SUPPLEMENTAL FIGURES AND TABLES

Targeting *Mycobacterium tuberculosis* and other microbial pathogens using improved synthetic antibacterial peptides

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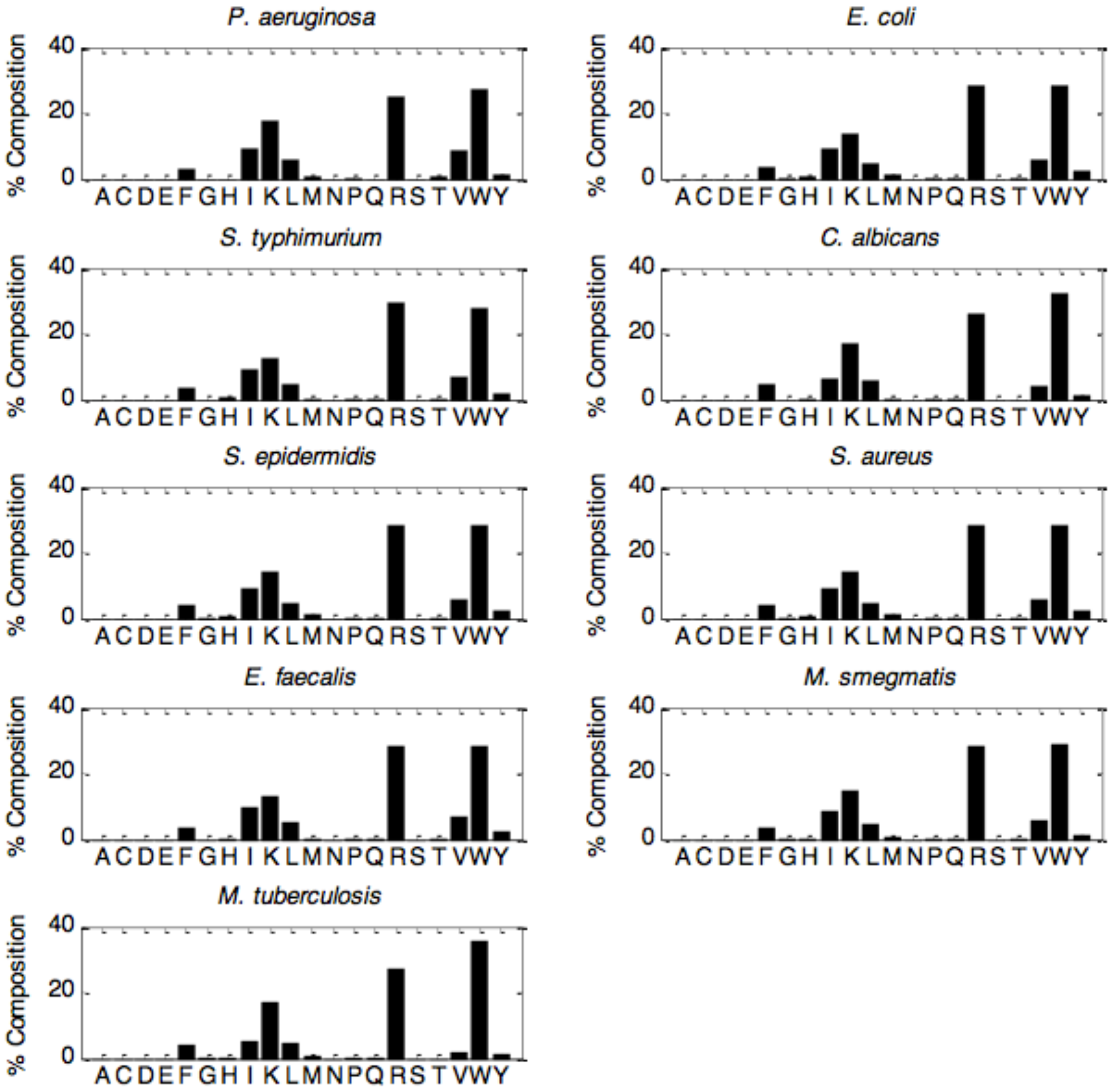
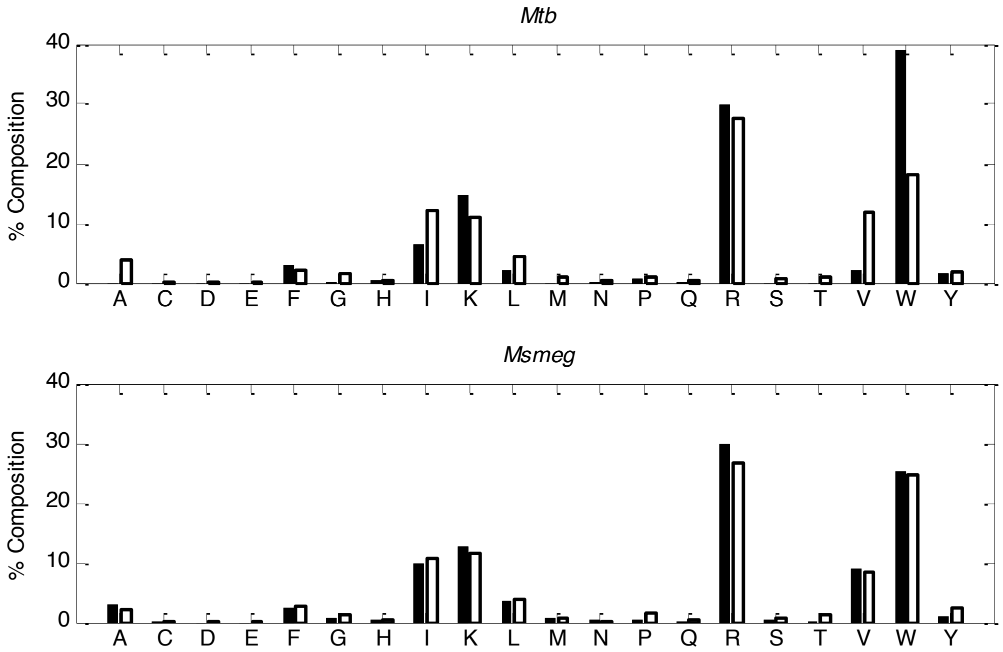


Supplemental Figure 1. Activities of peptides in PL-D as a function of their amino acid compositions. Amino acid compositions of positive peptides for all microbes tested. For further information see Supplemental Table 1.



Supplemental Figure 2. Activities against *Mtb* and *Msmeg* of peptides in PL-A as a function of their amino acid compositions. Amino acid compositions are shown for the activity classes "positive" (black bars) and "negative" (white bars). The two *Mtb* groups had statistically different A, I, L, V and W compositions while *Msmeg* groups had no significant variations for any amino acid (see Supplemental Table 1).

Supplemental Table 1. Distribution of activity classes in PL-D for the different bacterial species

	Number of peptides for "Positive" (MIC < 10 μM)	Number of peptides for "Negative" (MIC >20 μM)
P. aeruginosa	19	16
S. typhimurium	41	4
E. coli	47	2
E. faecalis	34	2
S. epidermidis	48	1
S. aureus	48	1
C. albicans	26	8
M. tuberculosis	26	15
M. smegmatis	44	1

Supplemental Table 2. Cytotoxic activities of peptides in PL-D library against mammalian cells (THP1) and activity ratios compared to *Mtb*.

Sequence[a]	*M. tuberculosis*		THP1 toxicity		Selectivity index (SI) THP1 / *Mtb*	
	MIC_{50} (µM)	MIC_{90} (µM)	IC_{50} (µM)	IC_{90} (µM)	SI_{50}	SI_{90}
WKWLKKWIK	0.8	1.1	24.3	24.3	32.0	21.3
ILRWKWRWWRWRR	1.2	2.4	25.2	50.4	21.3	21.3
ILPWKWRWWKWRR	1.3	2.6	56.4	56.4	42.7	21.3
RWRRKWWWW	0.9	2.9	73.0	145.9	85.3	51.2
WRKFWKYLK	0.6	3.0	47.3	47.3	85.3	16.0
KRWWKWWRR	0.9	3.1	79.2	158.4	85.3	51.2
RRWWKWWWR	0.9	3.6	152.6	152.6	170.7	42.7
KIWWWWRKR	1.0	4.1	173.9	173.9	170.7	42.7
RLWWWWRRK	2.0	4.1	87.0	173.9	42.7	42.7
KWKWWWRKI	2.1	4.2	90.4	90.4	42.7	21.3
RIRRWKFRW	2.1	4.3	182.5	182.5	85.3	42.7
RLKRWWKFL	1.5	4.5	96.1	48.0	64.0	10.7
RWWRWRKWW	1.7	4.6	147.5	147.5	85.3	32.0
KRWWWWRFR	2.0	5.2	83.4	166.7	42.7	32.0
KRWWRKWWR	2.0	5.3	84.4	84.4	42.7	16.0
RRWWRWVVW	1.0	5.6	179.1	179.1	170.7	32.0
WFKMRWWGR	0.7	5.9	189.3	189.3	256.0	32.0
KFKWWRMLI	2.3	6.1	49.0	49.0	21.3	8.0
FIKWKFRWWKWRK	2.8	7.4	14.8	59.1	5.3	8.0
RIKRWWWWR	1.3	7.8	167.2	167.2	128.0	21.3
RWRWWWRVY	4.0	8.0	171.5	171.5	42.7	21.3
HQFRFRFRVRRK	3.1	8.2	65.8	131.7	21.3	16.0
LKRRWKWWI	3.6	8.8	186.7	186.7	51.2	21.3
RRRIKIRWY	2.2	8.9	190.2	190.2	85.3	21.3
RLWWKIWLK	1.1	9.0	192.8	192.8	170.7	21.3
KRRWRIWLV	1.5	9.1	195.1	195.1	128.0	21.3
FFIYVWRRR	1.1	11.9	190.8	190.8	170.7	16.0
IRMRIRVLL	1.1	13.7	219.0	219.0	204.8	16.0
RWWRKIWKW	2.1	16.6	177.3	177.3	85.3	10.7
LRFILWWKR	0.7	17.0	181.0	181.0	256.0	10.7
RWWIRIRWH	1.4	17.0	181.8	181.8	128.0	10.7
RRRWWKLMM	3.7	17.6	47.0	94.0	12.8	5.3
LRRWIRIRW	0.7	17.7	94.5	189.1	128.0	10.7
RKFRWWVIR	2.2	17.8	190.2	190.2	85.3	10.7
WKIVFWWRR	7.3	23.3	186.0	186.0	25.6	8.0
RQRRVVIWW	2.3	24.7	197.2	197.2	85.3	8.0
RRWRVIVKW	1.5	24.7	98.6	197.2	64.0	8.0
RRWKIVVIRWRR	2.6	24.8	33.1	132.3	12.8	5.3
RLWRIVVIRVKR	2.7	25.9	69.2	138.4	25.6	5.3
RLRRIVVIRVFR	7.4	29.8	158.8	158.8	21.3	5.3
VRLRIRVRVIRK	7.5	30.1	20.1	40.2	2.7	1.3
RRYHWRIYI	1.0	33.2	176.9	176.9	170.7	5.3

RKWKIKWYW	2.2	34.5	91.9	183.8	42.7	5.3
YRLRVKWKW	3.7	36.0	191.9	191.9	51.2	5.3
WKWRVRVTI	19.3	51.5	206.0	206.0	10.7	4.0
RTKKWIVWI	4.1	78.1	208.3	208.3	51.2	2.7
NWRKLYRRK	10.9	109.3	174.9	174.9	16.0	1.6
YKFRWRIYI	16.2	130.0	173.3	173.3	10.7	1.3
KRKKRFKWW	8.8	141.0	188.0	188.0	21.3	1.3

[a] Peptides originating from PL-C are shown in bold