Supporting Information

Cyclotides from Brazilian *Palicourea sessilis* and Their Effects on Human Lymphocytes

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Table S1. Obtained masses of cyclotides from *Palicourea sessilis*.

Cyclotide	Leaves		Stem	
	Obtained mass	mg/g*	Obtained mass	mg/g*
pase A **(1)**	5.4	(0.21)	8.2	(0.07)
pase B **(2)**	6.7	(0.26)	1.0	(0.001)
pase C **(3)**	3.6	(0.14)	3.1	(0.03)
pase D **(4)**	-	-	2.5	(0.02)
pase E **(5)**	-	-	2.9	(0.02)
kalata S **(6)**	1.1	(0.04)	-	-

*Concentrations based on dried leaves (26.15 g, 198 mg 80%-C_{18} leave extract) and dried stems (111.35 g, 103 mg 80%-C_{18} stem extract).

Table S2. Sequence fragments of pase (A–E) and kalata S cyclotides, generated through enzymatic digestion and characterization using MALDI-TOF/TOF-MS/MS.

Cyclotide (Da)	Sequences identified in the precursor ion	Precursor Mass (Da)		Enzyme(s)
		obs.	calc.	
pase A 2889.01	NGLPVCGETCVGGTCNTPGCVCSWPVCTR	3255.07	3255.23	T
	VCSWPVCTR	3255.35	3255.23	E
pase B 2903.30	NGLPVCGETCVGGTCNTPGCVCSWPICTR	3269.04	3269.24	T
	TPGCVCSWPICTRNGLPV	3269.34	3269.24	E
pase C 2905.04	NGLPTCGETCVGGTCNTPGCVCSWPICTR	3271.12	3271.22	T
	PGCVCSWPICTRNGLT	3271.19	3271.22	E
pase D 2887.00	NGLPVCGETCVGGTCNTPGCVCAWPICTR	3253.10	3253.24	T
	GGTCNTPGCVCAWPICTRNGLPV	3253.30	3253.24	E
pase E 2983.08	RNGLPVCGE	1001.49	1001.46	E; T
	TCVTGSCYTPGCSCSWPVCK	2366.84	2366.82	E; T
kalata S 2977.00	NGLPVCGETCVGGTCNTPGCSCSWPVCTR	3242.89	3243.19	T
	SCSWPVCTRNGLPVCGE	3242.85	3243.19	E

obs. observed, calc. calculated, T: Trypsin and E: Endoproteinase GluC

Table S3. ^{1}H Chemical shifts (ppm) of pase A at pH 4.5 and 298K (BMRB code 50464).

Residue		NH	H_{α}	$H_{\beta a}$	$H_{\beta b}$	$H_{\gamma a}$	$H_{\gamma b}$	$H_{\delta a}$	$H_{\delta b}$	H_{ε}
1	**Gly**	8.98	3.6; 4.24							
2	**Leu**	7.74	5.08	1.70	1.93	1.50	0.92	0.99		
3	**Pro**		5.10	1.75	2.47	2.18	2.06	3.80		
4	**Val**	8.16	4.67	2.59		0.87	0.87			
5	**Cys**	8.05	4.44	3.03	3.37					
6	**Gly**	8.53	3.74; 3.84							
7	**Glu**	7.17	4.80	1.96	1.88	2.51	2.41			
8	**Thr**	8.47	4.56	4.44		1.16	1.16			
9	**Cys**	8.33	4.96	3.19	2.92					
10	**Val**	8.54	3.87	2.05		0.98	1.03			
11	**Gly**	8.72	3.85; 4.25							
12	**Gly**	8.27	4.06; 4.42							
13	**Thr**	7.87	4.71	4.10		1.15	1.15			
14	**Cys**	8.61	4.71	2.70	3.07					
15	**Asn**	10.42	4.71	2.78						
16	**Thr**	9.06	4.41	4.26		1.33	1.33			
17	**Pro**		4.26	1.90	2.32	2.15	2.01	3.71	4.71	
18	**Gly**	8.78	3.67; 4.19							
19	**Cys**	7.69	5.35	2.61	3.83					
20	**Val**	9.40	4.44	2.05		0.86	0.86			
21	**Cys**	8.97	4.59	2.80	3.08					
22	**Ser**	8.99	4.75	3.85	3.85					
23	**Trp**	7.34	4.09							10.41
24	**Pro**		3.45	-0.17	1.73	1.32	1.42	3.26	3.20	
25	**Val**	8.24	4.22	1.94		0.85	0.85			
26	**Cys**	7.70	5.07	2.75	3.22					
27	**Thr**	9.92	5.07							
28	**Arg**	8.76	4.75	1.69	1.61	1.41	1.41	3.18		6.96
29	**Asn**	9.6	4.40	2.85	3.09					

Table S4. ^{1}H Chemical shifts (ppm) of pase B at pH 3.5 and 298K.

Residue		NH	H_{α}	$H_{\beta a}$	$H_{\beta b}$	$H_{\gamma a}$	$H_{\gamma b}$	$H_{\delta a}$	$H_{\delta b}$	H_{ε}
1	**Gly**	8.99	3.60; 4.23							
2	**Leu**	7.76	5.07	1.70	1.94	1.49	0.92	0.99		
3	**Pro**		5.06	1.78	2.48	2.18	2.05	3.79		
4	**Val**	8.12	4.68	2.60		0.87	0.87			
5	**Cys**	8.09	4.44	3.05	3.38					
6	**Gly**	8.50	3.73; 3.82							
7	**Glu**	7.13	4.74	2.33	2.48	1.86				
8	**Thr**	8.48	4.57	4.45		1.15	1.15			
9	**Cys**	8.34	5.01	2.85	3.20					
10	**Val**	8.57	3.83	2.06		0.98	1.04			
11	**Gly**	8.67	3.85; 4.28							
12	**Gly**	8.27	4.06; 4.45							
13	**Thr**	7.87	4.71	4.09		1.14	1.14			
14	**Cys**	8.55	4.69	2.66	3.09					
15	**Asn**									
16	**Thr**									
17	**Pro**		4.22	1.91	2.32	2.15	2.01	3.70	4.22	
18	**Gly**	8.78	3.68; 4.18							
19	**Cys**	7.70	5.35	2.61	3.84					
20	**Val**	9.46	4.35	2.01		0.87	0.87			
21	**Cys**	8.94	4.61	2.78	3.07					
22	**Ser**	9.06	4.76	3.85	3.85					
23	**Trp**									10.41
24	**Pro**		3.46	-0.26	1.73	1.28	1.40	3.2		
25	**Ile**	8.23	4.26	1.80		1.12, 1.34	0.86	0.73		
26	**Cys**	7.63	5.18	2.74	3.22					
27	**Thr**	9.90	5.05							
28	**Arg**	8.77	4.76	1.62	1.70	1.40		3.18	3.18	6.94
29	**Asn**	9.62	4.40	2.86	3.09					

Table S5. [1]H Chemical shifts (ppm) of pase C at pH 4.7 and 298K.

Residue		NH	H_{α}	$H_{\beta a}$	$H_{\beta b}$	$H_{\gamma a}$	$H_{\gamma b}$	$H_{\delta a}$	$H_{\delta b}$	H_{ε}
1	**Gly**		3.71; 4.25							
2	**Leu**	7.81	5.06	1.69	2.02	1.50	0.92	0.99		
3	**Pro**		5.10	1.77	2.49	2.18	2.03	3.78		
4	**Thr**	8.40	4.60							
5	**Cys**	7.92	4.44	3.02	3.39					
6	**Gly**		3.73; 3.83							
7	**Glu**	7.15	4.73	1.83	1.83	2.46	2.31			
8	**Thr**	8.50	4.56	4.44		1.14	1.15			
9	**Cys**	8.34	5.03	3.20	2.83					
10	**Val**	8.59	3.82	2.07		0.99	1.05			
11	**Gly**									
12	**Gly**	8.29	4.06; 4.46							
13	**Thr**	7.86	4.71	4.08		1.14	1.14			
14	**Cys**	8.54	4.69	2.67	3.09					
15	**Asn**	10.42	4.71	2.78						
16	**Thr**	9.06	4.41	4.26		1.33	1.33			
17	**Pro**		4.24	1.91	2.32	2.15	2.00	3.66	4.71	
18	**Gly**	8.96	3.59; 4.25							
19	**Cys**	7.70	5.36	2.62	3.83					
20	**Val**	9.38	4.42	2.04		0.86	0.86			
21	**Cys**	8.94	4.61	2.78	3.07					
22	**Ser**	9.07	4.75	3.85	3.85					
23	**Trp**		4.09	3.28	3.28					10.41
24	**Pro**		3.47	-0.26	1.73	1.28	1.40	3.20	3.20	
25	**Ile**	8.23	4.27	1.81		1.12, 1.34	0.86			
26	**Cys**	7.64	5.16	2.76	3.23					
27	**Thr**	9.90	5.04							
28	**Arg**	9.3	4.75	1.77	1.59	1.37	1.37	3.09	3.24	6.96
29	**Asn**									

Table S6. ¹H Chemical shifts (ppm) of pase D at pH 3.5 and 298K.

Residue		NH	H_{α}	$H_{\beta a}$	$H_{\beta b}$	$H_{\gamma a}$	$H_{\gamma b}$	$H_{\delta a}$	$H_{\delta b}$	H_{ε}
1	**Gly**	8.96	3.68, 4.22							
2	**Leu**	7.77	5.08	1.69	1.93	1.49	0.92	0.98		
3	**Pro**		5.08	1.77	2.47	2.18	2.05	3.79		
4	**Val**	8.14	4.68	2.59		0.87	0.87			
5	**Cys**	8.12	4.42	3.09	3.39					
6	**Gly**	8.52	3.73, 3.82							
7	**Glu**	7.14	4.73	1.88	1.88	2.40	2.28			
8	**Thr**	8.44	4.58	4.44		1.15	1.15			
9	**Cys**	8.29	4.99	3.16	2.86					
10	**Val**	8.54	3.86	2.07		1.01	1.01			
11	**Gly**	8.72	3.85, 4.26							
12	**Gly**	8.28	4.03; 4.45							
13	**Thr**	7.84	4.70	4.08		1.14	1.14			
14	**Cys**	8.52	4.68	2.66	3.16					
15	**Asn**	10.42	4.71	2.78						
16	**Thr**	9.87	4.32			1.32	1.32			
17	**Pro**		4.21	1.91	2.32	2.15	2.01	3.71		
18	**Gly**	8.77	3.67; 4.18							
19	**Cys**	7.70	5.36	2.61	3.85					
20	**Val**	9.43	4.39	2.01		0.87	0.87			
21	**Cys**	8.93	4.57	2.81	3.06					
22	**Ala**	9.12	4.72	1.27	1.27					
23	**Trp**	7.33	4.10	3.27	3.27					10.39
24	**Pro**		3.50	-0.17	1.74	1.30	1.41	3.20	3.20	
25	**Ile**	8.26	4.30	1.85		1.15, 1.35	0.86	0.74		
26	**Cys**	7.58	5.18	2.75	3.20					
27	**Thr**	9.68	5.07				0.73			
28	**Arg**	8.86	4.81	1.77	1.61	1.40	1.40	3.18	3.18	6.96
29	**Asn**	9.58	4.40	2.86	3.09					

Table S7 [1]H Chemical shifts (ppm) of pase E at pH 4.5 and 298K.

Residue		NH	H_{α}	$H_{\beta a}$	$H_{\beta b}$	$H_{\gamma a}$	$H_{\gamma b}$	$H_{\delta a}$	$H_{\delta b}$	H_{ε}
1	**Gly**	8.69	3.58; 4.24							
2	**Leu**	7.88	5.16	1.70	1.95	1.51	0.95	0.99		
3	**Pro**		5.17	1.65	2.55	2.12	2.22	3.84	3.84	
4	**Val**	8.04	4.68	2.61		0.88	0.88			
5	**Cys**	8.19	4.42	3.35	3.11					
6	**Gly**	8.61	3.74; 3.85							
7	**Glu**	7.32	4.75	2.25	1.89	2.44	2.44			
8	**Thr**	8.59	4.59	4.49		1.19	1.19			
9	**Cys**	8.20	5.19	3.31	2.86					
10	**Val**	8.30	3.73	2.15		1.05	1.13			
11	**Thr**	7.91	4.63							
12	**Gly**	8.19	4.06; 4.42							
13	**Ser**	7.96	4.71	3.59	3.59					
14	**Cys**	8.27	4.55	2.62	3.07					
15	**Tyr**	9.02	4.80	3.69	3.89					
16	**Thr**	10.01	4.36	4.36		1.35	1.35			
17	**Pro**		4.24	1.92	2.32	2.16	2.04	3.73	4.17	
18	**Gly**	8.78	3.71; 4.16							
19	**Cys**	7.81	5.14	2.51	3.90					
20	**Ser**	9.35	4.68	3.80	3.80					
21	**Cys**	9.11	4.81	3.13	4.54					
22	**Ser**									
23	**Trp**									10.41
24	**Pro**		3.55	-0.32	1.77	1.30	1.38	3.22	3.18	
25	**Val**	8.43	4.19	1.93		0.88	0.88			
26	**Cys**	7.87	4.90	2.69	3.15					
27	**Lys**	9.25	5.05	1.81	1.81	1.53	1.37	0.77	0.77	2.80
28	**Arg**	8.78	4.75	1.63	1.72	1.39	1.39	3.20		6.92
29	**Asn**	9.65	4.40	2.83	3.11					

Table S8. Statistical analysis of pase A structures.

Energies (kcal/mol)	Pase A[a]
Overall	-847.01 ± 29.45
Bonds	10.64 ± 1.13
Angles	29.09 ± 4.00
Improper	10.75 ± 1.67
Dihedral	116.67 ± 1.92
van der Waals	-92.98 ± 8.75
NOE	0.011 ± 0.01
cDih	0.59 ± 0.47
Stereochemical quality[b]	
Clashes (all atoms)	10.23 ± 5.46
Poor rotamers	0.83 ± 1.73
Ramachandran outliers (%)	2.71 ± 1.69
Ramachandran favored (%)	86.42 ± 5.17
Overall Molprobity score	2.17 ± 1.69
RMSD from mean structure (Å)[c]	
Mean global backbone (residues 4-8, 19-27)	0.81 ± 0.25
Mean global heavy (residues 4-8, 19-27)	1.73 ± 0.41
Distance restraints	
Intraresidue (i-j=0)	95
Sequential (|i-j|=1)	84
Medium range (|i-j|<5)	4
Long range (|i-j|≥5)	2
Hydrogen bonds	16
Disulfide bonds	3
Total	204
Dihedral angle restraints	
φ	21
ψ	21
χ1	8
Total	50
Violations from experimental restraints	
Total NOE violations exceeding 0.2 Å	0
Total dihedral violations exceeding 2.0°	2 (highest 0.84)

[a]All statistics are given as mean ± SD.
[b]According to MolProbity.
[c]Mean RMSD was calculated using MOLMOL.

Figure S1. Multiple sequence alignment of reported Möbius cyclotides extracted from Cybase.[10]

Cter_4	CGETCFGG-TCYTPGCVCD-PWPICTKNGDPLA-	31
Cter_37	CGETCFGG-TCYTPGCVCD-PWPICTKNGSPT--	30
Cter_1	CGETCFGG-TCNTPNCVCD-PWPICTNNGLPI--	30
varv_peptide_B	CGETCFGG-TCNTPGCSCD-PWPMCSRNGLPV--	30
varv_peptide_G	CGETCFGG-TCNTPGCSCD-PWPVCSRNGVPV--	30
varv_peptide_H	CGETCFGG-TCNTPGCSCE-TWPVCSRNGLPV--	30
cycloviolacin_O23	CGETCFGG-TCNTPGCTCDSSWPICTHNGLPT--	31
kalata_B6	CGETCFGG-TCNTPGCSCS-SWPICTRNGLPT--	30
kalata_B10	CGETCFGG-TCNTPGCSCS-SWPICTRDGLPT--	30
kalata_B10_linear	CGETCFGG-TCNTPGCSCS-SWPICTRDGLPT--	30
kalata_B3	CGETCFGG-TCNTPGCTCD-PWPICTRDGLPT--	30
vhl-2	CGETCFTG-TCYTNGCTCD-PWPVCTRNGLPV--	30
cycloviolacin_O32	CGETCFGG-TCNTPGCTCD-PWPVCTNDGAPV--	30
cycloviolacin_O36	CGETCFGG-TCNTPGCTCD-PFPVCTHDGLPT--	30
cycloviolacin_O24	CGETCFGG-TCNTPGCTCD-PWPVCTHNGLPT--	30
Oak6_cyclotide_2	CGETCFGG-TCNTPGCICD-PWPVCTRDGLPI--	30
kalata_B14	CGESCFGG-TCNTPGCACD-PWPVCTRDGLPV--	30
kalata_B13	CGETCFGG-TCNTPGCACD-PWPVCTRDGLPV--	30
cycloviolacin_H3	CGETCFGG-TCNTPGCICD-PWPVCTRNGLPV--	30
vaby_D	CGETCFGG-TCNTPGCTCD-PWPVCTRNGLPV--	30
vaby_E	CGETCFGG-TCNTPGCSCD-PWPVCTRNGLPV--	30
Oak6_cyclotide_1	CGETCFGG-TCNTPGCACD-PWPVCTRNGLPV--	30
vitri_peptide_23	CGETCTLG-TCYTPGCTCS--WPLCTKNGLPT--	29
psybra_1	CGETCTLG-TCNTPGCTCS--WPICTKNGLPI--	29
Mobo_A	CGETCTLG-TCNTPGCTCS--WPICTRNGFPT--	29
Mden_A	CGETCTLG-TCNTPGCTCS--WPICTKNGIPT--	29
kalata_B7	CGETCTLG-TCYTQGCTCS--WPICKRNGLPV--	29
viphi_B	CGETCTIG-TCYTAGCTCS--WPICTRNGLPV--	29
vodo_N	CGETCTLG-KCYTAGCSCS--WPVCYRNGLPV--	29
Viba_16	CGETCTLG-TCYTVGCTCS--WPVCTRNGLPI--	29
varv_peptide_F	CGETCTLG-TCYTAGCSCS--WPVCTRNGVPI--	29
Vinc_A	CGETCTLG-TCYTAGCSCS--WPVCTRNGIPV--	29
vila_D	CGETCAFG-TCYTGGCSCS--WPVCTRNGIPV--	29
vibi_C	CGETCAFG-SCYTPGCSCS--WPVCTRNGLPV--	29
vitri_D	CGETCFTG-SCYTPGCSCN--WPVCNRNGLPV--	29
pase_E	CGETCVTG-SCYTPGCSCS--WPVCKRNGLPV--	29
cycloviolacin_O21	CGETCVTG-SCYTPGCTCS--WPVCTRNGLPV--	29
vitri_peptide_18a	CGETCFQG-TCNTPGCTCK--WPICERNGVPI--	29
psyleio_E	CGETCFGG-TCNTPGCSCS--WPICTKSVTPIV-	30
psyleio_B	CGETCFGG-TCNTPGCVCA--WPVCNRGDLPI--	29
psyleio_C	CGETCFGG-TCNTPGCVCA--WPVCTRGDLPV--	29
kalata_B15	CGESCFGG-SCYTPGCSCT--WPICTRDGLPV--	29
psyleio_A	CGETCFTG-TCNTPGCSCT--YPICTRDGLPI--	29
psyleio_D	CGESCFGG-TCNTPGCSCT--WPVCTRDGLPV--	29
kalata_B2	CGETCFGG-TCNTPGCSCT--WPICTRDGLPV--	29
kalata_B11	CGETCFGG-TCNTPGCSCT--DPICTRDGLPV--	29
paltet_1	CGETCFTG-TCNTPGCTCS--YPVCTRNGLPI--	29
vibi_A	CGETCFGG-TCNTPGCSCS--YPICTRNGLPV--	29
vibi_D	CGETCFGG-RCNTPGCTCS--YPICTRNGLPV--	29
vibi_B	CGETCFGG-TCNTPGCTCS--YPICTRNGLPV--	29
vaby_C	CGETCAGG-RCNTPGCSCS--WPVCTRNGLPV--	29
vaby_A	CGETCAGG-TCNTPGCSCS--WPICTRNGLPV--	29
vaby_B	CGETCAGG-TCNTPGCSCT--WPICTRNGLPV--	29
cycloviolacin_O22	CGETCVGG-TCNTPGCTCS--WPVCTRNGLPI--	29
vigno_2	CGETCAGG-TCNTPGCSCS--WPVCVRDGSSPL-	30
mech_7	CGETCTIG-TCNTPGCTCS--WPVCTRDGIPI--	29
Psysol_2	CGESCVGG-TCNTPGCTCT--WPVCTRNGLPI--	29
vitri_C	CGETCVGG-TCNTPGCFCT--WPVCTRNGLPI--	29
kalata_B4	CGETCVGG-TCNTPGCTCS--WPVCTRDGLPV--	29
cycloviolacin_O34	CGETCVGG-TCNTEYCTCS--WPVCTRDGLPV--	29
cycloviolacin_O35	CGETCVGG-TCNTPYCFCS--WPVCTRDGLPV--	29
cycloviolacin_O33	CGETCVGG-TCNTPYCTCS--WPVCTRDGLPV--	29
chacur_1	CGETCVGG-TCNTPGCTCS--WPICTRNGLPV--	29
riden_A	CGETCVGG-TCNTPGCTCT--WPVCTRNGLPV--	29
kalata_B1	CGETCVGG-TCNTPGCTCS--WPVCTRNGLPV--	29
Viba_15	CGETCVGG-TCNTPGCACS--WPVCTRNGLPV--	29
Viba_17	CGETCVGG-TCNTPGCGCS--WPVCTRNGLPV--	29
pase_A	CGETCVGG-TCNTPGCVCS--WPVCTRNGLPV--	29
pase_D	CGETCVGG-TCNTPGCVCA--WPICTRNGLPV--	29
pase_C	CGETCVGG-TCNTPGCVCS--WPICTRNGLPT--	29

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pase_B                         CGETCVGG-TCNTPGCVCS--WPICTRNGLPV--    29
vigno_5                        CGETCVGG-TCNTPGCSCG--WPVCVRNGLPL--    29
vigno_1                        CGETCAGG-TCNTPGCSCS--WPVCVRNGLPL--    29
vitri_B                        CGESCVGG-TCNTPGCSCS--WPVCTTNGYPI--    29
vigno_4                        CGETCVGG-TCNTPACSCS--WPVCTRNGLPL--    29
vigno_3                        CGETCVGG-TCNTPGCSCS--WPVCTRNGLPL--    29
varv_peptide_C                 CGETCVGG-TCNTPGCSCS--WPVCTRNGVPI--    29
varv_peptide_D                 CGETCVGG-SCNTPGCSCS--WPVCTRNGLPI--    29
cycloviolacin_O12              CGETCVGG-TCNTPGCSCS--WPVCTRNGLPI--    29
vocC                           CGETCVGG-TCNTPGCSCS--WPVCIRNGLPV--    29
cycloviolacin_O28              CGETCVGG-TCNTPGCSCS--WPVCFRDGLPV--    29
vitri_E                        CGETCVGG-TCNTPGCSCS--WPVCFRNGLPV--    29
viba_30_linear                 CGETCVGG-TCNTPGCSCS--WPVCTRNGPPV--    29
cycloviolacin_T1               CGETCVGG-TCNTPGCSCS--WPVCTRNGIPV--    29
cycloviolacin_O31              CGETCVGG-TCNTPGCSCS--IPVCTRNGLPV--    29
viba_32                        CGEACVGG-TCNTPGCSCS--WPVCTRNGLPV--    29
kalata_S                       CGETCVGG-TCNTPGCSCS--WPVCTRNGLPV--    29
vitri_peptide_24/28            CGDSCVFF-GCDDEGCTCG-PWSLCYRNGEPV--    30
Cter_36                        CGETCFGG-TCYTPNCVCD-PWPICTKNGSPT--    30
vitri_peptide_21               CQETCTLSDRCYTKGCTCN--WPICYKNGGPLD-    31
Cter_M                         CGETCTL-GTCYVPDCSCS--WPICMKNGLPT--    29
Mden_F                         CGETCFF-GKCNTPKCTCI--NPICYKNGLPI--    29
Mden_H                         CGETCFF-GKCNTPKCTCN--KPLCYKNGIPI--    29
Mobo_B                         CGETCAK-GKCYTPKCTCN--WPICYKNGKPI--    29
mech_2                         CGETCTL-GKCNTPKCTCN--WPICYKDGLPT--    29
mech_3                         CGETCTL-GKCNTPKCTCN--WPICYKNGLPT--    29
Mra25                          CGESCTL-GECYTPGCTCS--WPICTKNGSAIL-    30
cliotide_T19                   CGESCLL-GKCYTPGCTCS--RPICKKNGSVIK-    30
cliotide_T20                   CGESCLL-GKCYTPGCTCD--RPICKKNGSAIR-    30
cT31                           CGESCFA-GKCYTPGCTCD--RPICKKNGDPLK-    30
Cter_2                         CGESCFA-GKCYTPGCTCE--YPICMNNGDPLK-    30
Cter_7                         CGESCFA-GKCYTPGCTCE--YPICMNNGDPFK-    30
vitri_peptide_94b              CGETCTL-GTCYTPGCSCD--WPICKRNGVAV--    29
cliotide_T32                   CGETCFG-GTCYTPGCSCD--YPICKNNGDLFK-    30
cliotide_T2                    CGESCVQ-GECYTPGCSCD--WPICKKNGEFLK-    30
Cter_5                         CGESCVQ-GECYTPGCSCD--YPICKNNGEFLK-    30
vitri_peptide_29               CLETCFGG-KCNAHRCTCS-QWPLCAKNGVPSSD    32
cycloviolacin_O27              CGESCFKG-WCYTPGCSCS-KYPLCAKDGSIPA-    31
cycloviolacin_O26              CGESCFRG-KCYTPGCSCS-KYPLCAKDGSIPA-    31
cycloviolacin_O14              CGESCFKG-KCYTPGCSCS-KYPLCAKNGSIPA-    31
Vinc_B                         CGESCFKG-KCYTPGCTCS-KYPLCAKNGSIPA-    31
Cter_35                        CGETCVLG-TCYTPGCSCA-P-VICLNNGAF---    28
Panitide_L8                    CGETCVLG-TCYTPGCSCS-AYPLCVQD------    26
Panitide_L2                    CGETCVLG-RCYTPNCRC--QYPICVRQLPI---    28
Panitide_L1                    CGETCVLG-TCYTPGCRC--QYPICVRQLPI---    28
Panitide_L6                    CGETCVLG-TCYTPGCSC--AYPICVRQLPI---    28
Panitide_L5                    CGETCVLG-TCYTPGCSC--AYPICARQLPI---    28
Glopa_C                        CGETCFEGGNCRIPGCTCV--WPFCSKNGDIPL-    31
chassatide_C4                  CGETCFTG-ICFTAGCSCN-PWPTCTRNGAS---    29
chassatide_C1                  CGETCFTG-ICFTAGCSCN-PWPTCTRNGDA---    29
kalata_B12                     CGDTCFVL-GCNDSSCSCN--YPICVKDGSL---    28
vitri_peptide_38               CYETCFTG-FCFIGGCKCD--FPVCVKNGDT---    28
vitri_peptide_22a              CGETCFTG-LCYSSGCSCI--YPVCNRNGAPV--    29
vodo_M                         CGESCFTG-KCYTVQCSCS--WPVCTRNGAPI--    29
vitri_peptide_39               CGESCFTG-TCYTVQCSCS--WPVCTRNGAPI--    29
vitri_peptide_39_linear        CGESCFTG-TCYTVQCSCS--WPVCTRNGAPI--    29
Mra26                          CGETCVGN-KCYTPGCTCT--WPVCYRNGHPI--    29
Globa_E                        CGETCVKG-KCNTPGCVCS--WPVCKKNGSAFG-    30
Mra24                          CGETCLLG-TCYTPGCTCK--RPVCYKNGHPT--    29
violacin_A                     CGETCFKF-KCYTPRCSCS--YPVCKSAIS----    27
cliotide_T15                   CGETCFKT-KCYTKGCSCS--YPVCKRNGLPI--    29
Cter_30                        CGETCFKT-KCYTPGCSCS--YPVCKKNGFPI--    29
mela_5                         CGESCFKF-KCYTPGCSCS--YPICKKDGSAIA-    30
cycloviolacin_O16              CGETCFTG-KCYTPGCSCS--YPICKKINGLP--    29
mela_6                         CGETCFKG-KCYTPGCSCS--YPICKKDGIPT--    29
mela_7                         CGETCFKG-KCYTPGCSCS--YPICKKNGLPT--    29
cycloviolacin_O15              CGETCFTG-KCYTPGCSCS--YPICKKNGLVP--    29
cliotide_T18                   CGETCFTG-TCYTPGCTCS--YPVCKKNGLPI--    29
mela_2                         CGETCFKG-KCYTPGCTCS--YPLCKKDGKPT--    29
mela_1                         CGETCFKG-KCYTPGCTCS--YPICKKDGKYT--    29
Mden_B                         CGETCFTG-KCYTPGCTCS--YPICKKNGLPI--    29
mela_3                         CGETCFKG-KCYTPGCTCS--YPICKKDGKPI--    29
Mden_C                         CGETCFKG-KCYTPGCTCS--YPVCKKNGKPI--    29
mela_4                         CGETCFKG-KCYTPGCTCS--YPICKKNGKPI--    29
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