

# Distinct colicin M-like bacteriocin-immunity pairs in *Burkholderia*

## Supplementary information

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**Fig. S1. Multiple sequence alignment of BurM proteins.** Abbreviations for species names: Bamb, *Burkholderia ambifaria*; Bcen, *Burkholderia cenocepacia*; Bcep, *Burkholderia cepacia*; Bcon, *Burkholderia contaminans*; Bglu, *Burkholderia glumae*; Bokl, *Burkholderia oklahomensis*; Bpyr, *Burkholderia pyrrocinia*; Bubo, *Burkholderia ubonensis*; Burk, *Burkholderia* sp. Different shading indicates the degree of conservation. Predicted Sec signal sequences are boxed in red and Tat signal sequences in orange, the conserved motif at the amino-terminus in purple (see Sequence alignment and logo in Fig. 2), the ColM domain in yellow, conserved residues in the catalytic domain in green. The aspartate residue that was mutated in BurM2 is marked with an asterisk.

Burk A1 MGNSNDNNKFKIRSLIGAIASAALGMSGMSKSLA-----IQPEITLAPITIVGSGNVI-----TSSPADLPR-----MGHPALPPPELMTN  
Bamb AMMD (BurM2) MRKRKSSSDHVAEQTORHRKRLMLVAASPYLITIAALKQSTSLA-----OTMVEEIEISVAAPRL-----PSL--DGFS-----NKVGGGGAMSEAA  
Bcep GG4 MRKSNGLERAHAAEQTORHKRLVLTGAVSFLYAKRKSICLA-----QAMVEEIEISVAAPRL-----PSL--DGFS-----NKVGGGGAMSEAA  
Burk A9 MRKSNGLERAHAAEQTORHKRLVLTGAVSFLYAKRKSICLA-----QAMVEEIEISVAAPRL-----PSL--DGFS-----NKVGGGGAMSEAA  
Bubo Bu MKKRD TLVSA NV MNDNKRHONRKRFLIASTALDELGTLLKHTTSAVA-----QSVMVEEIEISVAAPRL-----PDFNFGDFK-----INSNEIPGANIGA  
Bpyr CH-67 MTRDRDSSAPENIERIAQTRHRERLRFVASSIVLLELIALKHSITCSA-----QSVMVEEIEISVAAPRL-----PSL--DGFS-----GKVGGGGAMSEAS  
Bamb MC40-6 MTERNPWKQTSPTS EGKQRLVLRFLVAASALIFSGMLKHA TAM A-----QNMVEEIEISVAAPRL-----PDFNFGDFG-----VNI NGGIPGANPGT  
Bcep ATCC 25416 MKRNP LKNTNHAS EEKQOPLMRFLIFASTALIFSGTLLKHA TAM A-----QSVMVEEIEISVAAPRL-----PDFNFGDFD-----IKANEIPGANPGA  
Bcon LMG 23361 MTRNP LKHVTRPS EENQOPLMRFLIFASTALIFSGTLLKHA TAM A-----QSVMVEEIEISVAAPRL-----PDFNFGDFG-----IKVNEIPGANPGA  
Bglu PG1 MINFH EEPNSRLSTRKAFIKNSGLLELIALMLNPKKSWG-----DINVEEIEISVAAPRL-----PDFNFGDFD-----LLTA  
Bamb MEX-5 (BurM1) MIKKLSKYERVVDNTRTRKAVIRASGAVIELLGLSSKSLA-----APPDFMVEEIEISVAAPRL-----TDMYYPGSGTGLTGLPSPRIPSVLNG  
Bcep DWS 37UF10B-2 MKRNFIFGASTAL-----LASSP IRLA-----OGHGPA DMLMVEEIEISVAAPRL-----LSLP IATPN-----GPAGGYHWAINGD  
Bcen CEIB S5-1 MKRNFIFGASTAF-----LMSNPVRLA-----OGHGPA DMLMVEEIEISVAAPRL-----LALP IATPN-----GPAGGYHWAINGD  
Bcep DWS 16B-4 MKRNFIFGASTAF-----LMSNPVRLA-----OGHGPA DMLMVEEIEISVAAPRL-----LALP IATPN-----GPAGGYHWAINGD  
Boki C6786 MEEKFRHS ISNRDRV MHVSKRSLIRTSIAFSAAMLPSVR IWAOTKGHGPA-----MVEEIEISVAAPRL-----TNLPVPSVG-----GPVGSYWTAGFD  
Boki EO147 MEEKLRHS ISNRDRV MHVSKRSLIRTSIAFSAAMLPSVR IWAOTKGHGPA-----MVEEIEISVAAPRL-----TNLPVPSVG-----GPVGSYWTAGFD

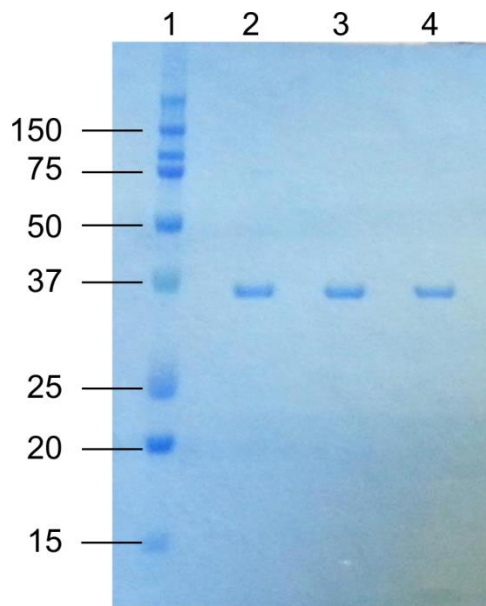
Burk A1 SGTTP ILLGLK VYLINGLN LGAAISQDITIGTLTALAQGI--VNASDMVLRADGTYASHS WIG IGE GKKNIA GATP YGLT--LNOSNI MSLFGVYAAOYYP  
Bamb AMMD (BurM2) LGYPKLLC FGRV--CSA TEMFNNDH GDMISVTEEFKFI--FEHRNEI FWRN OTLIGEHGHWARG--CYONFP GANS YNLNVA LAOHGD VSTLFGVYANOLNG  
Bcep GG4 LGYPKLLC FGRV--CSA TEMFNNDH GDMISVTEEFKFI--FEHRNEI FWRN OTLIGEHGHWARG--CYONFP GANS YNLNVA LAOHGD VSTLFGVYANOLNG  
Burk A9 LGYPKLLC FGRV--CSA TEMFNNDH GDMISVTEEFKFI--FEHRNEI FWRN OTLIGEHGHWARG--CYONFP GANS YNLNVA LAOHGD VSTLFGVYANOLNG  
Bubo Bu GIPPPSVC FNQY--CASNYMLL PANTNMVRA TEMFRYI PA IGRNDT FWRN OTLIGEHGHWARG--CYKYLP GANQYGFN FEPGOYAN MSLFGVYANOLNG  
Bpyr CH-67 LGYPKLLC FGRV--CSA TEMFNNDH GDMISVTEEFKFI--FEHRNEI FWRN OTLIGEHGHWARG--CYKHFP GANS YNLNVA LGH-AD VSTLFGVYANOLNG  
Bamb MC40-6 GTPAP TVCFN QY--C TS NFVLL PANTNMIRA TEMLKHIEI FGRNDT FWRN OTLIGEHGHWARG--CYKYLP GANQYGFN FEPGOYAN MSLFGVYANOLNG  
Bcep ATCC 25416 GMPAP S ICFN QY--C TS NFVLL PANTNMIRA TEMLKHIEI FGRNDT FWRN OTLIGEHGHWARG--CYKHFP GANQYGFN FEPGOYAN MSLFGVYANOLNG  
Bcon LMG 23361 GTPAP TVCFN QY--C TS NFVLL PANTNMVRA TEMLKHIEI FGRNDT FWRN OTLIGEHGHWARG--CYKHFP GANQYGFN FEPGOYAN MSLFGVYANOLNG  
Bglu PG1 GITAP LLQVGNLWLVNGAKILLTAACMPD IOVLVAHAEGII--IQARDGARS AMLYGTHS WANG--CYKTV DITG P YGLT--ASN LGN MSLFGVYANOLNG  
Bamb MEX-5 (BurM1) NISGGPVLRVGEL YLVNGKILDEA AER GDS NGTVL EHA TGI--EHA TESAVRA AAVYGLV IHWATG--CYINQP GANQYFA FT--RVG S MSLFGVYANOLNG  
Bcep DWS 37UF10B-2 NIRGG IYQIGKRLVNGKILDEA AAR GSRDVL EHG YGM--ELASKOVV QADIS TYALHS WADM--GWOGIS GATQYGLS--DIT FSG MSLFGVYANOLNG  
Bcen CEIB S5-1 NIRGG IYQIGKRLVNGKILDEA AAR GSRDVL EHG YGM--ELASKOVV QADIS TYALHS WADM--GWOGIS GATQYGLS--DIT FSG MSLFGVYANOLNG  
Bcep DWS 16B-4 NIRGG IYQIGKRLVNGKILDEA AAR GSRDVL EHG YGM--ELASKOVV QADIS TYALHS WADM--GWODIT GATQYGLS--DIT FSG MSLFGVYANOLNG  
Boki C6786 NIRGG IYQIGKRLVNGKILDEA AAR GSRDVL EHG YGM--ELASNNLV KADIA TYGLHWANN--GWOS IV GADQYGLS--NTOPSG MSLFGVYANOLNG  
Boki EO147 NIRGG IYQIGKRLVNGKILDEA AAR GSRDVL EHG YGM--ELASNNLV KADIA TYGLHWANN--GWOS IV GADQYGLS--NTOPSG MSLFGVYANOLNG

Burk A1 GMFLQPSN E QFYGTALLTTS A IYWHYEDGS MRSNIE SMND M G IAD EDP H K RVALD LANSRGT Y I DA QED DNI FSHGDKDI VVAG I LERVIG R V F EDV I I  
Bamb AMMD (BurM2) ---IRVSE E QFYGN E F M F I G A V Y W W F E N G E R S N I E S M N I M G S A D E F K L I O D S I D N P G Y E P G T Y S I D G P E S N I F P N H G A H D F W S A H T V G R V S G H V R G T I T M O  
Bcep GG4 ---IRVSE E QFYGN E F M F I G A V Y W W F E N G E R S N I E S M N I M G V S D F E L I R S S I D N P G Y E P G T Y P I D G P E S N I F P N H G A O D F W S A H T V G R V S G H V R G T I T M O  
Burk A9 ---IPATSE E QFYGN E F M F I G A V Y W W F E N G E R S N I E S M N I M G V S D F E L I R S S I D N P G Y E P G T Y P I D G P E S N I F P N H G A O D F W S A H T V G R V S G H V R G T I T M O  
Bubo Bu ---TPPTS E QFYGN E L M F I G A V N H W H F G N G V O R S N I E S M N I M G V S D F E L I R A N I D N P G Y E P G T Y P I N S G P S N I F P N H G T O D L W S A H T V G R V S G H V R G T I T M O  
Bpyr CH-67 ---IRVSE E QFYGN E L M F I G A V N H W H F G N G V O R S N I E S M N I M G V S D F E L I R A S I D N P G Y E P G T Y P I D G P E S N I F P N H G A O D F W S A H T V G R V S G H V R G T I T M O  
Bamb MC40-6 ---LPATSE E QFYGN E L M F I G A V N H W H F G N G V O R S N I E S M N I M G S A D F E N I A K A N E N P G Y E P G T Y P I D T A S N I F P N H S H G T O D L W S A S V F G R V S G H V R G T I T M O  
Bcep ATCC 25416 ---IPATSE E QFYGN E L M F I G A V N H W H F G N G V O R S N I E S M N I M G V A D E R E I T K A N E N P G Y E P G T Y P I D T A S N I F P N H G T O D L W S A S T F G R V S G H V R G T I T M O  
Bcon LMG 23361 ---IPATSE E QFYGN E L M F I G A V N H W H F G N G V O R S N I E S M N I M G V A D E R E I T K A N E N P G Y E P G T Y P I D T A S N I F P N H G T O D L W S A S T F G R V S G H V R G T I T M O  
Bglu PG1 QG FYL E V S E E K F Y G S P F T T S A I Y W W F E D G S T H M N I N A V N I V N I D E F G P V P E I I R G N P D M S P G T Y P I D A E R S F N I F N H - A S N L W T A L V N G R V S G H V R G T I T M O  
Bamb MEX-5 (BurM1) NLP SR P A S E E A F Y G S P F M S H A I Y W W F E D G S P R M N I O S I N H A M S L S D P A Q I N R A V E N P A Y S H T Y P F D S E F S N I F D H H T K D L W A A G V I G R V S G H V R G T I T M O  
Bcep DWS 37UF10B-2 HLPAP P I E S E K F Y A T E F F T S A Y Y N W H R E N G D P K S V D I K S I R I E H G A Q O I S P I R D I H V N D A M E R G T Y R I D A E S N I L S --D O E L I V G S A L G R V S G H H O G E N F I G  
Bcen CEIB S5-1 HLPAP P I E S E K F Y A T E F F T S A Y Y N W H R E N G D P K S V D I K S I R I E H G V Q O I S P I R D I H V N D A M E R G T Y R I D A E S N I L S --N O E L I V G S A L G R V S G H H O G E N F I G  
Bcep DWS 16B-4 HLPAP P I E S E K F Y A T E F F T S A Y Y N W H R E N G D P K S V D I K S I R I E H G V Q O I S P I R D I H V N D A M E R G T Y R I D A E S N I L S --D O E L I V G S A L G R V S G H H O G E N F I G  
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Boki EO147 HLP P T P I S E E Q F Y A T E F F T A A Y D W H R E N G S P R A V D I K S I R I E H G A N E I G P I R S I H V N D G M E R G A Y P I D A E S N I L S --D K E Y I V G S A L G R V S G H V G O I V I T

Burk A1 T D T H Y S H N G Y W H Y D R Y A Y P S T - E G Y O E V L N N E M N I G A K - S H N D Y D H T E N K G V T I S G O R P N - K E Q A V S - P T G O N T R P S F C G L P R N P P Y I D  
Bamb AMMD (BurM2) Q D N H Y R E V S Y H N N P K A A D S N - E P F I O E W M M V I R E F I G S M L G H A D Y O H Y E T E K E I S F S G O R P V - R N A E T R - P P Q A V H R P S F C G L M R P G P Q  
Bcep GG4 E D N H Y R E A G S Y H N N P K A A D R S N - E P F I O E W M M V I R E F I G S T L G H T D Y O H Y E T E K E I S F S G O R P V - R N A E T R - P P Q A V H R P S F C G L M R P R L W  
Burk A9 E D N H Y R E A G S Y H N N P K A A D R S N - E P F I O E W M M V I R E F I G S T L G H T D Y O H Y E T E K E I S F S G O R P V - R N A E T R - P P Q A V H R P S F C G L M R P R L W  
Bubo Bu A D N H Y R E N G Y W H N P R A D P S N - E P F I O E A A H H F A K I G S V L G H T D Y O H Y E T E K E I S F S G O R P V - R N A E I R - P P Q A V H R P S F C G L M R P G R F  
Bpyr CH-67 E D N H Y R E V S Y H N N P K A A D R S N - E P F I O E W M M V I R E F I G S V L G H T D Y O H Y E T E K E I S F S G O R P V - R N A E T R - P P Q A V H R P S F C G L M R P R L R  
Bamb MC40-6 E D H Y R E D G S Y S N N P R A D P S N - E P F I O E T A M M F I A K I G A I L G H K D Y O H N E E K K I S F S G O R P V - K N A D I R - P P Q A V H R P S F C G L M R P P R  
Bcep ATCC 25416 E D D H Y R E D G Y S N N P R A D P S N - E P F I O E A A H H F I A K I G A I L G R K D Y O H N E E K K I S F S G O R P V - K N A G T R - P P Q A V H R P S F C G L M R P L R  
Bcon LMG 23361 E D D H Y R E D G Y S N N P R A D P S N - E P F I O E A A H H F I A K I G S I L G H K D Y O H N E E K K I S F S G O R P V - K N A G V H - P P Q A V H R P S F C G L M R P P R  
Bglu PG1 G D E S Y A H N G E W H N N P R A Y P S N - A T E T O E V L H S F I S R I G S L - G H V D Y D H I L E T S K E V N L S G R P R P S - - K F F A S - P G A - - - R R S T C G L F E N R N V V N Y  
Bamb MEX-5 (BurM1) D K G D Y R E A G S H H N N P R A Y D S N - A T L T O E V L I K F I G L I G T F - G H K D Y D H I L E T S Q N I T F S G K R P S A N O M P V N - P G E A V H R P S F C G R P P S G T  
Bcep DWS 37UF10B-2 S D D S H Y R E G E W H N P K A A D S R S - P S H O B A L H H F V R K I G E F T D H K D E M I Y E T E S O P I N N I N G T R A S I K A T N P D G T P A A H H T A R P C G F G R R P  
Bcen CEIB S5-1 S D D S H Y R E G E W H N P K A A D S R S - P S H O B A L H H F V R K I G E F T D H K D E M I Y E T E S O P I N N I N G T R A S I K A T N P D G T P A A H H T A R P C G F G R R P  
Bcep DWS 16B-4 S D D S H Y R E G E W H N P K A A D S R S - P S H O B A L H H F V R K I G E F T D H K D E M I Y E T E S O P I N N I N G T R A S I K A T N P D G T P A A H H T A R P C G F G R R P  
Boki C6786 A D G G S H S S E C W H N N P K A A D S N S - P Y I H O E M L H M L V R K M G E I T G H T D E M I Y E K E S O P I N N I S G S R R N I K A M D E R - - - G I V H R P S M C G L P H L G M R D I I N G N V S G L I  
Boki EO147 A D G G S H S S E C W H N N P K A A D S N S - P Y I H O E M L H M L V R K M G E I T G H T D E M I Y E K E S O P I N N I S G S R R N I K A M D E R - - - G I V H R P S M C G L P H L G M R D I I N G N V S G L I

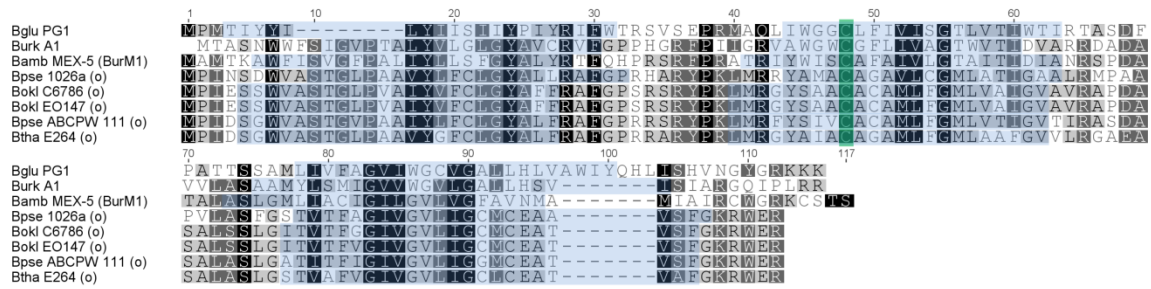
\*

**Fig. S2. Purification of BurM proteins.** SDS PAGE electrophoresis of purified BurM1 (lane 2), BurM2 (lane 3) and BurM2(D297A) (lane 4). Kaleidoscope ladder with size marks (kDa) is visible in line 1.

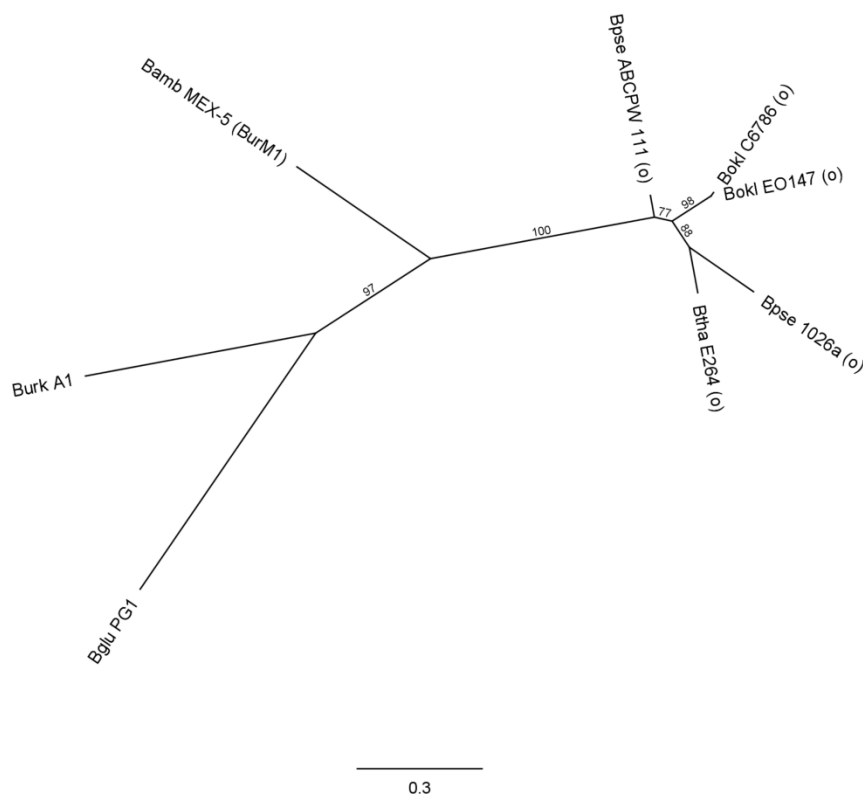


**Fig. S3. Homology and phylogeny of BmiA proteins.** Multiple sequence alignment (A) and unrooted maximum likelihood phylogenetic tree (B) of BmiA proteins. Encoded proteins without associated toxin (orphans) are marked with (o). Abbreviations for species names: Bpse, *Burkholderia pseudomallei*; Btha, *Burkholderia thailandensis*; other abbreviations as in Fig. S1. (A) Predicted transmembrane regions are boxed in blue and the conserved cysteine residue is colored green. Different grey shading indicates the degree of conservation. (B) Scale bar represents 0.3 substitutions per site. Bootstrap values (percentages of 1000 replicates) are shown at the branches.

**A**



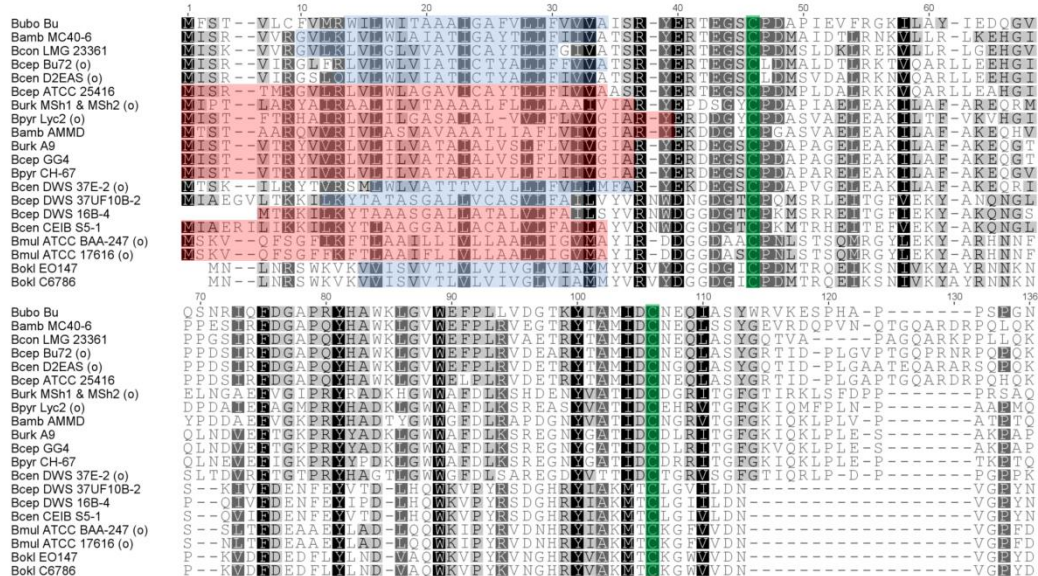
**B**



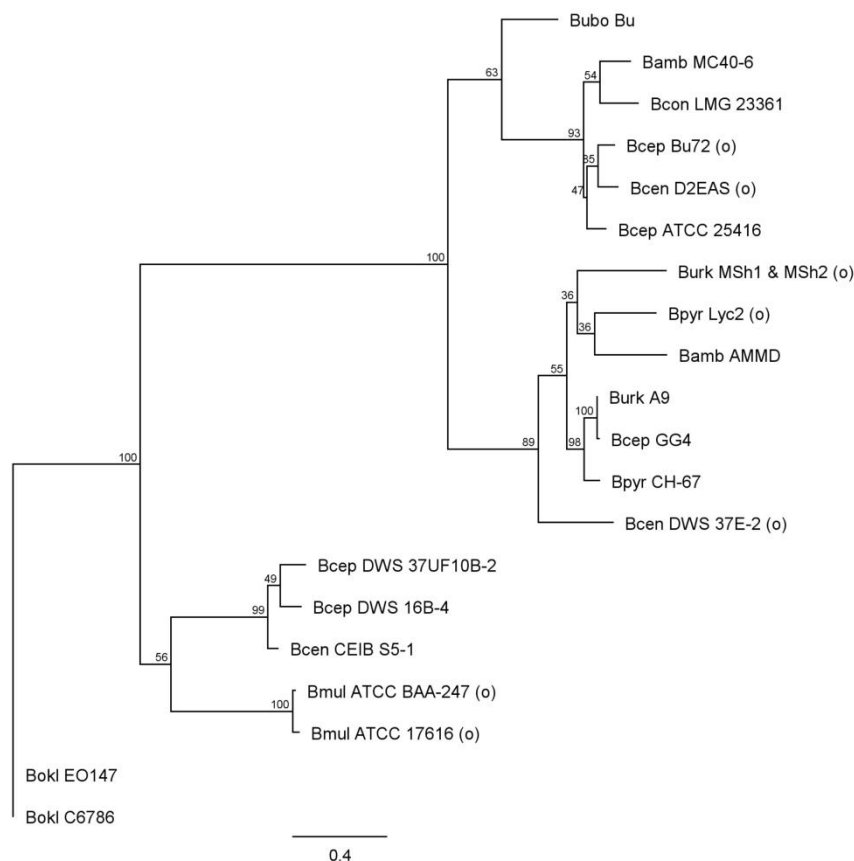


**Fig. S4. Homology and phylogeny of BmiB proteins.** Multiple sequence alignment (A) and unrooted maximum likelihood phylogenetic tree (B) of BmiB proteins. Encoded proteins without associated toxin (orphans) are marked with (o). Abbreviations for species names: Bmul, *Burkholderia multivorans*; other abbreviations as in Fig. S1. (A) Predicted transmembrane regions are boxed in blue, and predicted Sec-dependent signal peptide sequences in red. The conserved cysteine residues are highlighted in green boxes. Different shading indicates a different degree of conservation. (B) Scale bar represents 0.4 substitutions per site. Bootstrap values (percentages of 1000 replicates) are shown at the branches.

**A**



**B**



**Table S1. Susceptibility patterns of *Burkholderia* strains to BurM1 and BurM2.** +, clear halo; T, turbid halo: reduced cell density compared to cell lawn; -, no growth inhibition of the indicator strain; /, not informative.

Species	Strain number	BurM1	BurM2
<i>B. ambifaria</i>	LMG 17828	-	-
	LMG 17829	-	-
	LMG 19182 (or AMMD)	-	/
	LMG 19466	-	-
	LMG 19467	-	-
	LMG 26702 (or MEX-5)	/	-
<i>B. anthina</i>	LMG 20980	-	-
	LMG 20983	-	-
<i>B. arboris</i>	LMG 24066	-	-
<i>B. cenocepacia</i>	LMG 6986	-	-
	LMG 16656	-	-
	LMG 16659	+	-
	LMG 18826	-	-
	LMG 18827	-	-
	LMG 18828	-	-
	LMG 18829	+	+
	LMG 18830	+	-
	LMG 18863	-	-
	LMG 19230	-	-
	LMG 21461	+	-
	LMG 21462	+	-
	LMG 24506	-	-
	<i>B. cepacia</i>	LMG 1222	-
LMG 18821		-	-
<i>B. contaminans</i>	LMG 16227	+	-
<i>B. diffusa</i>	LMG 24065	-	-
	LMG 24266	-	-
<i>B. dolosa</i>	LMG 18941	+	T
	LMG 18943	+	T
<i>B. lata</i>	LMG 6992	-	-
<i>B. latens</i>	LMG 24064	-	-
<i>B. metallica</i>	LMG 24068	T	-
<i>B. multivorans</i>	LMG 13010	-	-
	LMG 18825	-	-
<i>B. pyrrocinia</i>	LMG 14191	T	-
	LMG 21824	-	-
<i>B. seminalis</i>	LMG 24067	+	-
	LMG 24272	-	-
<i>B. stabilis</i>	LMG 14086	-	-
	LMG 14294	-	-
<i>B. ubonensis</i>	LMG 20358	-	-
	LMG 24263	-	-
<i>B. vietnamensis</i>	LMG 10929	-	-
	LMG 18835	-	-

**Table S2. List of primers and plasmids used in this study.**

Primer/plasmid	Sequence <sup>a</sup> /characteristics	Purpose of use/origin
PGPRB-8001	AAGTTGGGTAACGCCAGGGT	Sequencing of inserts in pUC18
PGPRB-8002	GCACCCCAGGCTTTACACTTT	Sequencing of inserts in pUC18
PGPRB-8461	GCTCACTCATTAGGCACCC	Sequencing of inserts in pJB3Tc20
PGPRB-10029	TGGCAGCAGCCAACCTCAGCTT	Sequencing of inserts in pET28(a)
PGPRB-10030	TATAGGCGCCAGCAACCGCA	Sequencing of inserts in pET28(a)
PGPRB-10070	TGGCTACT <b>CGAGT</b> GTCCCGCTAGGACGCGGAC	Cloning of <i>burM1</i> in pET28(a)
PGPRB-10072	TGGCT <b>ACCATGGG</b> ACCTCCTGATCCTATGTTGCCCGT	Cloning of <i>burM1</i> in pET28(a)
PGPRB-10077	TGGCTACT <b>CGAGT</b> TGGGGTCCGGGGCGCATAA	Cloning of <i>burM2</i> in pET28(a)
PGPRB-10080	TGGCT <b>ACCATGGG</b> AACCAATGTGTTGCCGGAAATTTT	Cloning of <i>burM2</i> in pET28(a)
PGPRB-10117	GAGATGTTCAATAACGCTGACCACGGCGACATGATCTC CACCACGGA	Removal of internal NcoI site in <i>burM2</i>
PGPRB-10118	TCCGTGGTGGAGATCATGTCGCCGTGGTCAGCGTTATTG AACATCTC	Removal of internal NcoI site in <i>burM2</i>
PGPRB-10141	TGGCT <b>AGCATGCC</b> CAGTAGACTGCGATCAGTGTC	Cloning of <i>bmiB</i> in pJB3Tc20
PGPRB-10142	TGGCT <b>AGGATCCCC</b> CTGTGAGCGGAGTCATT	Cloning of <i>bmiB</i> in pJB3Tc20
PGPRB-10167	TGGCTACT <b>GCAGT</b> ATTTGACAGCGAAGGAGATGCAAAA TGA	Cloning of <i>burM2</i> in pUC18
PGPRB-10168	TGGCTAT <b>CTAGA</b> ACAGGGCCAATGTGACTGA	Cloning of <i>burM2</i> in pUC18
PGPRB-10179	TCCTACACGTTGAATCCAGCCAAATTCGACGCCGATAGC	Construction of a D297A mutant in <i>burM2</i>
PGPRB-10180	GCTATCGGCGTCAATTTGGCTGGATTCAACGTGTAGGA	Construction of a D297A mutant in <i>burM2</i>
PGPRB-10214	TGGCTACT <b>GCAGAT</b> GGATATTCGATCCCCAGGGGA	Cloning of <i>bmiA</i> in pJB3Tc20
PGPRB-10215	TGGCTAT <b>CTAGAT</b> TGGGTGGACGTCGTAGAGGAA	Cloning of <i>bmiA</i> in pJB3Tc20
pET28(a)	pBR322 origin, His-tag/thrombin/T7 tag ; Km <sup>R</sup>	Novagen
pJB3Tc20	Broad-host-range cloning vector; Ap <sup>R</sup> , Tc <sup>R</sup>	1
pUC18	ColE1 replicon, <i>lacZ</i> , cloning vector; Ap <sup>R</sup>	2
pCMPG6228	pET28(a) with 1013-bp PCR-amplified fragment containing BamMEX5DRAFT_6664 from <i>B. ambifaria</i> MEX-5 cloned in NcoI/XhoI	This study
pCMPG6229	pET28(a) with 983-bp PCR-amplified fragment containing BAMB_RS01670 from <i>B. ambifaria</i> AMMD cloned in NcoI/XhoI	This study
pCMPG6230	Mutant construct of pCMPG6229; D297A of the encoded BmiB	This study
pCMPG6231	pJB3Tc20 with 411-bp PCR-amplified fragment containing BamMEX5DRAFT_6663 from <i>B. ambifaria</i> MEX-5 cloned in PstI/XbaI	This study
pCMPG6232	pJB3Tc20 with 447-bp PCR-amplified fragment containing BAMB_RS01665 from <i>B. ambifaria</i> AMMD cloned in SphI/BamHI	This study

<sup>a</sup> Restriction sites incorporated in the primers are shown in bold: GGATCC, BamHI; CCATGG, NcoI; CTGCAG, PstI; GCATGC, SphI; TCTAGA, XbaI; CTCGAG, XhoI.

## References

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