

Short Antimicrobial Peptide Derived from the Venom Gland Transcriptome of *Pamphobeteus verdolaga* Increases Gentamicin Susceptibility of Multidrug-Resistant *Klebsiella pneumoniae*

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Table S1. Custom database (cDB) of arthropod antimicrobial peptides.

Peptide	Species	Sequence	# aa	Charge (+)	MIC <i>E. coli</i> (μM)	MIC <i>S. aureus</i> (μM)
AaeAP1	<i>Androctonus aeneas</i>	FLFSLIPSVIAGLVSAIRN	19	1		11.90
AaeAP1 [S4.8.15K; A11K. N19K]	<i>Androctonus aeneas</i>	FLFKLIPKVIKGLVKAIRK	19	6	10.85	8.14
AaeAP2	<i>Androctonus aeneas</i>	FLFSLIPSAIAGLVSAIRN	19	1		8.04
AaeAP2 [S4.8.15K; A11K. N19K]	<i>Androctonus aeneas</i>	FLFKLIPKAIKGLVKAIRK	19	6	10.99	8.24
AamAP1 [S4K.H8K.G11.12 K.A16K]	<i>Androctonus amoreuxi</i>	FLFKLIPKAIKKLISKFK	18	6	7.50	5.00
AamAP1 [H8K]	<i>Androctonus amoreuxi</i>	FLFSLIPKAIGGLISAFK	18	2	5.00	3.00
AcrAP1	<i>Androctonus crassicauda</i>	FLFSLIPHAISGLISAFK	18	1		8.00
AcrAP1a	<i>Androctonus crassicauda</i>	FLFKLIPKAIKGLIKAFK	18	6	4	8
AcrAP1a [S4K.H8K.S11K.S15K]	<i>Androctonus crassicauda</i>	FLFKLIPKAIKGLIKAFK	18	5	8.00	4.00
AcrAP2	<i>Androctonus crassicauda</i>	FLFSLIPNAISGLLSAFK	18	1		8.00

AcrAP2 [S4K.N8K.S11K.S 15K]	<i>Androctonus crassicauda</i>	FLFKLIPKAIKGLLKAFK	18	5	8.00	4.00
Agelaia-CP	<i>Agelaia pallipes</i>	ILGTILGLLKGL	12	1		12.00
Androctonin	<i>Androctonus australis</i>	RSVCRQIKICRRRGGCYYKCTNRPY	25	8	12.00	
Apidaecin-1A	<i>Apis mellifera</i>	GNNRPVYIPQRPHPHR	17	3	11.71	
Apidaecin-1B	<i>Apis mellifera</i>	GNNRPVYIPQRPHPHRL	18	3	0.32	
Apidaecin-2	<i>Apis mellifera</i>	GNNRPYIPQRPHPHRL	18	3	0.09	
Bicarinalin	<i>Tetramorium bicarinatum</i>	KIKIPWGVKVDLVLGGMKAV	20	4		10.45
BmKn1	<i>Mesobuthus martensii</i>	FIGAVAGLLSKIF	13	1		14.97
Bmkn2	<i>Mesobuthus martensii</i>	FIGAIARLLSKIFGKR	16	4	1.50	0.60
BmKn2OR	<i>Mesobuthus martensii</i>	FIGAIARLLSKIF	13	2		5.49
cGomesin	<i>Acanthoscurria gomesiana</i>	GCRRLCYQRCVITYCRGR	18	6	2.03	
Codesane	<i>Colletes daviesanus</i>	GMASLLAKVLPVVKLIK	18	3	3.70	3.70
Css54	<i>Centruroides suffusus suffusus</i>	FFGSLLSLGSKLLPSVFKLFQRKKE	25	4	4.35	4.35
Ctriporin	<i>Chaerilus tricostatus</i>	FLWGLIPGAISAVTSLIKK	19	2		4.34
Cupiennin-1d	<i>Cupiennius salei</i>	GFGSLFKFLAKKVAKTVAKQAAKQGAKYVANK HME	35	7	0.12	0.94
Cupiennin-2a	<i>Cupiennius salei</i>	GFGTILKALAKIAGKVVKLATKPGATYMLKENL K	35	7	0.16	0.16
Defensin-1	<i>Centruroides limpidus limpidus</i>	ACQFWSCNSSCISRGYRQGYCWGIQYKYCQCQ	32	3	13.08	13.08
Delta-Myrtoxin- Mp1a	<i>Myrmecia pilosula</i>	IDWKKVDWKKVSKKTCKVMLKACKFLG	27	7		4.80
Dominulin-A	<i>Polistes dominula</i>	INWKKIAEVGGKILSSL	17	2	4.31	
Dominulin-B	<i>Polistes dominula</i>	INWKKIAEIGKQVLSAL	17	2	4.19	
Eumenine mastoparan-AF	<i>Anterhynchium flavomarginatu m</i>	INLLKIAKGIIKSL	14	3	13.12	3.28
Eumenitin	<i>Eumenes rubronotatus</i>	LNLKGIFKKVASLLT	15	3	6.00	
Gomesin	<i>Acanthoscurria gomesiana</i>	CRRRLCYQRCVITYCRGR	17	6	0.80	12.10
Gomesin (4-18) [Q9p]	<i>Acanthoscurria gomesiana</i>	RLTYKPRTVTYTRGR	15	5	10.24	
Gomesin c(1- 18)[Gln1]	<i>Acanthoscurria gomesiana</i>	QCRRLCYQRCVITYCRGR	18	6	0.48	1.44
H/V-peptide (1- 11)(19-25)	<i>Hadrurus aztecus</i>	GILKTIKSIASKLKRKAK	18	7	9.37	
H/V-peptide (1- 28)	<i>Vaejovis mexicanus smithi</i>	GILKTIKSIASKVANTVQKLKRKAKNAV	28	8	1.20	
HAL-1	<i>Halictus sexcinctus</i>	GMWSKILGHLIR	12	2	3.80	7.70

HAL-1/10	<i>Halictus sexcinctus</i>	GMWKKILGKLIR	12	4	2.30	15
HAL-1/15	<i>Halictus sexcinctus</i>	GMWSKLLGHLLR	12	2	3.00	7.70
HAL-1/18	<i>Halictus sexcinctus</i>	GMWSKILKHLIR	12	3	2.30	3.70
HAL-1/19	<i>Halictus sexcinctus</i>	GKWKKILGHLIR	12	4	2.70	
HAL-1/20	<i>Halictus sexcinctus</i>	GKWSKILGKLIR	12	4	2.30	
HAL-1/21	<i>Halictus sexcinctus</i>	GKWKKILGKLIR	12	5	1.80	
HAL-1/26	<i>Halictus sexcinctus</i>	GMWSKILGHLI	11	1	7.00	
HAL-1/5	<i>Halictus sexcinctus</i>	GMWKKILGHLIR	12	3	1.80	8.40
HAL-1/6	<i>Halictus sexcinctus</i>	GMWSKILGHLIK	12	2	7.20	
HAL-1/9	<i>Halictus sexcinctus</i>	GMWSKILGKLIR	12	3	3.70	9.20
HAL-2	<i>Halictus sexcinctus</i>	GKWMSLLKHILK	12	3	2.50	8.10
HAL-2/1	<i>Halictus sexcinctus</i>	GKWKSLLKHILK	12	4	3.70	
HAL-2/10	<i>Halictus sexcinctus</i>	GKWWSLLKHILK	12	3	1.60	4.70
HAL-2/11	<i>Halictus sexcinctus</i>	GKWLSLLKHILK	12	3	1.80	5.50
HAL-2/12	<i>Halictus sexcinctus</i>	GKWMHLLKHILK	12	3	3.70	12.50
HAL-2/13	<i>Halictus sexcinctus</i>	GKWMTLLKHILK	12	3	2.70	5.30
HAL-2/14	<i>Halictus sexcinctus</i>	GKWMSLLKQILK	12	3	2.50	10.80
HAL-2/16	<i>Halictus sexcinctus</i>	SKWMSLLKHILK	12	3	2.30	9.20
HAL-2/17	<i>Halictus sexcinctus</i>	HKWMSLLKHILK	12	3	3.50	
HAL-2/2	<i>Halictus sexcinctus</i>	GKWMKLLKHILK	12	4	2.50	4.50
HAL-2/20	<i>Halictus sexcinctus</i>	GKWMSLWKHILK	12	3	8.00	
HAL-2/21	<i>Halictus sexcinctus</i>	GKWMSWLKHILK	12	3	3.90	10.10
HAL-2/24	<i>Halictus sexcinctus</i>	GKFMSLLKHILK	12	3	5.80	
HAL-2/4	<i>Halictus sexcinctus</i>	GKWMSLLKKILK	12	4	2.70	6.30
HAL-2/5	<i>Halictus sexcinctus</i>	KKWMSLLKHILK	12	4	6.30	
HAL-2/6	<i>Halictus sexcinctus</i>	GKWMSFLKHILK	12	3	4.00	6.40
HAL-2/9	<i>Halictus sexcinctus</i>	GKWQSLLKHILK	12	3	8.00	
Heterin 2	<i>Heterometrus spinifer</i>	FWGALAKGALKLIPSLVSSFTKGD	24	3		5.60
Hp1090	<i>Heterometrus petersii</i>	FKAIWSGIKSLF	12	2	15	
Hp1404	<i>Heterometrus petersii</i>	GILGKLWEGVKSIF	14	1		8.75

HYL	<i>Hylaeus signatus</i>	GIMSSLMKKLAASHIAK	16	3	15	
Im-5	<i>Isometrus maculatus</i>	FLGSLFSIGSKLLPGVIKLFQRKKQ	25	5	10.00	3.75
IsCT	<i>Opisthacanthus madagascariensis</i>	ILGKIWEGIKSLF	13	1	4.00	1.25
IsCT [EK7. GP8. SK11]	<i>Opisthacanthus madagascariensis</i>	ILGKIWKPIKKLF	13	4	2.00	1.17
IsCT [EK7]	<i>Opisthacanthus madagascariensis</i>	ILGKIWKGIKSLF	13	3	2.00	1.00
IsCT [WL6. SK11]	<i>Opisthacanthus madagascariensis</i>	ILGKILKGIKKLF	13	4	2.00	2.00
IsCT [WL6]	<i>Opisthacanthus madagascariensis</i>	ILGKILEGIKSLF	13	1		4.00
IsCT precursor	<i>Opisthacanthus madagascariensis</i>	ILGKIWKIKKLF	12	4	2.00	2.00
IsCT-P	<i>Opisthacanthus madagascariensis</i>	ILKKIWKPIKKLF	13	5	2.00	1.00
Ixosin	<i>Ixodes sinensis</i>	GLHKVMREVLGYERNSYKKFFLR	23	4	10.45	1.29
Jellein-1	<i>Apis mellifera</i>	PFKLSLHL	8	1	2.62	10.48
Jellein-2	<i>Apis mellifera</i>	TPFKLSLHL	9	1	14.21	
Lacrain	<i>Scolopendra viridicornis</i>	RYPAVGYT	8	1	5.80	
Lasiocepsin	<i>Lasioglossum laticeps</i>	GLPRKILCAIAKKKGKCKGPLKLVCCK	27	9	3.00	
Lasioglossin LL-I	<i>Lasioglossum laticeps</i>	VNWKVVLGKIIKVAK	15	5	1.70	14.3
Lasioglossin LL-II	<i>Lasioglossum laticeps</i>	VNWKILGKIIKVAK	15	5	1.40	9.00
Lasioglossin LL-III	<i>Lasioglossum laticeps</i>	VNWKILGKIIKVVK	15	5	1.40	3.90
Latarcin-1	<i>Lachesana tarabaei</i>	SMWSGMWRRKLKLRNALKKKLKGEK	26	10	0.85	
Latarcin-2a	<i>Lachesana tarabaei</i>	GLFGKLIKFGKRAISYAVKKARGKN	26	10	0.7	
Latarcin-3a	<i>Lachesana tarabaei</i>	SWKSMAKKLKEYMEKLKQRA	21	5	4.25	
Latarcin-4a	<i>Lachesana tarabaei</i>	GLKDKFKSMGEKLKQYIQTWKAKF	25	5	3.85	
Latarcin-4b	<i>Lachesana tarabaei</i>	SLKDKVKSMGEKLKQYIQTWKAKF	24	5	4.40	
Latarcin-5	<i>Lachesana tarabaei</i>	GFFGKMKEYFKKFGASFRRFANLKKRL	28	9	0.60	0.70
Longicin (53-73)	<i>Haemaphysalis longicornis</i>	SIGRRGGYCAGIHKQTCTCYR	21	4	2.00	2.00
Lycocitin-1	<i>Lycosa singoriensis</i>	GKLQAFIAKMEIAAQTL	19	2	4.80	
Lycocitin-2	<i>Lycosa singoriensis</i>	GRLQAFIAKMEIAAQTL	18	2	4.70	
Lycosin-I	<i>Lycosa singoriensis</i>	RKGWFKAMKSIKFIKKEKLKEHL	24	6		7.80

Lycosin-II	<i>Lycosa singoriensis</i>	VWLSALKFIGKHLAKHQLSKL	21	4	12.50	3.10
M-ctenitoxin-Cs1a	<i>Cupiennius salei</i>	GFGALFKFLAKKVAKTVAKQAAKQGAKYVVNKQME	35	7	0.47	0.47
M-lycotoxin-Hc1a	<i>Hogna carolinensis</i>	IWLTALKFLGKHAACHHLAKQQLSKL	26	5	15	
M-theraphotoxin-Gr1a	<i>Grammostola rosea</i>	GCLEFWWKCNPNDKCCRPKLKCSKLFKLCNFSF	34	4	12.00	3.00
Macropin 1	<i>Macropis fulvipes</i>	GFGMALKLLKKVL	13	3	3.00	3.70
Marmelittin	<i>Mesobuthus martensii</i>	FLFSLIPSAISGLISAFKGRR	21	3	6.21	6.48
Mastoparan B	<i>Vespa basalis</i>	LKLKSIVSWAKKVL	14	4		8.89
Mastoparan MP	<i>Mischocyttarus phthisicus</i>	INWLKLGKKMMSAL	14	3		9.00
Mastoparan PDD-A	<i>Polistes dorsalis dorsalis</i>	INWKKIFEKVKNLV	14	3	5.62	11.80
Mastoparan PMM	<i>Polistes major major</i>	INWKKIASIGKEVLKAL	17	3	4.93	
Mastoparan-A	<i>Vespa analis</i>	IKWKAILDAVKKVI	14	3	4.92	
Mastoparan-AF	<i>Vespa magnifica</i>	INLKAIAALAKKLF	14	3	3.96	
Mastoparan-L	<i>Vespa tropica</i>	INLKALAALAKKIL	14	3		14.6
Mastoparan-like peptide 12b	<i>Vespa magnifica</i>	INWKGIAAMKKLL	13	3	10.09	2.49
Mastoparan-like peptide 12c	<i>Vespa magnifica</i>	INLKAIAALAKKLLG	15	3	3.90	1.95
Mastoparan-like peptide 12d	<i>Vespa magnifica</i>	INLKAIAAMAKKLL	14	3	2.00	1.00
Mastoparan-M	<i>Vespa magnifica</i>	INLKAIAALAKKLL	14	3	5.41	
Mastoparan-T	<i>Vespa tropica</i>	INLKAIAAFACKLL	14	3	5.28	
Mastoparan-V	<i>Vespa magnifica</i>	INWKGIAAMAKKLL	14	3	5.13	
Mastoparan-VT2	<i>Vespa tropica</i>	NLKAIAALAKKLL	13	3	10.06	5.49
Mastoparan-VT3	<i>Vespa tropica</i>	INLKAITALAKKLL	14	3		3.86
Mastoparan-VT7	<i>Vespa tropica</i>	INLKAIAALARNY	13	2		13.98
Melectin	<i>Melecta albifrons</i>	GFLSILKKVLPKVMAMHK	18	4	10.37	12.80
Melittin	<i>Apis florea</i>	GIGAILKVLATGLPTLISWIKNRKQ	26	5	0.60	0.60
Melittin	<i>Apis mellifera</i>	GIGAVLKVLTTGLPALISWIKRKRQQ	26	5	2.72	2.78
Meucin-13	<i>Mesobuthus eupeus</i>	IFGAIAGLLKNIF	13	1	7.90	8.89
Meucin-18	<i>Mesobuthus eupeus</i>	FFGHLFKLATKIIPSLFQ	18	2	12.56	4.29
Midgut defensin G2	<i>Haemaphysalis longicornis</i>	ACHAHCQSVGRRGGYCGNFRMTCYCY	26	3	5.94	5.09
MP-VB1	<i>Vespa bicolor</i>	INMKASAAYAKKLL	14	3		2.15
Mucroporin	<i>Lychas mucronatus</i>	LFGLIPSLIGGLVSAFK	17	1		14.43
OcyC1	<i>Urodacus yaschenkoi</i>	ILSAIWSGIKSLF	13	1		6.50
OsDef2 (16-37)	<i>Ornithodoros savignyi</i>	KGIRGYKGGYCKGAFKQTCKCY	22	6		6.10

OsDef2 (16-37)[C26.34.36Del]	<i>Ornithodoros savignyi</i>	KGIRGYKGGYKGAFKQTKY	19	6		6.98
Osmin	<i>Osmia rufa</i>	GFLSALKKYLPVLKHV	17	3	1.56	
OxTx1	<i>Oxyopes takobius</i>	KFKWGKLFSTAKKLYKKGGKLSKNKNFKKALKF GK	35	15	0.19	0.93
Oxyopinin-4a	<i>Oxyopes takobius</i>	GIRCPKSWKCKAFKQRVLKRLAMLRLQHAF	31	9	0.50	10.00
Pandinin-2	<i>Pandinus imperator</i>	FWGALAKGALKLIPSLFSSFSKKD	24	3		12.34
Pandinin-2 [P14G]	<i>Pandinus imperator</i>	FWGALAKGALKLIGSLFSSFSKKD	24	3	12.50	12.50
Pantinin-1	<i>Pandinus imperator</i>	GILGKLWEGFKSIV	14	1		11.00
Pantinin-3	<i>Pandinus imperator</i>	FLSTIWNGIKSLL	13	1		14
Parapolybia Mastoparan	<i>Parapolybia indica</i>	INWKKMAATAALKMI	14	3	2.41	1.79
Pepcon	<i>Androctonus amoreuxi</i>	FLFSLIPSAIGGLISAFK	18	1		5.00
Peptide BmKb1	<i>Mesobuthus martensii</i>	FLFSLIPSAISGLISAFK	18	1		7.27
Pilosulin-1 (1-20)	<i>Myrmecia pilosula</i>	GLGSVFGRLARILGRVIPKV	20	4	3.33	2.50
Pilosulin-2	<i>Myrmecia pilosula</i>	GLLSKFGRLARKLARVIPKV	20	6	1.33	4.00
PNG-1	<i>Panurgus calcaratus</i>	LNWGAILKHHIK	12	2	3.70	10.60
PNG-1/1	<i>Panurgus calcaratus</i>	NLWAGILKHHIK	12	2	12.50	
PNG-1/12	<i>Panurgus calcaratus</i>	KNWGKILKHHIK	12	4	11.30	
PNG-1/13	<i>Panurgus calcaratus</i>	KNWKAILKHHIK	12	4	7.80	
PNG-1/17	<i>Panurgus calcaratus</i>	LNWGAFLKHFFK	12	2	5.00	
PNG-1/19	<i>Panurgus calcaratus</i>	LNWGALLKHLLK	12	2	3.80	6.70
PNG-1/22	<i>Panurgus calcaratus</i>	LNWGAWLKHWWK	12	2	7.20	
PNG-1/3	<i>Panurgus calcaratus</i>	LKWGAILKHHIK	12	3	3.70	11.70
PNG-1/5	<i>Panurgus calcaratus</i>	LNWKAILKHHIK	12	3	2.30	5.30
PNG-1/6	<i>Panurgus calcaratus</i>	LNWGKILKHHIK	12	3	4.00	8.70
PNG-1/9	<i>Panurgus calcaratus</i>	LNWGAILKKIHK	12	3	4.30	7.30
Polybia-CP	<i>Polybia paulista</i>	ILGTILGLLKSLL	12	1		4.00
Polybia-MP-II	<i>Polybia paulista</i>	INWLKLGKMVIDAL	14	1	4.96	2.36
Polyphemusin-2	<i>Limulus polyphemus</i>	RRWCFRVCYKGFCYRKCR	18	8	3.87	5.14
Polyphemusin-1	<i>Limulus polyphemus</i>	RRWCFRVCYRGFCYRKCR	18	8	0.9	0.3
Ponericin-G1	<i>Pachycondyla goeldii</i>	GWKDWAKKAGGWLKKKGPGMAKAALKAAAMQ	30	7		8.00
Ponericin-W1	<i>Pachycondyla goeldii</i>	WLGSALKIGAKLLPSVVGLFKKKKQ	25	6		8.00

Ponericin-W4	<i>Pachycondyla goeldii</i>	GIWGTALKWGVKLLPKLVGMAQTKKQ	26	5	7.25	12.50
Protonectarina Mastoparan	<i>Protonectarina sylveirae</i>	INWKALLDAAKKVL	14	2	4.93	2.46
Salivary glands defensin S2	<i>Haemaphysalis longicornis</i>	NCIQQCVSCKGAQGGYCTNEKCTCY	24	1	6.73	5.76
Scolopendin 2	<i>Scolopendra subspinipes mutilans</i>	AGLQFPVGRIGRLLRK	16	4	6.30	
Scolopin 1	<i>Scolopendra mutilans</i>	FLPKMSTKL RVPYRRGTKDYH	21	5	5.30	1.20
Scolopin 2	<i>Scolopendra mutilans</i>	GILKKFMLHRG TKVYKMRTL SKRSH	25	8	5.00	0.25
Smp24 - GVG	<i>Scorpio maurus palmatus</i>	IWSFLIKAATKLLGVGSLFGGKKDS	26	3		5.94
Smp24-T	<i>Scorpio maurus palmatus</i>	IWSFLIKAATKLLPSLFGG	19	2		7.76
Tachyplesin-3	<i>Tachyplesus gigas</i>	KWCFRVCYRGICYRKCR	17	7	7.1	1.8
Tachyplesin-2	<i>Tachyplesus tridentatus</i>	RWCFRVCYRGICYRKCR	17	7	4.1	1
Tachyplesin-1	<i>Tachyplesus gigas</i>	KWCFRVCYRGICYRRCR	17	7	1.8	1.3
Toxin LyeTx 1	<i>Lycosa erythrognatha</i>	IWLTALKFLGKNLGKHLAKQQLAKL	25	5	6.66	4.65
TsAP2	<i>Tityus serrulatus</i>	FLGMIPGLIGGLISAFK	17	1		7.50
Um3	<i>Urodacus manicatus</i>	GFWGKLWEGVKSAL	14	1	15	15
Um4	<i>Urodacus manicatus</i>	FFSALLSGIKSLF	13	1	8.00	15.00
Um5	<i>Urodacus manicatus</i>	IFKAIWSGIKSLF	13	2	15.00	
Uy192	<i>Urodacus yaschenkoi</i>	FLSTIWNGIKGLL	13	1	15.00	
Uy192 [G11S.L13F]	<i>Urodacus yaschenkoi</i>	FLSTIWNGIKSLF	13	1		8.00
Uy234 [Ins 5.9.12.16K]	<i>Vaejovis punctatus</i>	FPFLKLSLKIPKSAIKSAIKRL	22	6	8.00	
UyCT1	<i>Urodacus yaschenkoi</i>	GFWGKLWEGVKNAI	14	1		6.75
UyCT1 - 3K	<i>Urodacus yaschenkoi</i>	GFWGKLWEGVKNAIKKK	17	4	4.00	
UyCT1 [W7L.N12K]	<i>Urodacus yaschenkoi</i>	GFWGKLLEGVKKAI	14	2	15.00	
UyCT3 [L2F.S3G]	<i>Urodacus yaschenkoi</i>	IFGAIWSGIKSLF	13	1	8.00	
UyCT5	<i>Urodacus yaschenkoi</i>	IWSAIWSGIKGLL	13	1		2.75
VCP 5f	<i>Vespa magnifica</i>	FLPIRPILLGGL	13	1		6.84
VCP 5g	<i>Vespa magnifica</i>	FLIIRRPIVLGGL	13	2		6.57
VCP-VT2	<i>Vespa tropica</i>	FLPIIGKLLSG	11	1	8.64	5.04
Ves-CP-M	<i>Vespa magnifica</i>	FLPIIGKLLSGLL	13	1		8.00
Ves-CP-X	<i>Vespa magnifica</i>	FLPIIAKLLGGLL	13	1		3.66
VESP-VB1	<i>Vespa bicolor</i>	FMPIIGRLMSGSL	13	1	7.91	1.56

VmCT1 [N7K]	<i>Vaejovis mexicanus smithi</i>	FLGALWKVAKSVF	13	2	1.56	6.56
VmCT1 [A9W]	<i>Vaejovis mexicanus smithi</i>	FLGALWNVWKS VF	13	1	1.56	1.56
VmCT1 [G3K]	<i>Vaejovis mexicanus smithi</i>	FLKALWNVAKSVF	13	2	1.56	3.12
VmCT1 [S11K]	<i>Vaejovis mexicanus smithi</i>	FLGALWNVAKKVF	13	2	1.56	1.56
VmCT2	<i>Vaejovis mexicanus smithi</i>	FLSTLWNAAKSIF	13	1		10.00
VpAmp1.0	<i>Vaejovis punctatus</i>	LPFFLLSLIPSAISAIKKI	19	2		2.50
VpAmp1.1	<i>Vaejovis punctatus</i>	FFLLSLIPSAISAIKKI	17	2		5.00
VpAmp2.0	<i>Vaejovis punctatus</i>	FWGFLGKLAMKAVPSLIGGNKSSSK	25	4		10.00
VpAmp2.1	<i>Vaejovis punctatus</i>	FWGFLGKLAMKAVPSLIGGNKK	22	4		5.00
Xac-2	<i>Xylocopa appendiculata</i>	GFVALLKKLPLILKHL P	17	3	3.12	3.12

Table S2. List of *P. verdolaga*'s hypothetical AMPs.

Id.	Candidate	A	B	C	Homologous to	D	Contig id
PvAMP0	CFYKCTN	7	2	1.25	Androctonin	85.71	Pv_tr_17126.t1
PvAMP1	CRPKLRC	7	4	1.22	M-theraphotoxin-Gr1a	85.71	Pv_sp_5188.t1
PvAMP2	QRAVTCY [†]	7	2	1.25	cGomesin	85.71	Pv_tr_14213.t1
PvAMP3	IQTIKAK [†]	7	3	1.23	M-zodatoxin-Lt4a	85.71	Pv_sp_1494.t1
PvAMP5	KQKCVTY	7	3	1.95	Gomesin	85.71	Pv_so_5570.t1
PvAMP6	YKCTYRP	7	3	2.32	Androctonin	85.71	Pv_tr_16614.t1
PvAMP7	SLWGMWR	7	2	2.33	M-zodatoxin-Lt1a	75	Pv_sp_3683.t1
PvAMP8	SLFKFLA	7	2	0.52	Cupiennin-1d	100	Pv_tr_9174.t1
PvAMP9	NSLRKVQ	7	3	1.05	Lt4a	85.71	Pv_tr_16907.t1
PvAMP11	INRKLLE	7	2	1.06	Lt4b	85.71	Pv_sp_4704.t1
PvAMP12	AKMREIA	7	2	1.06	Lycocitin 1	85.71	Pv_so_4563.t1
PvAMP13	DKFKAMG	7	2	1.05	M-zodatoxin-Lt4a	85.71	Pv_tr_17094.t1
PvAMP14	KEKLKEH	7	2	2.14	Lycosin-I	100	Pv_so_3998.t1
PvAMP15	FLGKNLG	7	2	0.52	Lycosin-I	100	Pv_sp_6402.t1
PvAMP16	LLSKIFG [†]	7	2	0.52	Bmkn2	100	Pv_tr_2228.t1
PvAMP17	GMISAFK	7	2	0.52	TsAP2	85.71	Pv_sp_6035.t1
PvAMP18	KIIPNLF	7	2	0.52	Meucini-18	85.71	Pv_sp_2233.t1
PvAMP19	FVFKLIP	7	2	0.52	AcrAP2a	85.71	Pv_tr_2209.t1
PvAMP20	IKKLISK	7	4	1.57	AamAP1	100	Pv_sp_1634.t1
PvAMP21	LVKAVRK	7	4	1.4	AaeAP1 [S4.8.15K; A11K. N19K]	85.71	Pv_sp_6551.t1
PvAMP22	LLPSIFK	7	2	0.52	Css54	85.71	Pv_sp_192.t1
PvAMP23	RIGRILR	7	4	1.05	Scolopendin 2	85.71	Pv_sp_225.t1
PvAMP24	VTYTRDR	7	2	1.42	Gomesin (4-18) [Q9p]	85.71	Pv_tr_1752.t1
PvAMP25	IWKIKKL	7	4	2.56	IsCT precursor	100	Pv_sp_743.t1
PvAMP26	VLGKIWK	7	3	2.04	IsCT precursor	85.71	Pv_sp_13985.t1
PvAMP27	GLLKNVF	7	2	0.52	Meucini-13	85.71	Pv_sp_7193.t1
PvAMP28	KLLSKIF	7	3	1.05	Bmkn2	100	Pv_sp_556.t1
PvAMP29	IFKSLWS	7	2	1.51	Um5	71.43	Pv_sp_550.t1
PvAMP30	LLTGIKS	7	2	0.52	Um4	85.71	Pv_sp_8010.t1
PvAMP31	ILGKILR	7	3	0.87	IsCT [WL6. SK11]	100	Pv_so_7688.t1
PvAMP32	IIKKIWK	7	4	2.56	IsCT-P	85.71	Pv_so_7981.t1
PvAMP33	RVAKSVF	7	3	0.87	VmCT1	100	Pv_tr_5074.t1
PvAMP34	LWNVVKK	7	3	2.04	VmCT1 [S11K]	85.71	Pv_tr_5073.t1
PvAMP35	NIWKSIV	7	2	2.24	VmCT1 [A9W]	71.43	Pv_sp_1355.t1
PvAMP36	VCYKGHCY [†]	8	2	1.9	Polyphemusin-2	87.5	Pv_tr_15238.t1
PvAMP37	KILKHVIK [†]	8	4	1.56	PNG-1/6	87.5	Pv_sp_2023.t1
PvAMP38	YIQTWHTK [†]	8	2	2.3	M-zodatoxin-Lt4b	100	Pv_tr_7193.t1
PvAMP39	RGYKGGHC [†]	8	3	1.58	OsDef2 (16-37)	87.5	Pv_sp_11752.t1
PvAMP41	KCEGNRR	8	3	1.23	κ-theraphotoxin-Gr4a	72.73	Pv_sp_3172.t1
PvAMP42	FADLKRL	8	3	1.22	M-zodatoxin-Lt5a	87.5	Pv_tr_11159.t1
PvAMP43	VAKTVTKQ	8	3	1.07	M-ctenitoxin-Cs1a	87.5	Pv_sp_67.t1
PvAMP45	RKLMEINL	8	2	0.92	Lt4a	75	Pv_tr_7666.t1
PvAMP46	DRKLMQII	8	2	0.92	Lt4a	62.5	Pv_sp_3014.t1
PvAMP47	LTKMKEIA	8	2	1.08	Lycocitin 1	87.5	Pv_sp_2708.t1
PvAMP48	KAMKAIK	8	4	1.38	Lycosin-I	87.5	Pv_tr_4264.t1
PvAMP49	KDKLKEHM	8	2	1.72	Lycosin-I	75	Pv_tr_3957.t1
PvAMP50	FKAMKGVA	8	3	0.92	Lycosin-I	75	Pv_tr_1918.t1
PvAMP51	LLSRIFGK	8	3	0.76	Bmkn2	87.5	Pv_tr_9659.t1
PvAMP52	VRNAIRKK	8	5	1.53	UyCT1 - 3K	75	Pv_tr_9657.t1
PvAMP53	KLAAKIIP	8	3	0.92	Meucini-18	87.5	Pv_sp_1006.t1
PvAMP54	SGMISAFK	8	2	0.46	Marmelittin	87.5	Pv_sp_6035.t1
PvAMP56	KGLLKDFK	8	3	1.38	AcrAP2a	87.5	Pv_sp_2642.t1
PvAMP57	PGAIIKLI	8	3	0.92	AamAP1	87.5	Pv_sp_2640.t1
PvAMP58	IPKVVKGM	8	3	0.92	AaeAP1 [S4.8.15K; A11K. N19K]	75	Pv_sp_5515.t1
PvAMP59	FPVGRVAR	8	3	0.61	Scolopendin 2	75	Pv_sp_6943.t1
PvAMP60	GAIAKLLS	8	2	0.46	Bmkn2	87.5	Pv_tr_6401.t1

PvAMP61	LSTRWNGI	8	2	1.17	Uy192	87.5	Pv_tr_13580.t1
PvAMP62	LGKILDIK	8	2	0.92	IsCT [WL6]	77.78	Pv_tr_13579.t1
PvAMP63	ALNVAKSV	8	2	0.46	VmCT1 [G3K]	88.98	Pv_tr_7191.t1
PvAMP64	KALWNILK	8	3	1.78	VmCT1 [G3K]	75	Pv_so_8363.t1
PvAMP65	ALWNILKK	8	3	1.78	VmCT1 [S11K]	75	Pv_so_8363.t1
PvAMP66	WKKIKKFF	8	5	2.7	IsCT [EK7. GP8. SK11]	75	Pv_tr_5073.t1
PvAMP67	KLLNGVKK	8	4	1.38	UyCT1 [W7L.N12K]	87.5	Pv_sp_1577.t1
PvAMP68	LEGVKRAV	8	2	0.92	UyCT1 [W7L.N12K]	75	Pv_sp_5735.t1
PvAMP69	YRARCVIYC	9	3	1.67	Gomesin c(1-18)[Gln1]	66.67	Pv_tr_6713.t1
PvAMP70	QAVLKRLLA	9	3	0.82	Oxyopinin-4a	88.89	Pv_tr_6712.t1
PvAMP71	TKPYMLKDN	9	2	1.38	Cupiennin-2a	66.67	Pv_tr_4146.t1
PvAMP72	AKIPGKVVR	9	4	1.09	Cupiennin-2a	77.78	Pv_tr_4145.t1
PvAMP73	NKDFKTLK	9	4	1.63	OxTx1	77.78	Pv_sp_260.t1
PvAMP74	FLSKMKEIA [†]	9	2	0.96	Lycocitin 1	88.89	Pv_tr_8904.t1
PvAMP75	RHLVKQQLS	9	3	1.12	M-lycotoxin-Hc1a	87.5	Pv_tr_15055.t1
PvAMP77	LYSMIPKAV	9	2	0.97	AamAP1 [H8K]	66.67	Pv_so_8056.t1
PvAMP78	IPKALKNLI	9	3	0.82	AamAP1	77.78	Pv_tr_16804.t1
PvAMP79	PKKGLVRAI	9	4	1.09	AaeAP1 [S4.8.15K; A11K. N19K]	72.73	Pv_so_5175.t1
PvAMP80	VFKLFHKKK	9	5	1.79	Css54	77.78	Pv_sp_716.t1
PvAMP81	FSGNKLLPG	9	2	0.41	Im-5	80	Pv_so_3641.t1
PvAMP82	GRIFRLLRK	9	5	1.22	Scolopendin 2	88.89	Pv_so_3638.t1
PvAMP83	GRIGRLVLR	9	4	0.82	Scolopendin 2	88.99	Pv_sp_5222.t1
PvAMP84	ILKPFMLRR	9	4	0.95	Scolopin 2	77.78	Pv_sp_312.t1
PvAMP85	KPHHRTVTY	9	3	1.56	Gomesin (4-18) [Q9p]	77.78	Pv_so_1476.t1
PvAMP86	WSSIWAGMK	9	2	1.95	UyCT5	66.67	Pv_tr_75378.t1
PvAMP87	IAALLKSIY	9	2	0.97	Meucin-13	66.67	Pv_sp_3763.t1
PvAMP88	GPFWTGIKS	9	2	1.18	UyCT3 [L2F.S3G]. D1	66.67	Pv_sp_3762.t1
PvAMP89	LWQGSKSAI	9	2	1.32	Um3	77.78	Pv_tr_1841.t1
PvAMP91	GKLLEGLKK	9	3	1.36	UyCT1 [W7L.N12K]	88.89	Pv_sp_2709.t1
PvAMP92	LLDGVKKFI	9	2	0.82	UyCT1 [W7L.N12K]	85.71	Pv_tr_10673.t1
PvAMP95	DKCCDNCTRK	10	2	0.98	κ-theraphotoxin-Gr4c	62.5	Pv_sp_13803.t1
PvAMP164	RSVLKAHCRICRRRG	15	7	1.16	Androctonin	61.11	Pv_so_8460.t1
PvAMP169	CRRVCYKNRCVTYCRG [†]	16	6	1.47	Gomesin c(1-18)[Gln1]	87.5	Pv_sp_11662.t1
PvAMP170	CNKLRSDHFHLCNFQF	16	2	0.64	M-theraphotoxin-Gr1a	56.25	Pv_sp_11936.t1
PvAMP172	CRKLCFRNRCLTYCRGR	17	7	1.23	cGomesin	70.59	Pv_tr_7912.t1
PvAMP177	QCRKLCFRNRCLTYCRGR	18	7	1.24	Gomesin c(1-18)[Gln1]	72.22	Pv_tr_7912.t1
PvAMP179	VKMCRWTKSMLRGRGGCY	18	6	1.48	Androctonin	50	Pv_sp_11670.t1
PvAMP183	QCRKLCFRNRCLTYCRGRG	19	7	1.17	Gomesin c(1-18)[Gln1]	72.22	Pv_tr_7912.t1

Note: [†] Sequence predicted from the HMMER3 strategy. A: Peptide length. B: Peptide positive charge. C: Amphipathic index. D: Peptide identity percentage towards homologous peptide within the cDB.

Table S3. LC/MS analysis of *P. verdolaga*'s AMPs.

			m/z ratio								
AMP	Sequence	Theoric mass	+1	+2	+3	+4	+5	+6	Observed ions		
PvAMP7	SLWGMWR-NH ₂	934.12 Da	935.1	468.1	312.4	234.5	187.8	156.7	934.6	468.9	
PvAMP32	IIKKIWK-NH ₂	927.23 Da	928.2	464.6	310.1	232.8	186.4	155.5	464.6	310	
PvAMP66	WKKIKKFF-NH ₂	1123.43 Da	1124	562.7	375.5	281.9	225.7	188.2	375.4		
PvAMP69	YRARCVIYC-NH ₂	1145.41 Da	1146	573.7	382.8	287.4	230.1	191.9	573.5		
PvAMP82	GRIFRLLRK-NH ₂	1157.46 Da	1159	579.7	386.8	290.4	232.5	193.9	579.7	386.7	
PvAMP164	RSVLKAHCRICRRRG-NH ₂	1810.22 Da	1811	906.1	604.4	453.6	363	302.7	604	453.3	
PvAMP172	CRKLCFRNRCLTYCRGR-NH ₂	2147.63 Da	2149	1074.8	716.9	537.9	430.5	358.9	716.9		
PvAMP177	QCRKLCFRNRCLTYCRGR-NH ₂	2275.76 Da	2277	1138.9	759.6	569.9	456.2	380.3	570.1	457	
PvAMP183	QCRKLCFRNRCLTYCRGRG-NH ₂	2332.82 Da	2334	1167.4	778.6	584.2	467.6	389.8	583.5	467	

Table S4. IC₅₀ values for isobologram analysis.

Gentamicin (μM)	50	25	12.50	6.25	3.12	1.56	0.39	0.1
PvAMP66 (μM)	17.01	29.096	31.75	29.27	9.85	15.53	NC	NC
	(10.01 - 23.19)	(25.59 - 32.62)	(26.89 - 37.26)	(26.52 - 32.23)	(7.81 - 11.89)	(13.50 - 17.77)		

Note: In parentheses 95% confidence intervals. NC = Logistic or linear regression with Pearson’s correlation coefficient (R^2) < 0.70.

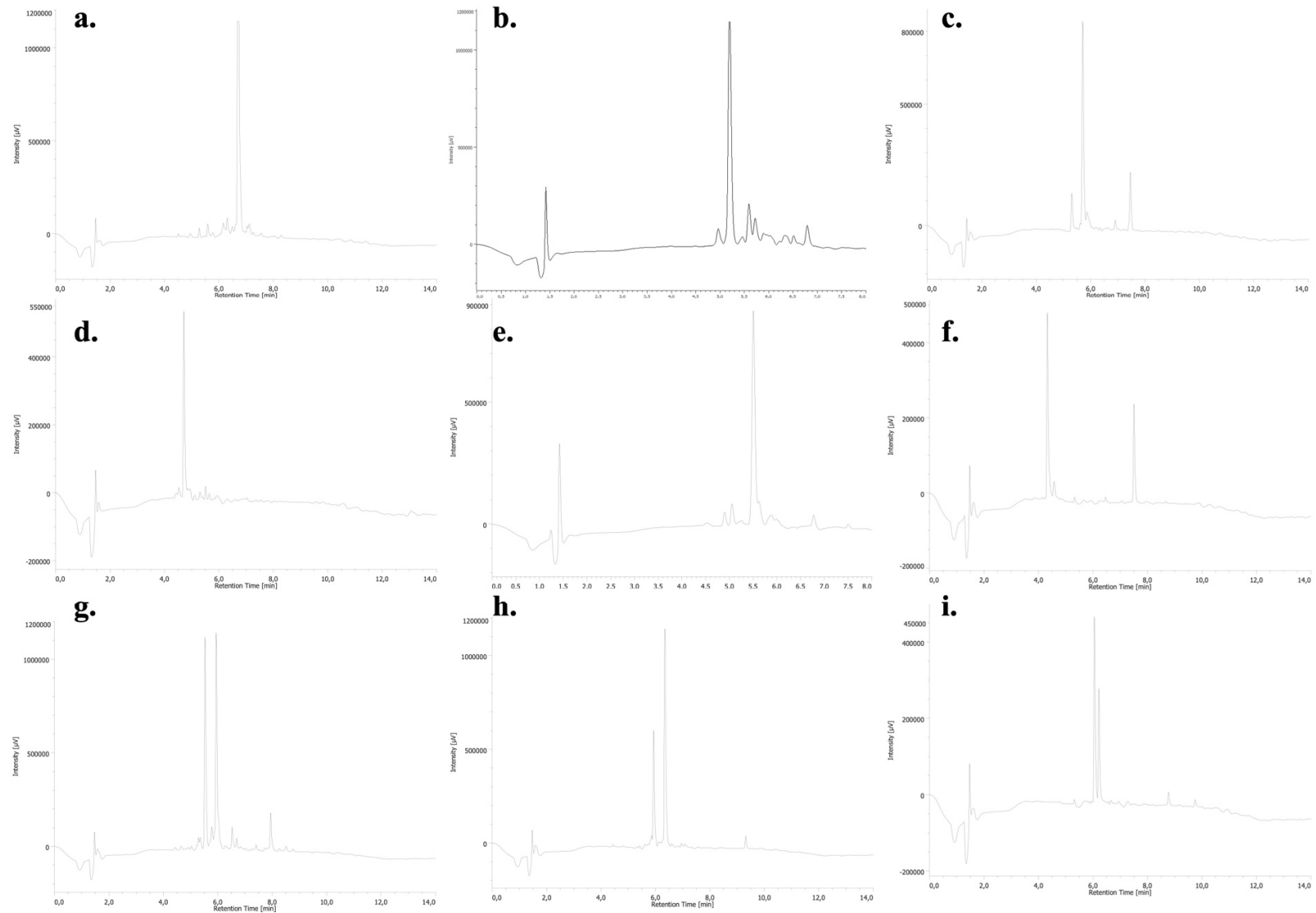


Figure S1. RP-HPLC analysis of *P. verdolaga*'s AMPs: (a) Peptide PvAMP7. (b) Peptide PvAMP32. (c) Peptide PvAMP66. (d) Peptide PvAMP69. (e) Peptide PvAMP82. (f) Peptide PvAMP164. (g) Peptide PvAMP172. (h) Peptide PvAMP177. (i) Peptide PvAMP183.

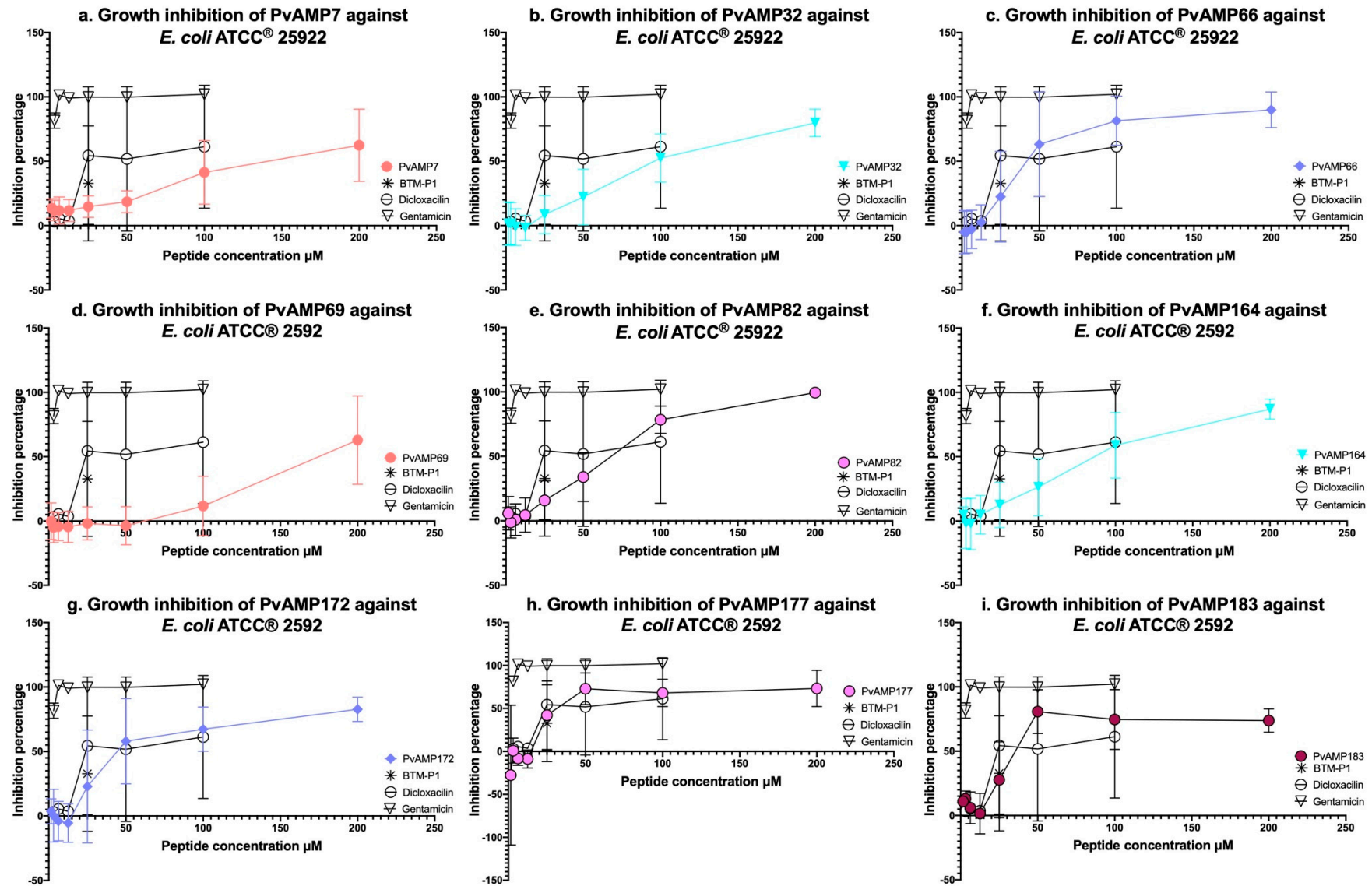


Figure S2. Dose-response curves of *P. verdolaga*'s AMPs against *E. coli* ATCC® 25922: (a) PvAMP7; (b) PvAMP32; (c) PvAMP66; (d) PvAMP69; (e) PvAMP82; (f) PvAMP164; (g) PvAMP172; (h) PvAMP177; (i) PvAMP183.

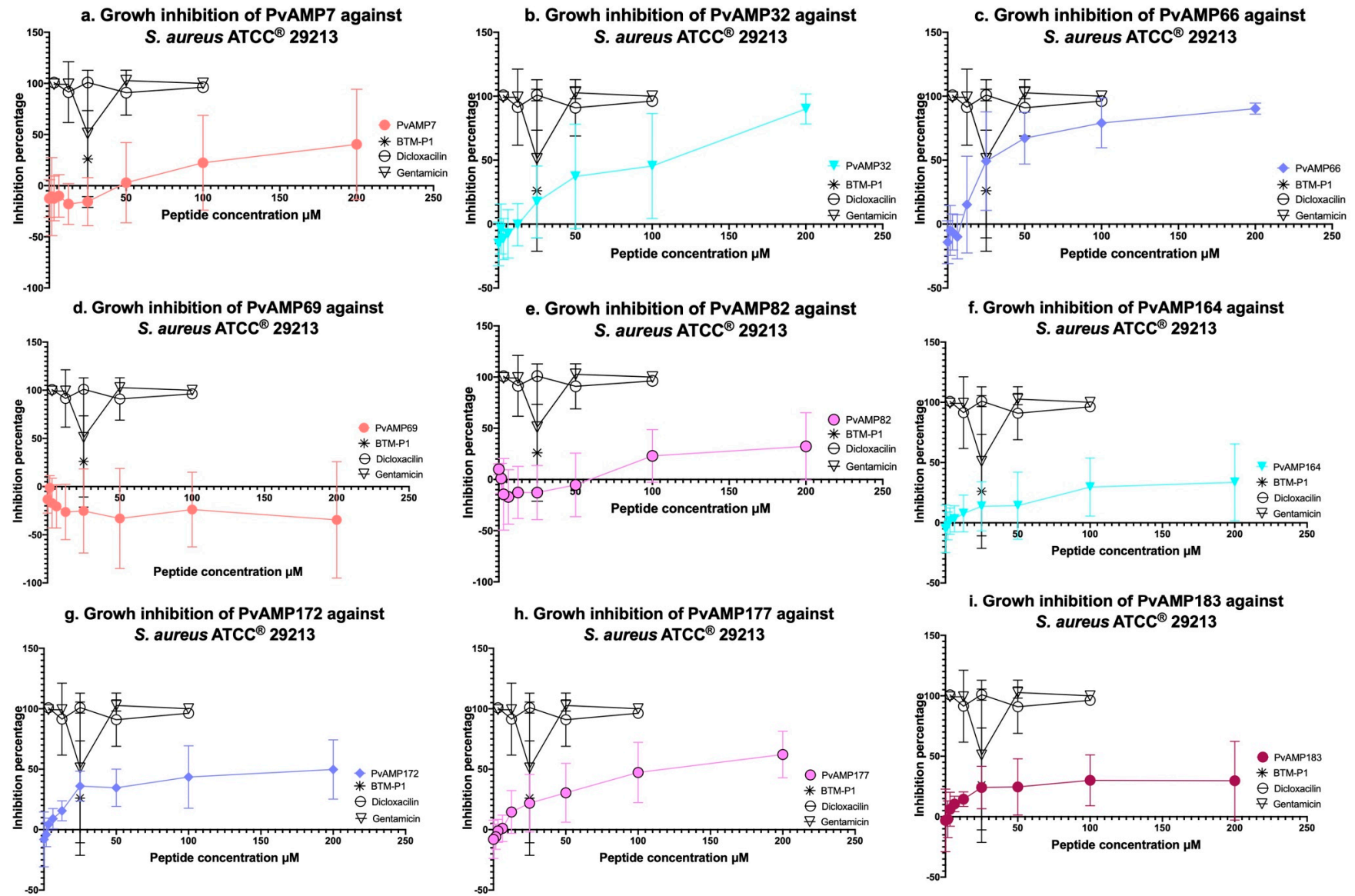


Figure S3. Dose-response curves of *P. verdolaga*'s AMPs against *S. aureus* ATCC® 29213: (a) PvAMP7; (b) PvAMP32; (c) PvAMP66; (d) PvAMP69; (e) PvAMP82; (f) PvAMP164; (g) PvAMP172; (h) PvAMP177; (i) PvAMP183.

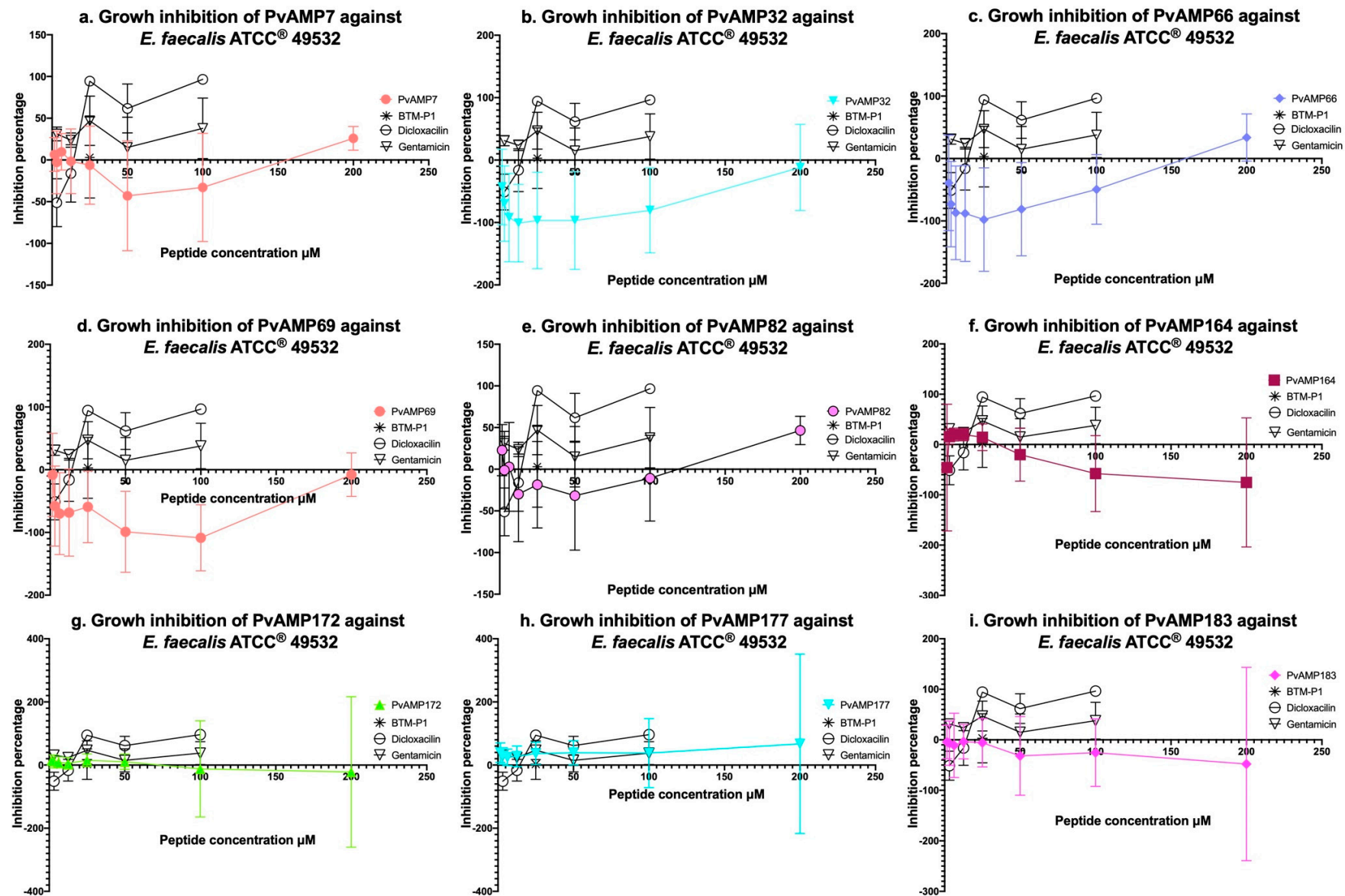


Figure S4. Dose-response curves of *P. verdolaga*'s AMPs against *E. faecalis* ATCC® 49532: (a) PvAMP7; (b) PvAMP32; (c) PvAMP66; (d) PvAMP69; (e) PvAMP82; (f) PvAMP164; (g) PvAMP172; (h) PvAMP177; (i) PvAMP183.

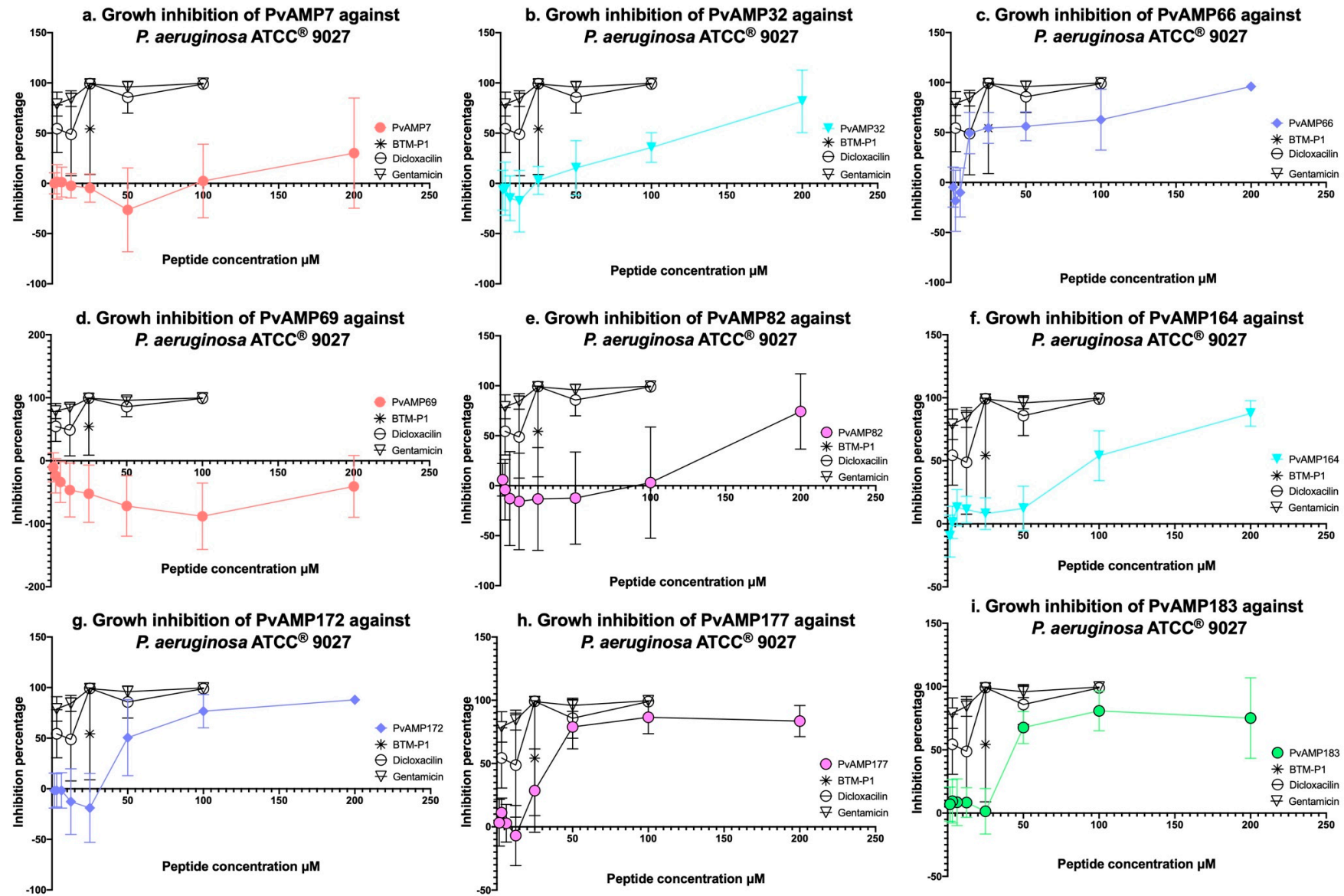


Figure S5. Dose-response curves of *P. verdolaga*'s AMPs against *P. aeruginosa* ATCC® 9027 (a) PvAMP7; (b) PvAMP32; (c) PvAMP66; (d) PvAMP69; (e) PvAMP82; (f) PvAMP164; (g) PvAMP172; (h) PvAMP177; (i) PvAMP183.

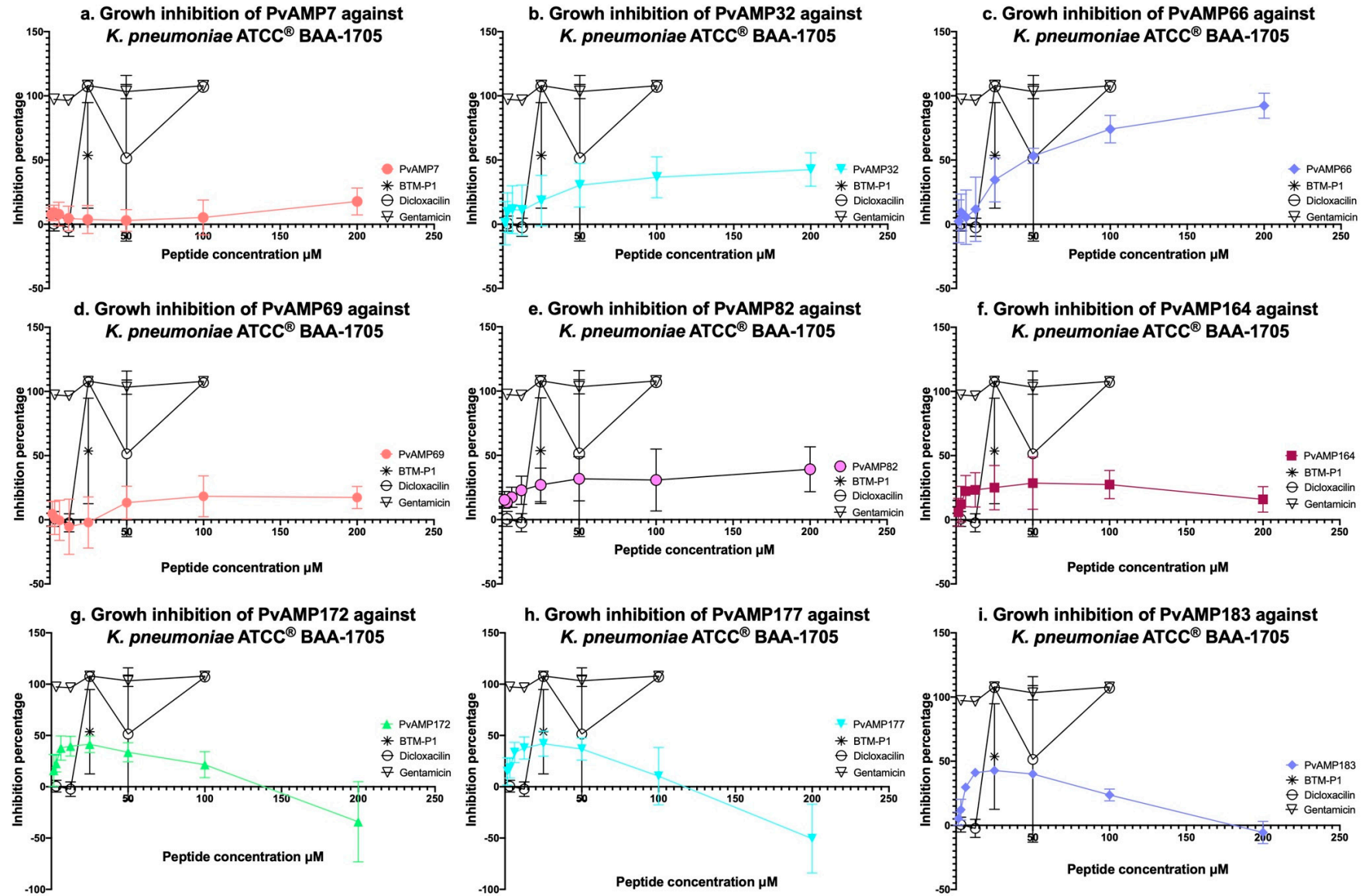


Figure S6. Dose-response curves of *P. verdolaga*'s AMPs against *K. pneumoniae* ATCC® BAA-1705: (a) PvAMP7; (b) PvAMP32; (c) PvAMP66; (d) PvAMP69; (e) PvAMP82; (f) PvAMP164; (g) PvAMP172; (h) PvAMP177; (i) PvAMP183.

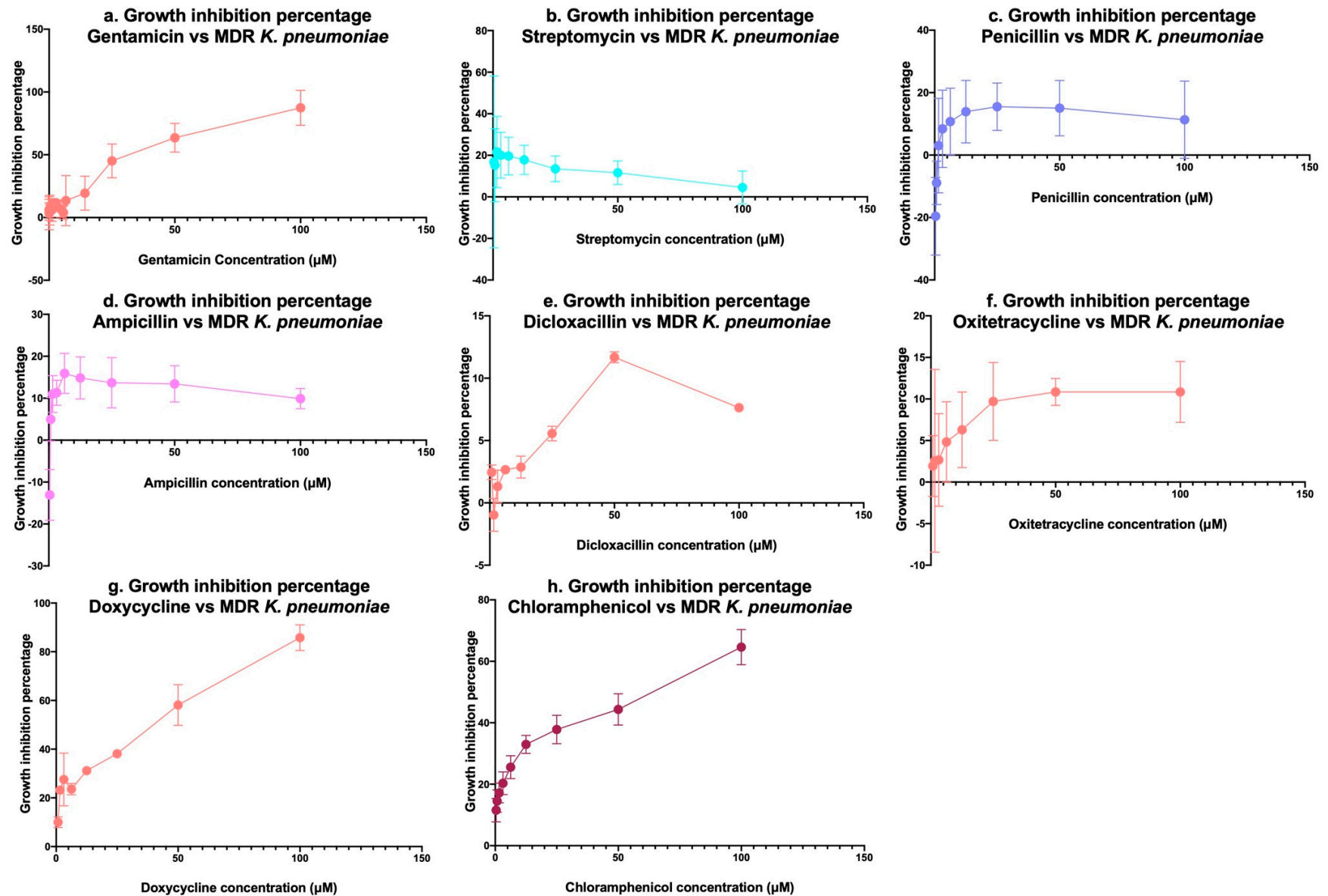


Figure S7. Dose-response curves of MDR *K. pneumoniae* against: (a) Gentamicin; (b) Streptomycin; (c) Penicillin; (d) Ampicillin; (e) Dicloxacillin; (f) Oxytetracycline; g(g) Doxycycline; (h) Chloramphenicol.

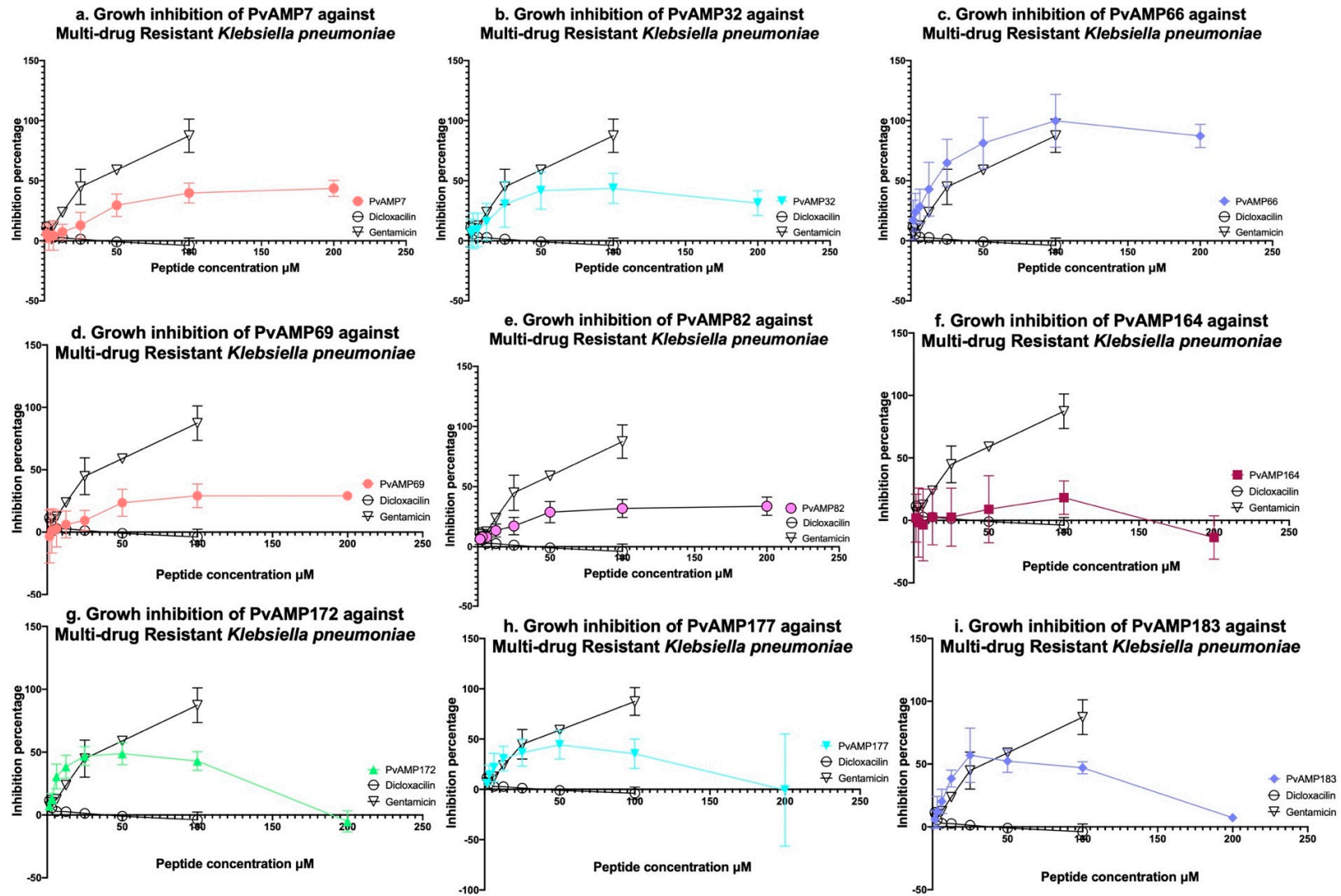


Figure S8. Dose-response curves of *P. verdolaga*'s AMPs against MDR *K. pneumoniae* (a) PvAMP7; (b) PvAMP32; (c) PvAMP66; (d) PvAMP69; (e) PvAMP82; (f) PvAMP164; (g) PvAMP172; (h) PvAMP177; (i) PvAMP183.

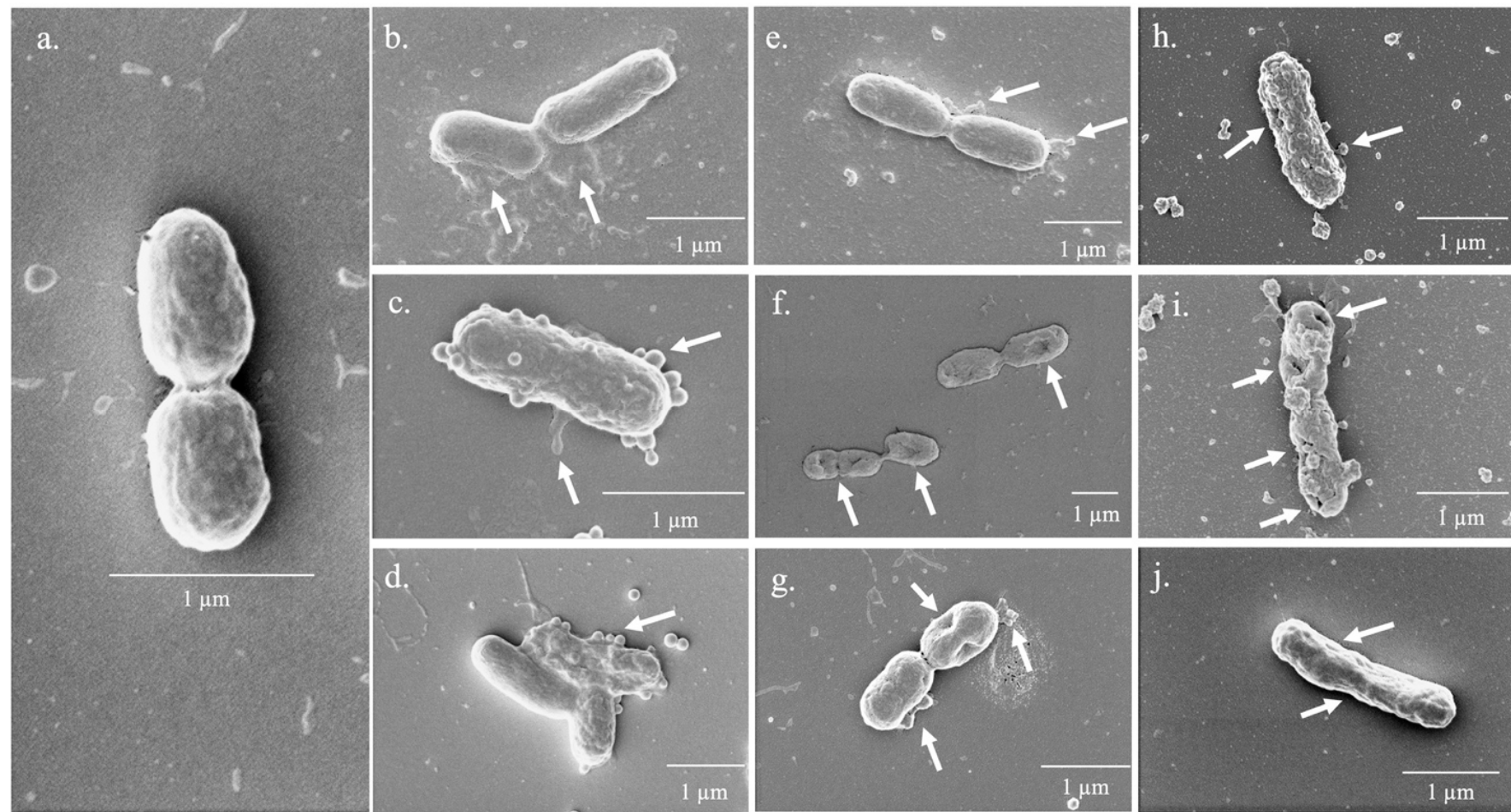


Figure S9. SEM analysis: (a) the multidrug resistant *K. pneumoniae* strain in media; and against (b) P7; (c) P32; (d) P66; (e) P69; (f) P82; (g) P164; (h) P172; (i) P177; (j) P183.

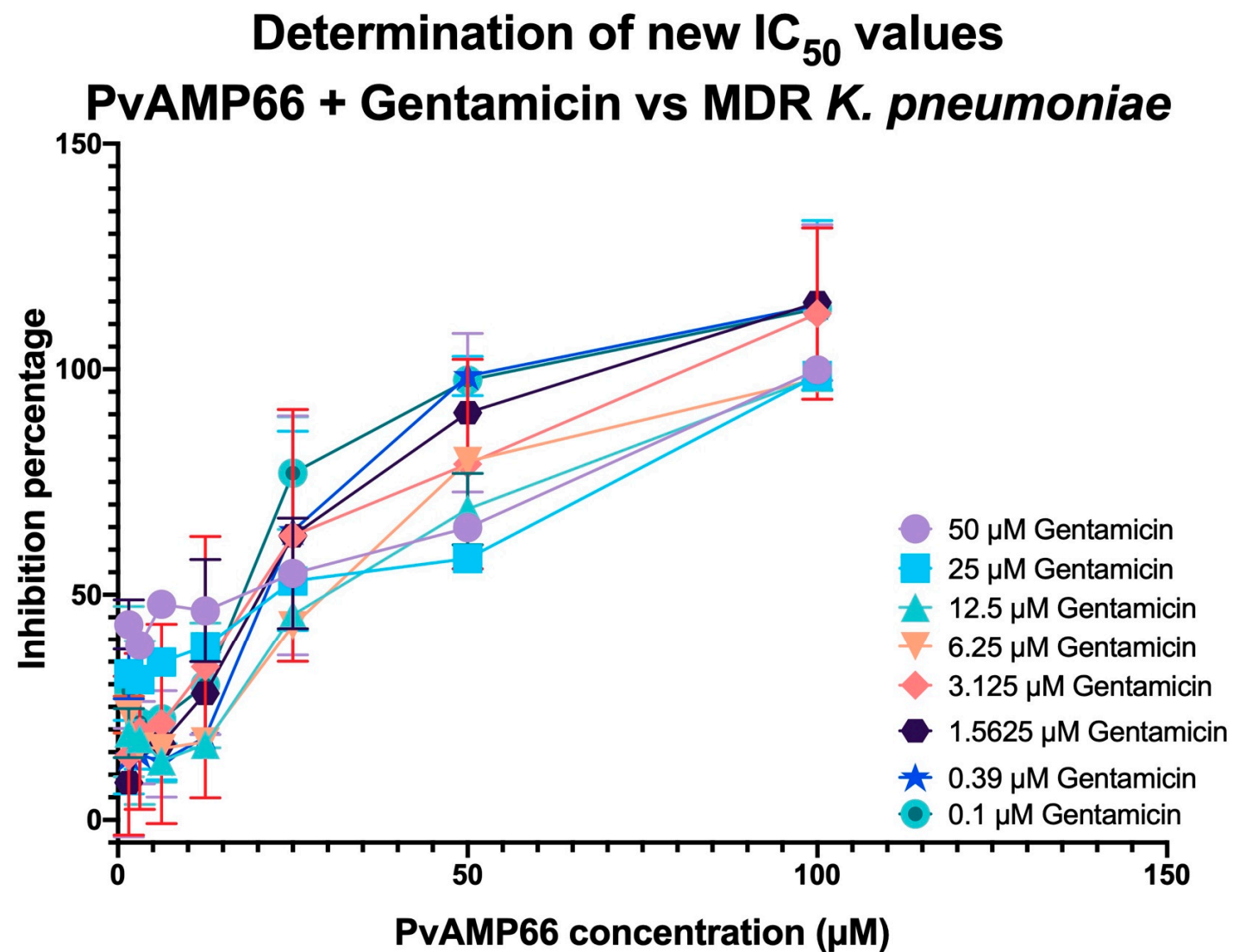


Figure S10. Dose-response curves of the isobologram analysis