFGKAFVGEIMNS	20.0	49.3
NM8	GMATKAGTALGKVAKAVIGAAL	25.0	50.0
ATCC 15308	KESRAKKFQRQHMDSDSSPSSSTYSNQMMRRRNMTQGRSK PVNTFVH	9.0	50.7
NM8	ILGKLLSTAAGLLKNL	32.0	52.0
ATCC 15308	KPKDMTSSQWFKTQHVQPSPQASNSAMSIINKYTERSKDLNT FLH	10.0	52.1
ATCC 15308	KPPQFTWAQWFETQHINMTSQQSTNAMQVINNYQRRSKNQ NTFLL	10.0	54.6
ATCC 15308	QDNSRYTHFLTQHYDAKPQGRDDRYSESIMRRRLTSPSKDI NTFIH	10.0	56.4
ATCC 19606	WW	145.5	56.8
NA	GIWDTIKSMGKVFAGLILQNL	25.0	57.6
ATCC 19606	KGIVGMLGKLF	50.0	58.1
NA	FWGKLWEGVKNAI	38.0	58.8
NA	LGAWLAGKVAGTVATYAWNRYV	25.0	59.2
NA	GLASTIGSLLGKFAKGGQAQAFLQPK	25.0	61.5
ATCC 15308	GLFDKWAWWRWRR	33.5	62.5
ATCC 15308	FLGGLIKWPWWPWRR	31.3	62.5
NA	SKVWRHWRRFWHRAHRLH	25.0	63.8
ATCC 19606	GCRRWKKFRWRYRGKFWFWCG	22.0	64.0
ATCC 19606	GCRRFKFKKWRYRGRFWFWCFG	20.3	64.0
Q12	KFVRLKIYCRDKNKGRGISF	26.3	64.0
ATCC 19606	GIGKFLHSAGKFGKAFVGEIMKS	26.6	64.0
ATCC 19606	GCKKYRRFRWKFKGKF FWFG	23.1	64.0
ATCC 19606	GCKKYRRFRWKFKGKF FWFG	24.1	64.0
Q12	VLHTGYRKFLHRSKRFFHLR	24.6	64.0
NA	KLLK	127.8	64.0
DSM 3008	TWLKKRRWKKVKPP	34.6	64.0
ATCC 19606	KKKLKKLKKKKLK	50.0	75.6
ATCC 19606	FVQWFSKFLRLIL	48.0	81.5
ATCC 19606	FVPWFSKFLPRIL	50.0	82.5
DSM 30007	RWRWRW	85.0	88.8
ATCC 19606	DDALKHLLKHLLKHL	50.0	89.7

ATCC 19606	KKKLLLLLLLLLKKK	50.0	90.3
ATCC 19606	LLLLKKKKKKLLLL	50.0	90.3
NA	GLVGTLLGHIGKAILG	62.5	94.9
NA	GLVGTLLGHIGKAILS	62.5	96.8
NA	KVANTVQKLKRKAKNAVA	50.0	98.4
NM8	ILGKLLSTAAGLNSL	64.0	101.4
ATCC 19606	FSFLSRIF	100.0	101.6
NM8	ILGKLLKTAAGLNSL	64.0	104.0
ATCC 19606	FFFLSRIF	100.0	107.6
NA	SAVGRHGRRFGLRKHRKH	50.0	107.8
NA	IASKVANTVQKLKRKAKNAV	50.0	108.4
NA	LKFLKFG	128.0	109.1
ATCC 19606	FFFLLRIF	100.0	114.5
NA	LKWLKWG	128.0	119.1
ATCC 19606	KAAAKWAAKAAK	100.0	121.4
ATCC 15308	FLGGLIKWPWWPWRR	69.0	125.0
NA	LRWLRWG	128.0	126.2
NA	LRDLVCYCRTGCKRRERMNGTCRKGHLMYTLCCR	30.1	128.0
NA	GIGDPVTCLKSGAICHPVFCPRRYKQIGTCGLPGTKCCKP	29.5	128.0
ATCC 19606	KKIMRTFLRR	94.9	128.0
ATCC 19606	SMATPHVAGAAALILSKHPTWTNAQVRDRLESTATYLGNSF YYGK	26.1	128.0
ICU 63169	PRPRPRP	146.3	128.0
ICU 63169	PRPGPRP	165.0	128.0
ATCC 19606	KILRGVSKRLTGKK	75.4	128.0
Q13	GTAWRWHYRARS	82.8	128.0
ICU 63169	PRPLPRP	153.8	128.0
NA	AKRHGYKRKFH	81.8	128.0
Q13	RSITRPVLVRRRWVRPVF	52.2	128.0
ATCC 19606	KWKIFKKIEKVGRNIRNGIIKAGPAVALGEAKAL	33.5	128.0
ICU 63169	PRPWPRP	141.4	128.0
ATCC 19606	AGYLLPKINLKPLAKLPKKIL	54.9	128.0
NA	KRFKKFFKKVKKSV	71.2	128.0
ATCC 19606	KVVVKWVVKVVK	100.0	141.1
ATCC 19606	WPRFPKPRKPTYPGPTYPGPTWPRPTWRRSATIDTEH	32.0	141.8
ATCC 19606	KLLLKWLLKLLK	100.0	150.9
NM8	GFSSIFRGVAKFASKGLKDLAKLGVDLVA	50.0	152.6
ATCC 19606	DDALHHLLHHLLHHL	100.0	182.1
ATCC 19606	DDALRHLLRHLLRHL	100.0	187.8
ATCC 19606	DDALRRLRLRRLRRL	100.0	193.5
NA	KKCGFFCKLNKLNKSTGSRSNIAAGTHGGTFRV	56.4	200.0
NA	KKCKFFCKVKKKIKSICFGQIPIVSIPFK	60.9	200.0
NA	TRWLWLLRGGLKAAGWGIRAHLRNRQ	65.7	200.0
NA	KFFKRLLKSVRRAVKKFRKKPRLIGLSTLL	55.1	200.0
NM8	ILGKLLSTAAGLSSL	128.0	204.5
CICC 22934	SKVGRHGRRFGHRAHRKL	100.0	215.6
NM8	ILGAILPLVSGLLSNKL	128.0	220.3
CICC 22934	SAVGRHLRREGGLRKHRKH	100.0	221.2
CICC 22934	SKVGRHLRREGFHRAHRKL	100.0	221.2

CICC 22934	SAVGRHLRRFLLRKHRKH	100.0	226.8
CICC 22934	SKVGRHLRRFLHRAHRKL	100.0	226.8
CICC 22934	SAVLRHLLRFLRKHRKH	100.0	232.4
CICC 22934	SKVLRHLRRFLHRAHRKL	100.0	232.4
ATCC 19606	NPEKALEPLIAIQIAIKGMLNGWFTGVGFRRKR	64.0	238.4
ATCC 15308	FLGGLIKRPAMICAVRKKC	113.5	250.0
ATCC 15308	FLGGLIKRVPMICAVRKKC	113.4	250.0
ATCC 15308	FLGGLIKPVPMICAVRKKC	116.6	250.0
ATCC 15308	FLGGLIKIVPAMICAVRKKC	115.7	250.0
NA	PPPVIKFNRPFMLWIVERDTRSILFMGKIVNPKAP	60.8	250.0
ATCC 15308	RLPWRWPWRPWRR	130.3	250.0
NA	KTRNWFSEHFKKVKEKLKDFA	90.3	250.0
NA	FSTKTRNWFSEHFKKVKEKLKDFA	80.6	250.0
ATCC 15308	RRPWRWPWRPWRR	125.5	250.0
ATCC 15308	RRPWRWPWWPWRR	123.7	250.0
ATCC 15308	LLPWKWPWWKWRR	129.0	250.0
ATCC 19606	FASGIAGMAGKLF	200.0	253.9
ATCC 19606	DHYNCVSSGGQCLYSACPIFTKIQGTCYRGAKCCK	65.1	256.0
ATCC 19606	KISKKIMRTFLRR	152.6	256.0
ATCC 19606	AGRQKQGGKVRAKAKTRSSRAGLQFPVGRVHRLLRKGNY	60.1	256.0
ATCC 19606	ISKRLITGKK	223.9	256.0
ATCC 19606	FAKGIAGMAGKLF	200.0	262.1
NM124	KFASKGLGKDLAKLGVDLVACKISKQC	100.0	282.1
ATCC 19606	KLAKLAKKLAKLAK	196.9	300.0
ATCC 19606	AVAGEKLWLLPHLLKMLLTPTP	163.8	400.0
ATCC 19606	FLSLIPHIVSGVASLAIHF	200.0	404.3
ATCC 19606	WKRRRIKIWKKIR	256.0	438.1
NM8	GLGKDLAKLGVDLVACKISKQC	200.0	452.0
NM8	KGLGKDLAKLGVDLVACKISKQC	200.0	477.6
NM35	RGVAKFASKGLGKDLAKLGVDLVACKISKQC	200.0	641.0