Accesion[1]	NAME	SEQUENCE (size)	GRAVY	NZC	μH	3D-HM (ÅkT/e)	θ	μ (D)	TOTAL ELECTROSTATIC ENERGY (kJ/mol)	mBf	W-W INDEX (kcal/mol)	BOMAN INDEX (kcal/mol)
1465 (**Q6JQN2**)	BmKn2	FIGAIARLLSKIF-NH_2 (13)	1.59	(+1/+2)	0.76	10.54	125.37°	135	1.08 E4	1.59	–2.03	–0.86
1466 (**Q718F4**)	BmKb1, NDBP-4.2, Toxin peptide 6, MeuFSPL-1	FLFSLIPSAISGLISAFK-NH_2 (18)	1.54	(+1/+1)	0.44	6.19	91.59°	121	1.15 E4	1.67	–3.69	–1.32
2143 (**E4VP07**)	Meucin-13, VAP-6	IFGAIAGLLKNIF-NH_2 (13)	1.70	(+1/+1)	0.71	7.39	137.83°	121	1.05 E4	1.57	–2.54	–1.83
2144 (**E4VP50**)	Meucin-18, VAP-9	FFGHLFKLATKIIPSLFQ (18)	0.85	(0/+2)	0.54	8.55	119.72°	261	1.27 E4	1.73	–3.19	–0.66
2159 (**Q8MMJ7**)	IsCT	ILGKIWEGIKSLF-NH_2 (13)	0.77	(+1/+1)	0.77	9.86	117.44°	125	9.98 E3	1.97	–0.88	–0.80
2160 (**Q8MMJ7**)	IsCT [WA6]	ILGKIAEGIKSLF-NH_2 (13)	0.98	(+1/+1)	0.73	10.27	117.45°	124	9.64 E3	2.01	1.14	–0.76
2161 (**Q8MMJ7**)	IsCT [WL6]	ILGKILEGIKSLF-NH_2 (13)	1.13	(+1/+1)	0.76	10.06	115.79°	124	9.90 E3	2.00	0.41	–1.00
2162	IsCT [EK7]	ILGKIWKGIKSLF-NH_2 (13)	0.74	(+1/+3)	0.80	13.35	117.44°	163	9.20 E3	2.00	–1.91	–0.90
2163	IsCT [WL6, SK11]	ILGKILKGIKKLF-NH_2 (13)	0.86	(+1/+4)	0.85	14.33	118.38°	170	9.16 E3	2.15	0.24	–0.93
2164	IsCT [EK7, GP8, SK11]	ILGKIWKPIKKLF-NH_2 (13)	0.41	(+1/+4)	0.86	14.15	117.38°	170	9.16 E3	2.21	–0.61	–0.66
3246	IsCT2f	IFGAIWNGIKS (11)	0.74	(0/+1)	0.64	7.46	140.16°	125	9.02 E3	1.75	–2.18	–0.74
3247	IsCT2	IFGAIWNGIKSLF-NH_2 (13)	1.13	(+1/+1)	0.71	7.61	131.47°	118	1.04 E4	1.66	–3.87	–1.23
3248	IsCTf	ILGKIWEGIKS (11)	0.31	(0/+1)	0.71	8.76	127.30°	134	8.50 E3	2.18	0.81	–0.23
3343	Mastoparan-L	INLKALAALAKKIL-NH_2 (14)	1.15	(+1/+3)	0.39	11.34	69.04°	151	1.04 E4	1.80	1.21	–0.96
3353	Hp1090, Um5	IFKAIWSGIKSLF-NH_2 (13)	1.07	(+1/+2)	0.72	11.93	127.17°	161	9.99 E3	1.77	–3.18	–0.98
3354	Hp1035	IFSAIGGFLKSIF-NH_2 (13)	1.63	(+1/+1)	0.69	8.35	132.16°	119	9.39 E3	1.65	–3.44	–1.53
3475	VmCT1	FLGALWNVAKSVF-NH_2 (13)	1.20	(+1/+1)	0.57	7.13	139.04	119	8.33 E3	1.60	–3.20	–1.16
3476	VmCT2	FLSTLWNAAKSIF-NH_2 (13)	0.82	(+1/+1)	0.60	8.22	135.35°	117	8.56 E3	1.75	–3.39	–0.39
3477	VsCT1	FLKGIIDTVSNWL-NH_2 (13)	0.76	(+1/0)	0.76	8.66	126.18°	164	1.23 E4	1.87	–1.73	–0.23
3478	VsCT2	FLKGIIDTVSKLF-NH_2 (13)	1.01	(+1/+1)	0.76	10.67	124.25°	141	8.65 E3	1.97	–0.44	–0.37
3479	CT1-NDBP-5.17, UyCT1	GFWGKLWEGVKNAI-NH_2 (14)	–0.05	(+1/+1)	0.69	8.84	52.41°	140	1.32 E4	1.95	–1.01	–0.11
3480	CT1-NDBP-5.17, UyCT2	FWGKLWEGVKNAI-NH_2 (13)	–0.02	(+1/+1)	0.74	9.21	116.41°	131	8.55 E3	1.98	–1.02	–0.05
3481	CT3-NDBP-5.15, UyCT3, OcyC1, NDBP-5.7	ILSAIWSGIKSLF-NH_2 (13)	1.39	(+1/+1)	0.66	8.00	131.62°	116	1.01 E4	1.70	–3.47	–1.30
3482	CT5-NDBP-5.16, UyCT5	IWSAIWSGIKGLL-NH_2 (13)	1.13	(+1/+1)	0.69	8.82	124.08°	116	1.07 E4	1.66	–4.31	–1.58
3489	Pantinin-2	IFGAIWKGISSLL-NH_2 (13)	1.42	(+1/+1)	0.71	9.82	118.77°	142	1.09 E4	1.67	–3.59	–1.63
3490	Pantinin-1	GILGKLWEGFKSIV-NH_2 (14)	0.67	(+1/+1)	0.69	9.53	54.71°	137	1.16 E4	1.96	–0.49	–0.75
3491	Pantinin-3	FLSTIWNGIKSLL-NH_2 (13)	0.93	(+1/+1)	0.70	8.99	131.34°	119	9.21 E3	1.84	–3.46	–0.71
3599	CT1	GFWGSLWEGVKSVV-NH_2 (14)	0.51	(+1/0)	0.61	9.08	63.20°	121	9.12 E3	1.85	–1.88	–0.59
3615	CT2, Um3	GFWGKLWEGVKSAI-NH_2 (14)	0.14	(+1/+1)	0.65	9.11	54.47°	138	1.24 E4	1.95	–1.30	–0.34
3752	Mucroporin	LFGLIPSLIGGLVSAFK-NH_2 (17)	1.61	(+1/+1)	0.58	5.44	142.18°	110	1.10 E4	1.68	–3.15	–1.87
3753	Mucroporin-M1, Mucroporin [G3,11R, P6K, G10K]	LFRLIKSLIKRLVSAFK-NH_2 (17)	0.79	(+1/+5)	0.74	13.85	134.29°	196	1.39 E4	0.52	–0.03	0.70
3754	Imcroporin	FFSLLPSLIGGLVSAIK-NH_2 (17)	1.59	(+1/+1)	0.58	7.11	132.72°	116	1.10 E4	1.70	–3.03	–1.61
3884	1, AamAP1	FLFSLIPHAIGGLISAFK-NH_2 (18)	1.43	(+1/+1)	0.43	5.95	89.48°	119	1.13 E4	1.57	–3.77	–1.49
3885	2, AamAP2	FPFSLIPHAIGGLISAIK-NH_2 (18)	1.22	(+1/+2)	0.39	6.68	85.75°	125	1.11 E4	1.71	–1.94	–1.33
3886	AamAP1 [H8K]	FLFSLIPKAIGGLISAFK-NH_2 (18)	1.39	(+1/+1)	0.49	7.95	76.71°	137	1.12 E4	1.70	–2.95	–1.44
3935	Ctriporin	FLWGLIPGAISAVTSLIKK-NH_2 (19)	1.16	(+1/+2)	0.45	5.87	93.98°	83	1.28 E4	1.77	–2.33	–1.25
4297	TsAP-1	FLSLIPSLVGGSISAFK-NH_2 (17)	1.32	(+1/+1)	0.47	4.95	139.47°	111	1.11 E4	1.84	–2.34	–1.12
4298	TsAP2	FLGMIPGLIGGLISAFK-NH_2 (17)	1.54	(+1/+1)	0.59	4.94	146.06°	109	9.88 E3	1.65	–3.32	–2.02
4299	TsAP-1 [S7K] [G10K] [G11K] [S12I] [S14K]	FLSLIPKLVKKIIKAFK-NH_2 (17)	0.85	(+1/+5)	0.75	12.52	158.80°	170	1.07 E4	2.06	0.90	–0.59
4300	TsAP-2 [G7K] [G10K] [G11K] [S14K]	FLGMIPKLIKKLIKAFK-NH_2 (17)	0.74	(+1/+5)	0.77	12.59	161.49°	179	1.01 E4	2.04	0.48	–0.75
4330	Peptide Hp1036	ILGKIWEGIKSIF-NH_2 (13)	0.83	(+1/+1)	0.78	9.90	117.49°	125	9.77 E3	1.95	–0.63	–0.80
4331	Peptide Hp1239	ILSYLWNGIKSIF-NH_2 (13)	0.94	(+1/+1)	0.68	7.90	133.44°	119	1.05 E4	1.66	–4.29	–0.90

4572	Kn2–7	FIKRIARLLRKIF-NH_2 (13)	0.55	(+1/+5)	0.90	16.61	124.49°	199	1.20 E4	1.84	0.27	1.8
7227	AamAP1 [S4K, H8K, G11,12K, A16K]	FLFKLIPKAIKKLISKFK-NH_2 (18)	0.51	(+1/+6)	0.60	12.06	60.99°	174	1.11 E4	2.20	0.69	–0.19
8151	AaeAP1	FLFSLIPSVIAGLVSAIRN-NH_2 (19)	1.58	(+1/+1)	0.45	5.68	89.36°	135	1.40 E4	1.60	–2.31	–0.86
8152	AaeAP2	FLFSLIPSAIAGLVSAIRN-NH_2 (19)	1.45	(+1/+1)	0.42	5.56	88.22°	136	1.39 E4	1.61	–2.21	–0.74
8153	AaeAP1 [S4,8,15K; A11K, N19K]	FLFKLIPKVIKGLVKAIRK-NH_2 (19)	0.77	(+1/+6)	0.66	13.29	76.17°	216	1.25 E4	2.01	1.66	–0.19
8154	AaeAP2 [S4,8,15K; A11K, N19K]	FLFKLIPKAIKGLVKAIRK-NH_2 (19)	0.64	(+1/+6)	0.64	13.18	75.43°	214	1.24 E4	2.03	1.76	–0.07
8199	Stigmurin	FFSLIPSLVGGLISAFK-NH_2 (17)	1.53	(+1/+1)	0.57	6.42	131.60°	113	1.08 E4	1.69	–3.60	–1.50
8437	VpAmp1.0	LPFFLLSLIPSAISAIKKI-NH_2 (19)	1.52	(+1/+2)	0.41	5.51	164.94°	95	1.13 E4	1.79	–2.13	–1.45
8438	VpAmp1.1	FFLLSLIPSAISAIKKI-NH_2 (17)	1.57	(+1/+2)	0.37	5.42	17.12°	92	1.13 E4	1.73	–2.02	–1.33
8864	Hp1404	GILGKLWEGVKSIF-NH_2 (14)	0.67	(+1/+1)	0.67	9.40	54.60°	136	1.10 E4	1.96	–0.49	–0.75
9867	ToAP3, Im–4	FIGMIPGLIGGLISAIK-NH_2 (17)	1.68	(+1/+1)	0.59	5.37	145.06°	110	9.63 E3	1.65	–2.25	–2.14
9869	ToAP1	FIGMIPGLIGGLISAFK-NH_2 (17)	1.58	(+1/+1)	0.59	4.85	148.15°	107	9.67 E3	1.64	–3.07	–2.02
9870	OcyC2, NDBP-5.8	GILGKIWEGVKSLI-NH_2 (14)	0.79	(+1/+1)	0.68	10.03	55.71°	137	1.15 E4	1.97	0.33	–0.89
9945	Uy17	ILSAIWSGIKGLL-NH_2 (13)	1.50	(+1/+1)	0.66	8.61	128.03°	115	1.06 E4	1.68	–3.02	–1.78
9946	Uy192	FLSTIWNGIKGLL-NH_2 (13)	0.96	(+1/+1)	0.70	9.14	128.68°	117	8.94 E3	1.80	–3.58	–1.04
9947	Uy234	FPFLLSLIPSAISAIKRL-NH_2 (18)	1.32	(+1/+2)	0.46	4.84	95.63°	92	1.15 E4	1.79	–2.00	–0.74
9951	Um2	ISQSDAILSAIWSGIKSLF-NH_2 (19)	0.83	(+1/0)	0.50	8.84	74.18°	113	1.48 E4	1.89	–1.54	–0.13
9952	Um4	FFSALLSGIKSLF-NH_2 (13)	1.49	(+1/+1)	0.65	8.09	130.51°	121	7.79 E3	1.70	–3.82	–1.20
9953	UyCT3 [L2F,S3G], D1	IFGAIWSGIKSLF-NH_2 (13)	1.36	(+1/+1)	0.67	7.46	131.27°	117	9.63 E3	1.65	–4.16	–1.48
9954	Uy192 [G11S,L13F], D2	FLSTIWNGIKSLF-NH_2 (13)	0.86	(+1/+1)	0.71	8.55	130.65°	118	8.53 E3	1.82	–4.03	–0.56
9955	UyCT1 [E8K,G9P,N12K], D4	GFWGKLWKPVKKAI-NH_2 (14)	–0.19	(+1/+4)	0.73	12.10	37.32°	173	1.15 E4	2.17	–1.03	–0.21
9956	UyCT1 [W7L,N12K], D5	GFWGKLLEGVKKAI-NH_2 (14)	0.25	(+1/+2)	0.70	9.31	40.87°	121	1.23 E4	2.08	0.85	–0.37
9957	UyCT1 – 3K, D11	GFWGKLWEGVKNAIKKK-NH_2 (17)	–0.72	(+1/+4)	0.59	5.42	34.90°	52	1.34 E4	2.47	1.96	0.88
10158	NDBP-5.5	IFSAIAGLLSNLL-NH_2 (13)	1.93	(+1/0)	0.65	8.14	123.31°	134	8.50 E3	1.56	–2.96	–1.81
10462	IsCT1 [I5,9A]	ILGKAWEGAKSLF-NH_2 (13)	0.36	(+1/+1)	0.56	9.46	114.16°	125	9.87 E3	2.04	0.07	–0.32
10463	IsCT1 [I5,9V]	ILGKVWEGVKSLF-NH_2 (13)	0.73	(+1/+1)	0.69	9.75	115.63°	125	1.01 E4	1.99	–0.12	–0.67
10464	IsCT1 [I5,9L]	ILGKLWEGLKSLF-NH_2 (13)	0.66	(+1/+1)	0.76	9.94	119.27°	126	1.03 E4	2.02	–1.38	–0.80
10465	IsCT1 [K10E]	ILGKIWEGIESLF-NH_2 (13)	0.80	(+1/–1)	0.76	9.26	133.65°	177	1.13 E4	1.94	0.15	–0.70
10466	IsCT2 [F2L;I5,9A]	ILGAAWNGAKSLF-NH_2 (13)	0.80	(+1/+1)	0.49	7.21	130.56°	116	1.05 E4	1.73	–2.34	–0.90
10467	IsCT2 [F2L;I5,9V]	ILGAVWNGVKSLF-NH_2 (13)	1.16	(+1/+1)	0.62	7.50	131.89°	116	1.08 E4	1.69	–2.54	–1.25
11211	MeuFSPL-2	FLFSLIPSAISGLINAFK-NH_2 (18)	1.39	(+1/+1)	0.47	6.12	90.98°	124	1.22 E4	1.68	–3.40	–1.14
11223	Spiniferin	ILGEIWKGIKDIL-NH_2 (13)	0.70	(+1/0)	0.83	9.45	136.26°	132	1.15 E4	2.02	1.04	–0.54
11224	Spiniferin [E4K,D11N]	ILGKIWKGIKNIL-NH_2 (13)	0.66	(+1/+3)	0.84	13.35	118.37°	170	1.03 E4	2.02	–0.80	–0.80
11270	Stigmurin [S7K,G10K], StigA6	FFSLIPKLVKGLISAFK-NH_2 (17)	1.14	(+1/+3)	0.66	10.36	142.96°	152	1.09 E4	1.85	–1.76	–0.99
11271	Stigmurin [S3,7K; G10K], StigA16	FFKLIPKLVKGLISAFK-NH_2 (17)	0.96	(+1/+4)	0.72	14.63	135.00°	209	1.09 E4	1.93	–0.90	–0.86
12239	HAP-1 (1–19)	QKDDEEESRFFFNFIFSAE-NH_2 (19)	–0.93	(+1/–4)	0.22	10.15	90.35°	146	1.96 E4	2.94	7.81	3.28
12417	Stigmurin [G10,11K; S14K], StigA25	FFSLIPSLVKKLIKAFK-NH_2 (17)	0.94	(+1/+4)	0.70	9.91	167.31°	132	1.08 E4	1.97	–0.78	–0.61
12418	Stigmurin [S3,6,14K; G10,11K], StigA31	FFKLIPKLVKKLIKAFK-NH_2 (17)	0.57	(+1/+6)	0.80	15.39	148.69°	222	1.08 E4	2.16	0.94	–0.35
12573	1, AamAP1[P7R; H8K]	FLFSLIRKAIGGLISAFK (18)	1.23	(+1/+3)	0.51	8.08	88.82°	217	1.33 E4	1.68	–2.59	–0.61
13647	AcrAP1, AP1–Z1	FLFSLIPHAISGLISAFK-NH_2 (18)	1.41	(+1/+1)	0.43	6.19	90.11°	121	1.16 E4	1.60	–3.65	–1.25
13648	AcrAP1 [S4K, H8K, S11K, S15K]	FLFKLIPKAIKGLIKAFK-NH_2 (18)	0.85	(+1/+5)	0.64	14.16	78.24°	211	1.06 E4	1.94	–0.25	–0.84
13649	AcrAP2	FLFSLIPNAISGLLSAFK-NH_2 (18)	1.35	(+1/+1)	0.47	6.54	88.16°	121	1.23 E4	1.68	–3.65	–1.14
13650	AcrAP2 [S4K, N8K, S11K, S15K]	FLFKLIPKAIKGLLKAFK-NH_2 (18)	0.81	(+1/+5)	0.63	14.33	77.66°	212	1.07 E4	1.95	–0.50	–0.84
14214	IsCT [G3K, E7K, G8NAla, S11K]	ILKKIWKXIKKLF-NH_2 (13) [2]	0.40	(+1/+5)	0.91	17.56	120.76°	208	9.54 E3	2.17	0.09	–0.30
14497	QnCs-BUAP	FFSLIPSLISGLI-NH_2 (13)	2.00	(+1/0)	0.60	7.92	114.19°	132	8.00 E3	1.65	–4.02	–2.01
14624	Marcin-18	FFGHLFKLATKIIPSLFR-NH_2 (18)	0.80	(+1/+3)	0.59	10.81	115.48°	176	1.24 E4	1.72	–2.96	–0.14

14625	Megicin-18	FFGALFKLATKIIPSLFR-NH_2 (18)	1.07	(+1/+3)	0.58	10.78	116.52°	180	1.26 E4	1.72	–2.96	–0.50
14626	VmCT1 [G3R]	FLRALWNVAKSVF-NH_2 (13)	0.89	(+1/+2)	0.63	11.54	133.00°	158	9.36 E3	1.62	–2.40	0.05
14627	VmCT1 [N7R]	FLGALWRVAKSVF-NH_2 (13)	1.13	(+1/+2)	0.60	9.52	141.05°	133	8.69 E3	1.59	–2.81	–0.53
14634	VmCT1 [S11R]	FLGALWNVAKRVF-NH_2 (13)	0.92	(+1/+2)	0.63	7.86	136.92°	105	8.93 E3	1.60	–2.52	–0.28
14635	VmCT1 [F1G]	GLGALWNVAKSVF-NH_2 (13)	0.96	(+1/+1)	0.51	7.82	128.75°	123	8.59 E3	1.67	–2.06	–1.01
14636	VmCT1 [V8P]	FLGALWNPAKSVF-NH_2 (13)	0.76	(+1/+1)	0.57	6.85	139.33°	118	8.12 E3	1.76	–2.82	–0.85
14637	VmCT1 [A9L]	FLGALWNVLKSVF-NH_2 (13)	1.36	(+1/+1)	0.67	7.64	137.84°	121	8.56 E3	1.59	–3.93	–1.40
14638	VmCT1 [A9F]	FLGALWNVFKSVF-NH_2 (13)	1.28	(+1/+1)	0.68	7.23	137.40°	121	8.42 E3	1.57	–4.95	–1.25
14639	VmCT1 [V12L]	FLGALWNVAKSLF-NH_2 (13)	1.17	(+1/+1)	0.60	7.56	137.68°	120	8.42 E3	1.60	–3.83	–1.23
14640	VmCT1 [V12Y]	FLGALWNVAKSYF-NH_2 (13)	0.78	(+1/+1)	0.56	5.85	140.91°	122	1.10 E4	1.58	–4.21	–0.84
15558	Eval418	LWGEIWNTVKGLI-NH_2 (13)	0.50	(+1/0)	0.74	8.09	125.59°	96	9.52 E3	1.85	–1.78	–0.66
15559	Eval418-FH2	LWGHIWNFVHGLI-NH_2 (13)	0.85	(+1/0)	0.67	7.84	115.70°	134	8.63 E3	1.39	–5.72	–1.32
15560	Eval418-FH3	LWHHIWNFVHGLI-NH_2 (13)	0.63	(+1/0)	0.67	8.28	115.70°	135	8.97 E3	1.32	–5.56	–0.89
15561	Eval418-FH4	LWHHIWNTVHHLI-NH_2 (13)	0.15	(+1/0)	0.66	7.74	114.70°	136	9.61 E3	1.32	–4.13	–0.04
15562	Eval418-FH5	LWHHIWHTVHHLI-NH_2 (13)	0.17	(+1/0)	0.60	7.54	112.18°	136	9.09 E3	1.25	–4.38	–0.19
16149	MK049518	FLGLLGSVLGSVLPSIFK-NH_2 (18)	1.57	(+1/+1)	0.46	6.79	119.62°	127	1.14 E4	1.75	–3.37	–1.70
16150	MK049518 [S7,11,15K]	FLGLLGKVLGKVLPKIFK-NH_2 (18)	1.06	(+1/+4)	0.57	11.76	113.76°	176	1.15 E4	1.94	–0.79	–1.34
16151	MK049518 [G3,6,10K; S7,11,15K]	FLKLLKKVLKKVLPKIFK-NH_2 (18)	0.47	(+1/+7)	0.62	15.71	125.63°	240	1.19 E4	2.34	2.15	–0.26
16788	VmCT1 [F1K]	KLGALWNVAKSVF-NH_2 (13)	0.69	(+1/+2)	0.49	11.37	95.58°	160	8.31 E3	1.80	–1.08	–0.51
16789	VmCT1 [A9K]	FLGALWNVKKSVF-NH_2 (13)	0.76	(+1/+2)	0.48	5.25	134.06°	108	8.60 E3	1.81	–2.38	–0.60
16790	VmCT1 [F1K,V12K]	KLGALWNVAKSKF-NH_2 (13)	0.06	(+1/+3)	0.43	9.35	80.68°	126	8.43 E3	2.08	–0.16	0.22
16791	VmCT1 [G3K,N7K]	FLKALWKVAKSVF-NH_2 (13)	0.90	(+1/+3)	0.66	14.20	134.77°	151	8.20 E3	1.79	–1.65	–0.75
16792	VmCT1 [G3K,S11K]	FLKALWNVAKKVF-NH_2 (13)	0.70	(+1/+3)	0.69	11.64	133.94	138	8.37 E3	1.79	–1.36	–0.50
16793	VmCT1 [N7K,S11K]	FLGALWKVAKKVF-NH_2 (13)	0.93	(+1/+3)	0.66	10.77	137.16°	180	7.53 E3	1.74	–1.77	–1.08
16794	VmCT1 [G3K,N7K,S11K]	FLKALWKVAKKVF-NH_2 (13)	0.66	(+1/+4)	0.72	14.20	136.13°	115	7.85 E3	1.87	–0.79	–0.58
17518	BmKn1	FIGAVAGLLSKIF-NH_2 (13)	1.88	(+1/+1)	0.63	7.56	116.56°	108	9.98 E3	1.58	–2.45	–2.01
17527	Im-6	FFFLPSLIGGLVSAIK-NH_2 (16)	1.68	(+1/+1)	0.43	5.02	67.12°	118	1.06 E4	1.63	–3.73	–1.80
18163	VpCT1	FWSTLLSIGKSLL-NH_2 (13)	1.09	(+1/+1)	0.58	8.57	128.82°	118	8.80 E3	1.86	–4.0	–0.96
18164	VpCT2	FWSTIWNAAKSLI-NH_2 (13)	0.59	(+1/+1)	0.63	8.65	126.28°	102	9.05 E3	1.74	–3.86	–0.34
18165	VpCT3	FLQGIIDTVGKWL-NH_2 (13)	0.79	(+1/0)	0.75	7.37	117.28°	102	1.18 E4	1.84	–1.69	–0.65
18166	VpCT3 [I6W]	FLQGIWDTVGKWL-NH_2 (13)	0.37	(+1/0)	0.76	7.08	123.17°	119	1.21 E4	1.82	–3.23	–0.45
18167	VpCT4	LWGALLGLGSTLLSKL-NH_2 (16)	1.25	(+1/+1)	0.53	5.37	110.98°	140	1.34 E4	1.78	–4.18	–1.65
18168	VpCTconsensus	FLSKIWDGVKSLL-NH_2 (13)	0.66	(+1/0)	0.73	11.02	118.93°	120	8.41 E3	2.01	–1.42	–0.25
18292	Ctri9594	GVVDTLKNLLMGLL-NH_2 (14)	1.20	(+1/0)	0.55	9.90	83.02°	141	1.41 E4	1.79	–0.09	–0.95
20289	IsCT [E7P]	ILGKIWPGIKSLF-NH_2 (13)	0.92	(+1/+2)	0.67	10.45	111.51°	161	8.77 E3	1.93	–2.45	–1.32
20290	IsCT [G3K,G8P]	ILKKIWEPIKSLF-NH_2 (13)	0.41	(+1/+2)	0.82	13.39	117.82°	172	1.02 E4	2.24	0.54	–0.23
20291	IsCT [I1A; G3,8K; I5F]	ALKKFWEKIKSLF-NH_2 (13)	–0.1	(+1/+3)	0.80	14.51	103.94°	159	8.24 E3	2.36	0.74	0.58
20292	IsCT [I1A, I5F, E7P, G8K]	ALGKFWPKIKSLF-NH_2 (13)	0.32	(+1/+3)	0.67	12.61	95.27°	170	7.03 E3	2.10	–1.81	–0.44
20293	IsCT [G3K,E7K,I9K]	ILKKIWKGKKSLF-NH_2 (13)	–0.17	(+1/+5)	0.64	14.77	117.33°	169	9.78 E3	2.79	0.37	0.40
20294	IsCT [G3K, E7K, G8P, I9K]	ILKKIWKPKKSLF-NH_2 (13)	–0.26	(+1/+5)	0.65	14.76	117.22°	193	9.67 E3	2.86	0.81	0.47
21142	Hp1470	IFKAIWSGINRLF (13)	0.82	(0/+2)	0.77	8.72	142.80°	108	1.23 E4	1.69	–3.07	–0.01
21411	TtAP-2	IFGMIPGLIGGLISAFK-NH_2 (17)	1.59	(+1/+1)	0.59	4.92	146.20°	115	9.79 E3	1.64	–3.07	–2.02
21412	TtAP-3	FFSLIPSLIGGLVSAIK-NH_2 (17)	1.64	(+1/+1)	0.59	7.16	131.28°	135	1.08 E4	1.69	–2.78	–1.61

[1] Database of Antimicrobial Activity and Structure of Peptides, DBAASP and (Uniprot); [2] X: Sarcosine