

1 Investigating the specificity of the dehydration and cyclization reactions
2 in engineered lanthipeptides by synechococcal SyncM

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15 **Supporting Information for Publication**

16

17 **FIGURES AND TABLES**

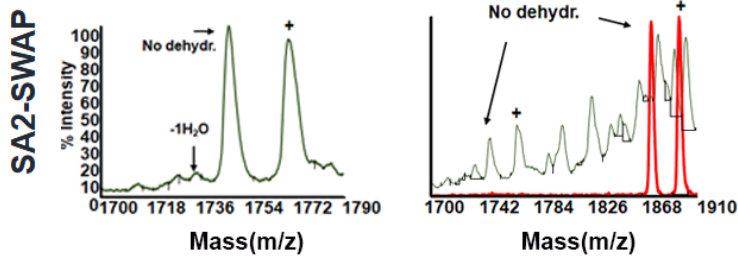
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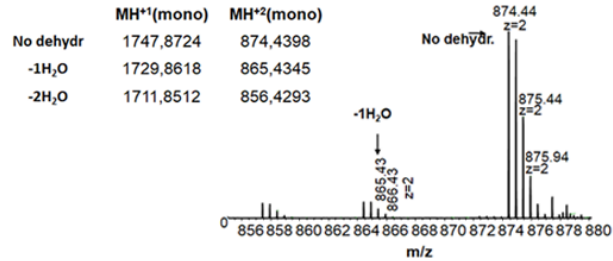
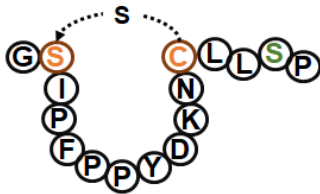
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A) MALDI-TOF and Ring analysis NEM

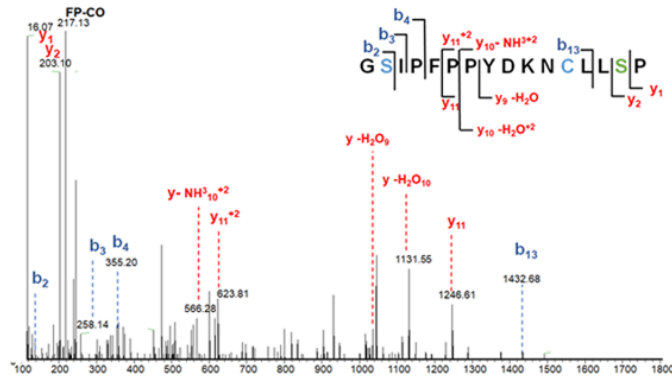
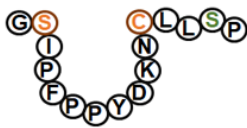
■ Control
■ NEM



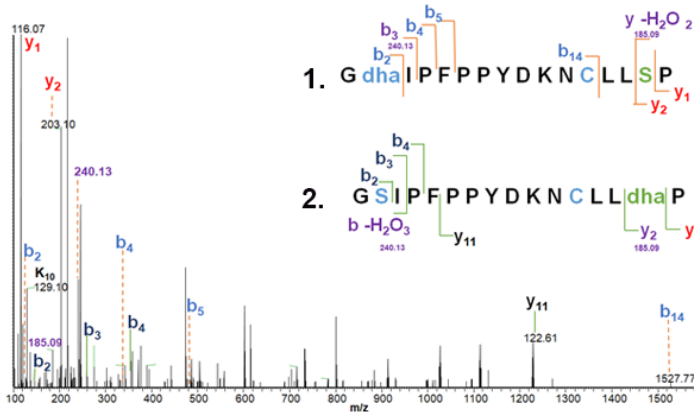
B) LC-MS



C) No dehy MH+2 874.43



D) -1H₂O MH+2 865.44



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22 **Supplementary Figure S1.** Overview of SA2-SWAP of SyncA2 mutants. Dehydration
 23 and cyclization state analysis. A) MALDI-TOF spectra of SA2-SWAP; the dehydration
 24 state is depicted by arrows. Ring analysis with N-ethylmaleimide (NEM, red spectra
 25 correspond after NEM reaction). (+) Na-adduct B) LC-MS spectra. Detected masses

26 were found to correspond to non-dehydrated and -1H₂O peptides. C) MS² spectra of
27 the non-dehydrated peptide. Ion fragments of the unmodified peptide are indicated. D)
28 MS² spectra of the -1H₂O peptide. Ion fragments of -1H₂O unmodified peptide are
29 indicated. Two options for dehydration were found. Form 1 with the S2 dehydrated.
30 Form 2 with the S15 dehydrated. Ion fragments of each form are differentiated with
31 color. (1-Orange, 2-Dark blue, same ion-Red). Masses that could correspond to both
32 peptides are identified in purple.

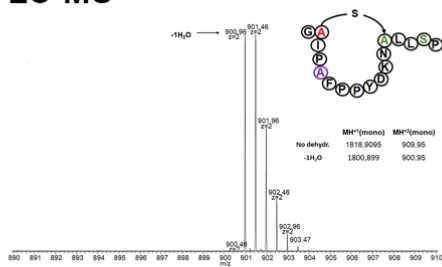
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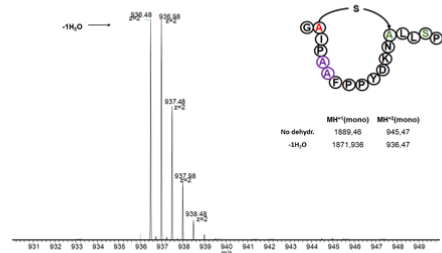
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A) LC-MS

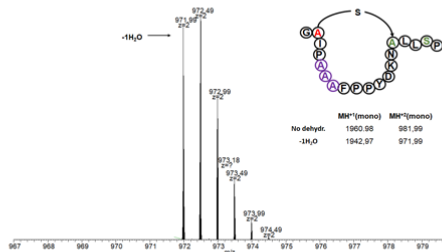
SA2-+1A



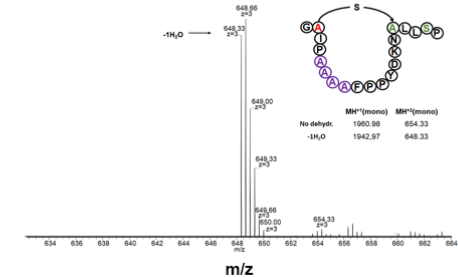
SA2-+2A



SA2-+3A

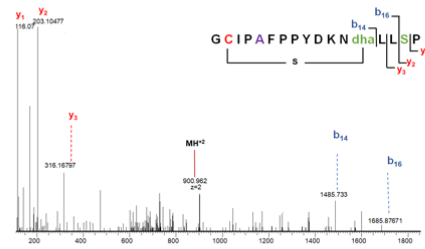


SA2-+4A

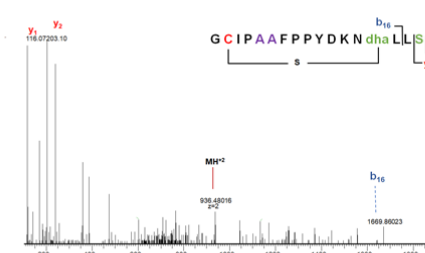


B) MS/MS

SA2-+1A



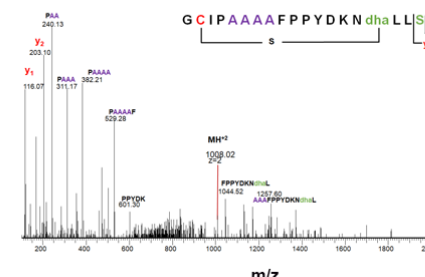
SA2-+2A



SA2-+3A



SA2-+4A



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37 **Supplementary Figure S2.** LC-MS/MS spectra of SyncA2 macrocycle variants. A)

38 Shows the LC-MS chromatograms. Expected dehydration was found in all mutants.

39 SA2-+1A, SA2-+2A, SA2-+3A and SA2-+4^a. B) Ring formation analysis showing MS²

40 spectra of each macrocycle mutant: SA2-+1A, SA2-+2A, SA2-+3A, and SA2-+4^a

41 Fragmented ions, corresponding with the two-time mass charge in each mutant, are

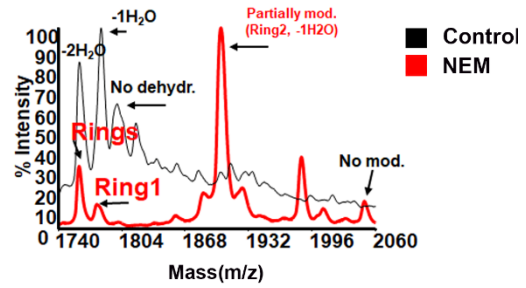
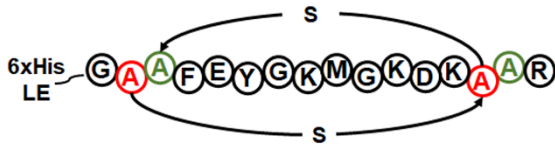
42 depicted. A lanthionine ring was installed by SyncM in all variants.

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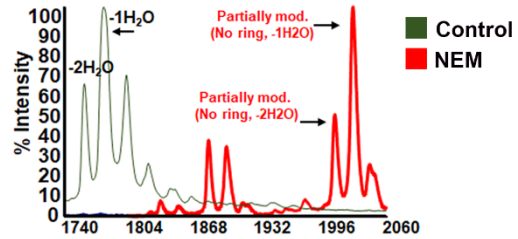
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A) Ring analysis SyncA6

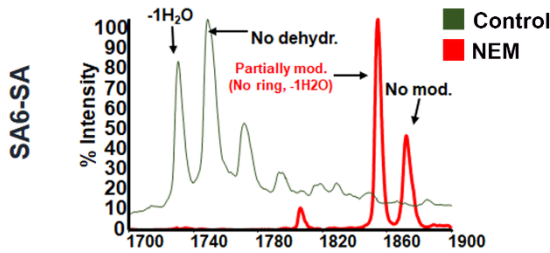
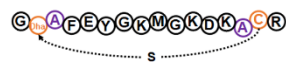


B) Ring Analysis NEM

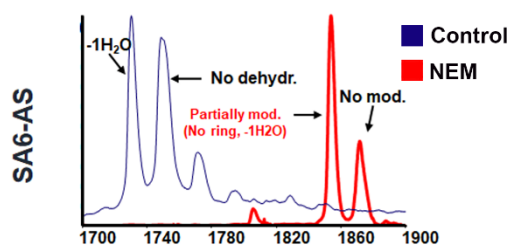
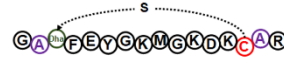


C) Ring Analysis NEM

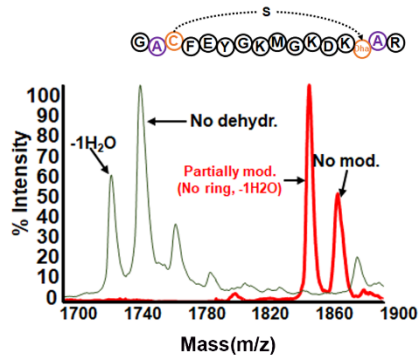
Ring swap (single-ring)



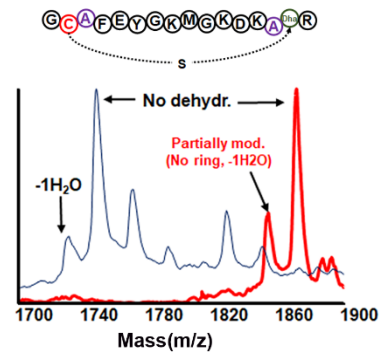
Ring original (single-ring)



SA6-AC



SA6-CA



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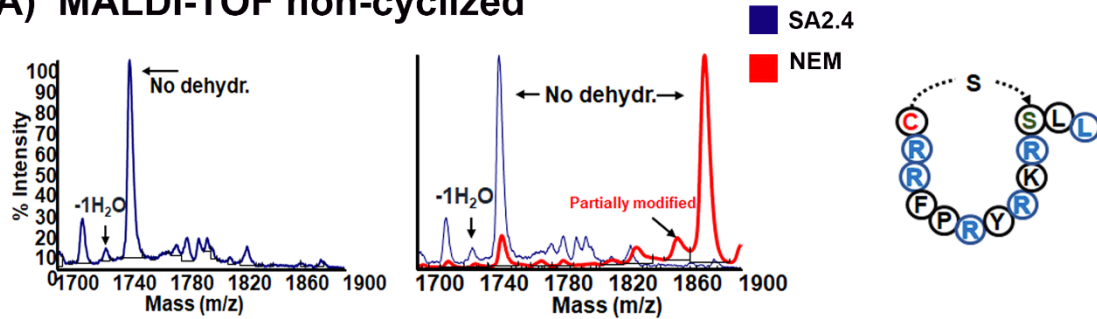
47 **Supplementary Figure S3.** Ring analysis of SyncA6 mutants with the NEM reaction.

48 A) SyncA6 control. B) Mutants with a change in the dehydration and ring direction. C)

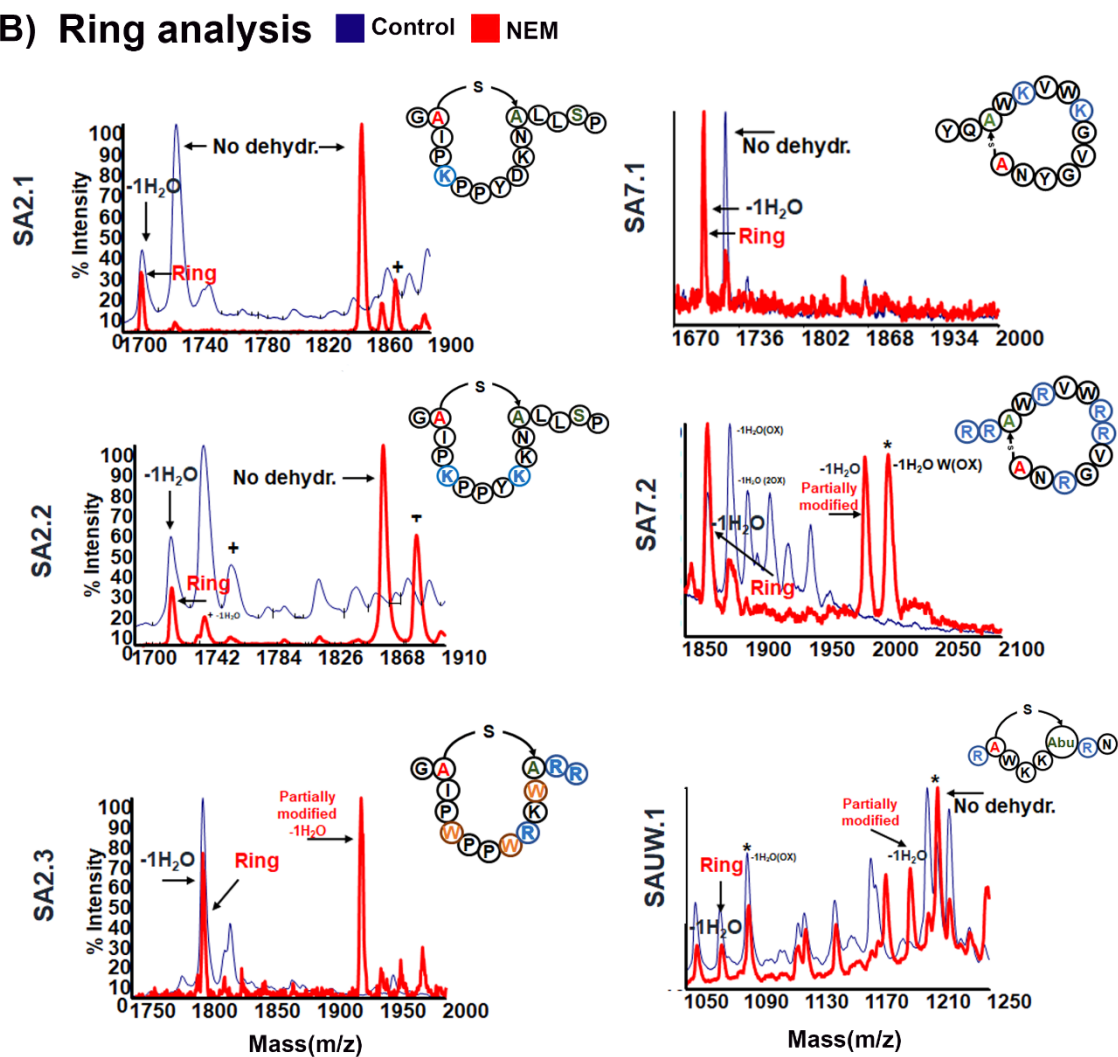
49 Single-ring mutants. Red lines correspond to spectra after NEM reaction and back line

50 (black, green and blue) depicts control spectra. No ring was formed in any of the
 51 mutants.

A) MALDI-TOF non-cyclized



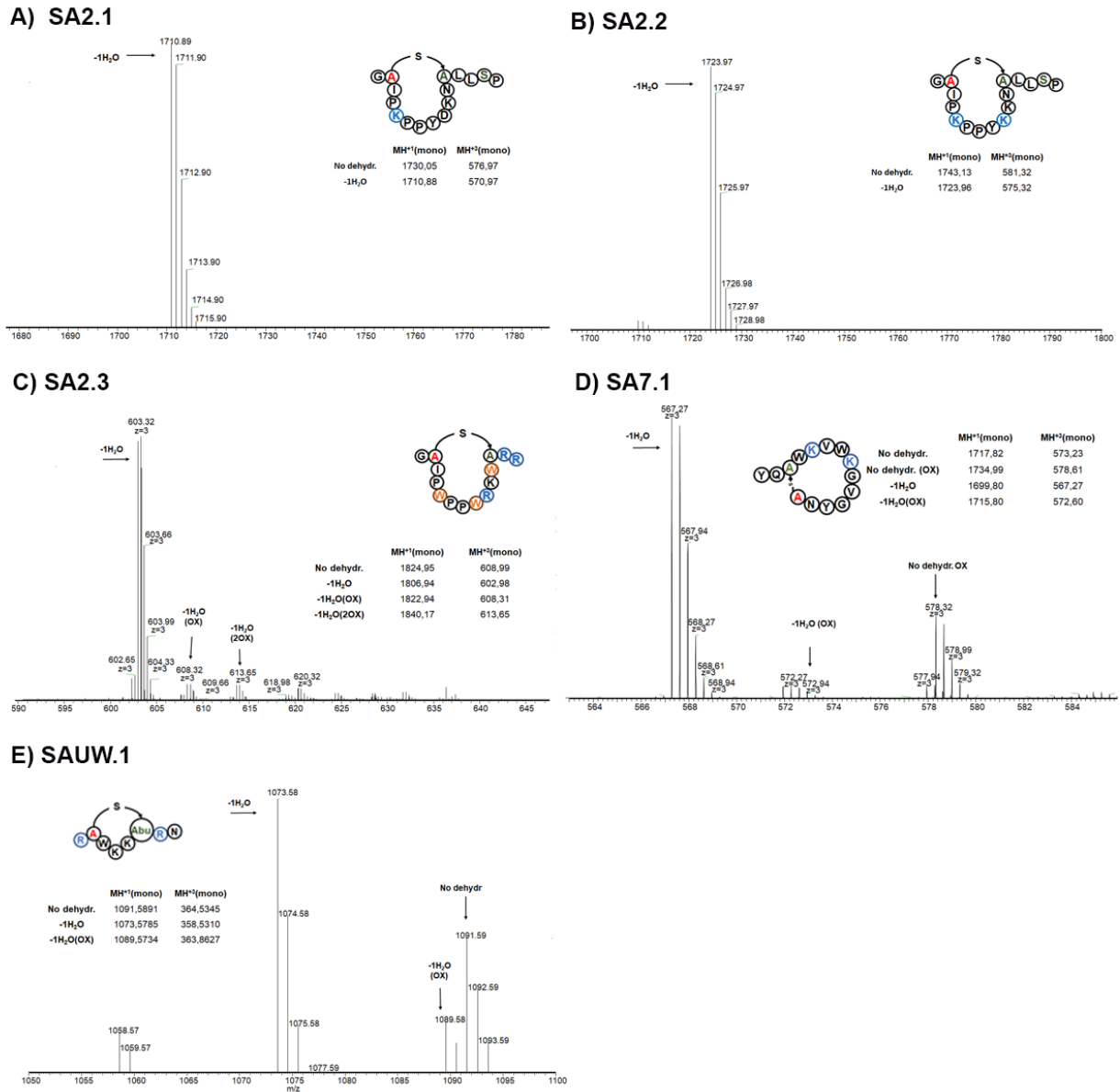
B) Ring analysis



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53 **Supplementary Figure S4.** Ring analysis of single-ringed engineered SyncA's with
 54 the NEM reaction. (+) Na adduct . A) The SA2.4 MALDI-TOF dehydration state is

55 depicted by arrows. Ring analysis with N-ethylmaleimide (NEM, red spectra
 56 correspond to the situation after NEM reaction). B) Single-ring variants with a ring
 57 installed. SA2.1, SA2.2, SA2.3, SA7.1, SA7.2, SAUW.1.



58

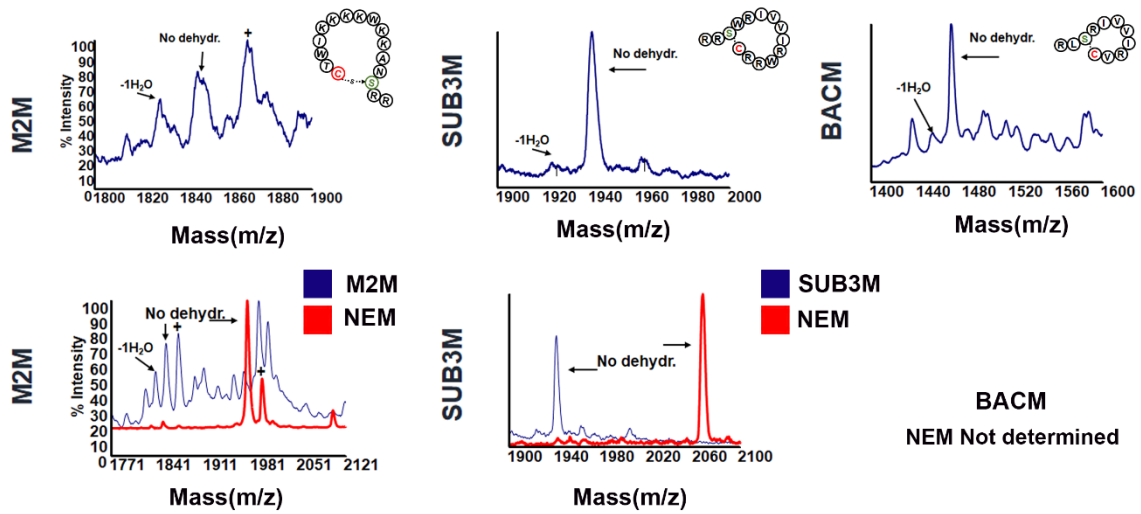
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60 **Supplementary Figure S5.** LC-MS Spectra of SyncA2 engineered single-ringed
 61 SyncA's. A) SA2.1 B) SA2.2, C) SA2.3, D) SA7.1. E) SAUW.1.

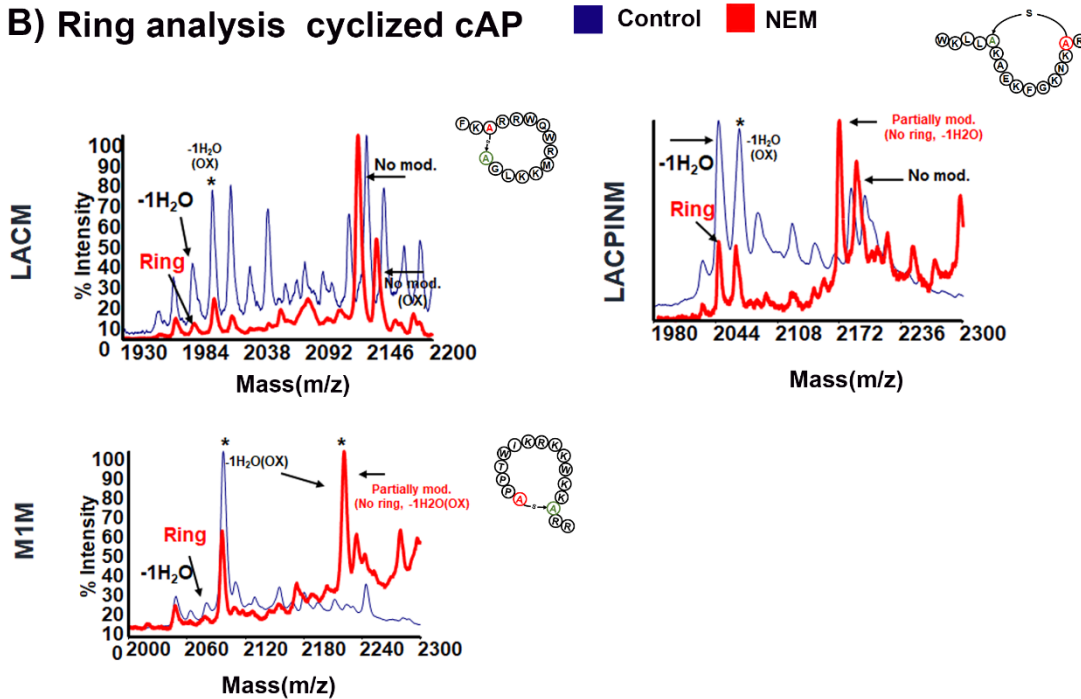
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A) MALDI-TOF non cyclized cAP



B) Ring analysis cyclized cAP



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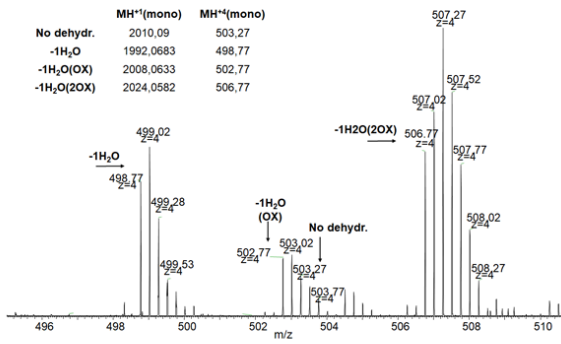
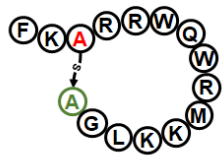
66 **Supplementary Figure S6.** Ring analysis of non-prochlorosin peptides co-expressed

67 with SyncM. A) MALDI-TOF and NEM of non-modified AMPs B) Ring analysis of cAMP

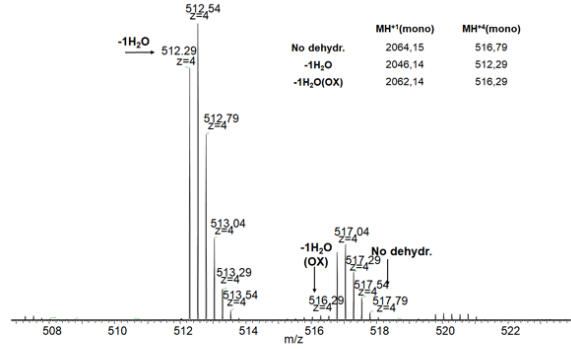
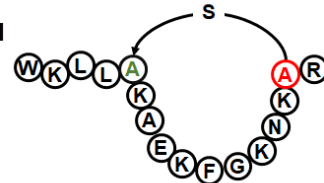
68 with NEM. LACM, M1M, and LACPINM.

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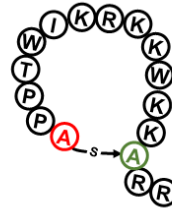
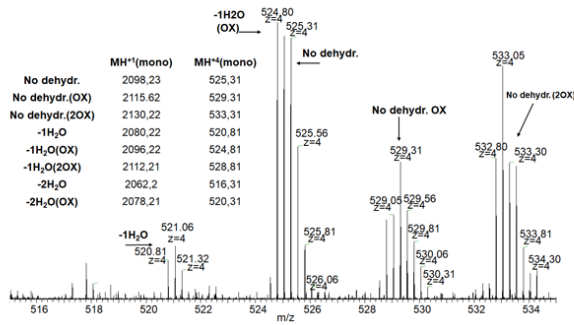
A) LANM



B) LACPINM



C) M1M



70

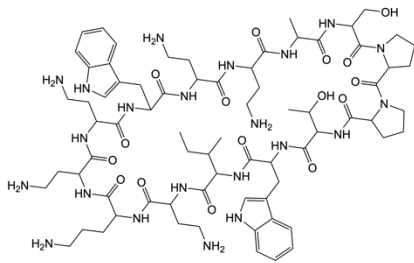
71 **Supplementary Figure S7** LC-MS analysis of non-prochlorosin peptides co-
 72 expressed with SyncM A) LACTO_+S15, B) LACPIN_S16C- and C) SyncAUW.1.

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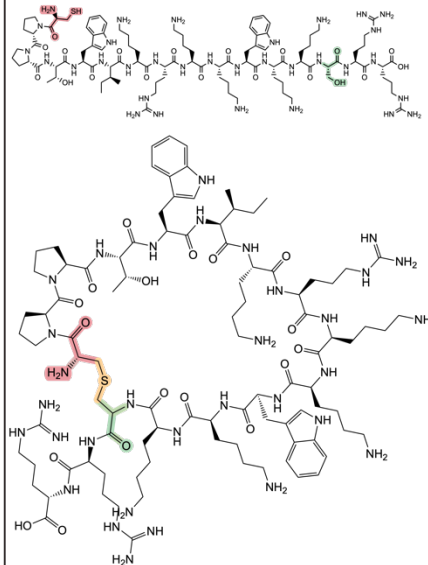
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A) Murepavadin

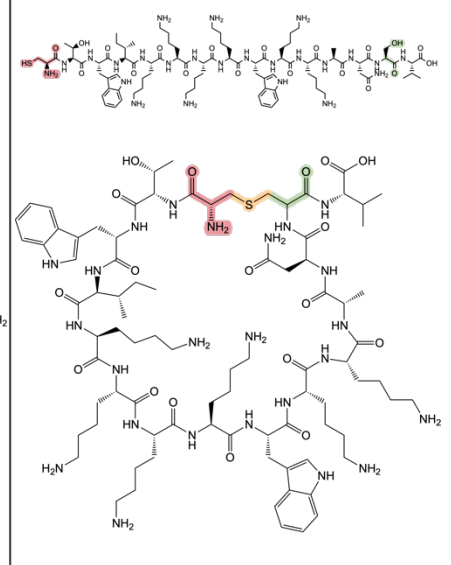
cyclo[Ala-Ser-D-Pro-Pro-Thr-Trp-Ile-Dab-Orn-D-Dab-Dab-Trp-Dab-Dab]



B) M1M **C** **P** **T** **W** **I** **K** **R** **K** **K** **W** **K** **R** **S** **R**



C) M2M **C** **T** **W** **I** **K** **K** **K** **R** **W** **L** **L** **A** **N** **S** **V**



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76 **Supplementary figure S8. Chemical structure of Murepavadin¹ and proposed**
 77 **chemical structure of M1M and M2M with the lanthionine ring. A) Murepavadin**
 78 **sequence and known structure; B) M1M amino acid sequence, linear chemical**
 79 **structure Cys (Highlighted in Red) and Ser (Highlighted in green) and macrocyclic**
 80 **structure after SyncM (lanthionine ring in yellow); C) M1M amino acid sequence, linear**
 81 **chemical structure Cys (Highlighted in Red) and Ser (Highlighted in green) and**
 82 **macrocyclic structure after SyncM (lanthionine ring in yellow).**

83 **Supplementary Table S1.** Core peptide sequences and amino acid profiles of 79 SyncA's from *Synechococcus* M19509. Residues
 84 involved in ring formation are highlighted in selected peptides (red for (C) and green for (T/S)). Blue numbers highest occurrence and
 85 red numbers lowest occurrence.

86

#	Core Peptide Sequence	AA ^a	Ala	Ile	Val	Leu	Met	Phe	Trp	Tyr	Pro	Gly	Cys	Ser	Thr	Asn	Gln	Arg	Lys	His	Asp	Glu	CHARGE
1	TIPPVNWIG EKMDKGC GTLFAASYT SCVAMGTAN KECG	40	5	3	2	1	2	1	1	1	2	5	3	2	4	2	0	0	3	0	1	2	0
SA1	AGSANPQG GDPWCTWD FPICINHK	24	2	2	0	0	0	1	2	0	3	3	2	1	1	2	1	0	1	1	2	0	1
SA2	GCIFFPPYD KNSLLSP	16	0	1	0	2	0	1	0	1	4	1	1	2	0	1	0	0	1	0	1	0	0
4	RRCDSGIW GWIGMAKTC KGPTQG IPGVATTPQL THVLSNLTS QNPdffngf DFFSSLTNPI	24	1	2	0	0	1	0	2	0	1	5	3	1	2	0	1	2	2	0	1	0	3
5	DKPPIPGTIE RINYLLKTLQ DIVAITVKDS QYPYQKSTS TLSCFAIDGR QQLTSRKSC GDCVLGRAL SCLLLGSYA KQKR	96	3	8	4	9	0	6	0	3	8	4	2	10	11	5	7	3	5	1	6	1	1
6	TNILNSAGFC NDNPESRSL QP	22	2	0	1	5	0	0	0	1	0	3	2	2	0	0	1	2	2	0	1	0	3
7	EYECLCHCT WDDVTSCTY NTWGLG	21	1	1	0	2	0	1	0	0	2	1	1	3	1	4	1	1	0	0	1	1	-1
8		0	0	0	2	2	0	0	2	1	0	2	0	0	0	0	0	0	0	0	0	0	-4

9	GACPSTFTID ACAATGCNP KDL	22	4	1	0	1	0	1	0	0	2	2	3	1	3	1	0	0	1	0	2	0	-1
10	AASAIVGDC QSQEGHVCF SEGEVCGK R	28	3	1	4	0	0	1	0	0	0	4	3	3	0	0	2	1	1	1	1	3	-2
11	TAWNSNCY	8	1	0	0	0	0	0	1	1	0	0	1	2	1	1	0	0	0	0	0	0	0
12	CDIELVSLCS KTHNVLC	17	0	1	2	3	0	0	0	0	0	0	3	2	1	1	0	0	1	1	1	1	-1
13	GLSIWGCTE CVDGTFHCK RCDLSNLF	26	0	1	1	3	0	2	1	0	0	3	4	2	2	1	0	1	1	1	2	1	-1
14	NSWGWCRG FTGLEGCSA WCNRFCHG RQTR	29	1	0	0	1	0	2	3	0	0	5	4	2	2	2	1	4	0	1	0	1	3
15	EYTGNDTGP TNMYGVCHI PKCPEWAAS KG	29	2	1	1	0	1	0	1	2	3	4	2	1	3	2	0	0	2	1	1	2	-1
16	SGWAGYKP GQACLGVDT MAPPSPGEF YLSYDGSER	26	3	0	1	1	1	1	1	1	4	5	1	2	1	0	1	0	1	0	1	1	-1
SA9	TFGCGGKGC GWVEPPTKI GGGECRDN KLR	38	0	1	1	2	0	1	1	2	2	9	3	2	2	1	0	3	3	0	2	3	1
18	GVRGGTAAY MCPTDRNKT CKPVATCPG LK	21	3	0	2	1	1	0	0	1	3	4	1	1	0	0	0	0	0	0	0	0	4
19	AEGGWQCQL FPVPTACQV TWN	20	2	0	2	1	0	1	2	0	2	2	2	0	2	1	2	0	0	0	0	1	-1
20	DSGGDYLSY AGCDTGRCC ACSWGCPG	26	2	0	0	1	0	0	1	2	1	7	4	3	1	0	0	1	0	0	3	0	-2
21	LDALKQCNF TGTCWDTLL	18	1	0	0	4	0	1	1	0	0	1	2	0	3	1	1	0	1	0	2	0	-1
SA18	SDTNWITEV SKCPWWRR S	18	0	1	1	0	0	0	3	0	1	0	1	3	2	1	0	2	1	0	1	1	1
SA13	CWMNTCWG YGPGTAAAP DWN	20	3	0	0	0	1	0	3	1	2	3	2	0	2	2	0	0	0	0	1	0	-1

SA14	TDNALNKCT TGCSPSGEV PGYTKPCDN All	30	2	2	1	1	0	0	0	0	1	3	3	3	2	4	3	0	0	2	0	2	1	-1
25	ANICTGCQIA TTCIDDSQIL QYTNSG	26	2	4	0	1	0	0	0	0	1	0	2	3	2	4	2	3	0	0	0	2	0	-2
26	GACEVLTGP VIESYVGDS WHDYCCRIT	27	1	2	3	1	0	0	1	2	1	3	3	3	2	2	0	0	1	0	1	2	2	-3
SA4	EGSWRAGW GPCRVRLSM SPQHKNCRG EQCPLNTGC	26	1	0	1	1	1	0	2	0	2	4	2	2	3	0	1	1	4	1	1	0	1	4
SA5	PLHTGWWC TGVLVDQQP HRSAASNI	40	2	1	2	3	0	0	2	0	3	3	3	3	2	4	2	0	0	3	0	1	2	-1
SA8	SDDELTDF GCKDYERY NKSHYYCEP	17	0	0	0	1	0	1	0	2	0	1	1	1	1	2	0	0	1	1	0	4	2	-4
SA3	IPAPFA	15	2	1	0	0	0	1	0	2	3	0	1	1	0	1	0	0	1	1	0	1	0	0
31	EPTPWDPE WYN	11	0	0	0	0	0	0	2	1	3	0	0	0	0	1	1	0	0	0	0	1	2	-3
32	ECGNVSCVN IYLLTLGKDK EVEL	23	0	1	3	4	0	0	0	1	0	2	2	2	1	1	2	0	0	2	0	1	3	-2
33	KVSDFC TSDI VSYCCW	16	0	1	2	0	0	1	1	1	0	0	3	3	3	1	0	0	0	1	0	2	0	-1
34	ASWSGPMW NTTCIGG	15	1	1	0	0	1	0	2	0	1	3	1	2	2	2	1	0	0	0	0	0	0	0
35	DYCTVETAT VCYIREPGC DTSYGC	25	1	1	2	0	0	0	0	3	1	2	4	4	1	4	0	0	1	0	0	3	2	-4
36	RSYNWASW CSE	11	1	0	0	0	0	0	2	1	0	0	1	3	0	0	1	0	1	0	0	0	1	0
SA12	YYCACTRIPV YNHTN	15	1	1	1	0	0	0	0	3	1	0	2	0	2	2	0	1	0	1	0	0	0	1
38	GTGRHTCGT GSCGCFCSI YEC	24	0	1	0	0	0	1	0	1	0	5	2	2	1	1	2	1	0	1	1	2	0	0
39	ICRQSCIWRS IFKAAPE	17	2	3	0	0	0	1	1	0	1	0	2	2	0	0	0	1	2	1	0	0	1	2
4	VGGVCGAFT SEANGTP	16	2	0	2	0	0	1	0	0	1	4	1	1	2	2	1	0	0	0	0	0	1	-1
41	GTDVNHCFY ATAYGPHTC SGACAK	24	4	0	1	0	0	1	0	2	1	3	3	3	1	3	1	0	0	1	2	1	0	0
42	TACALRVGT VFIGSCWN	17	2	1	2	1	0	1	1	0	0	2	2	2	1	2	1	0	1	0	0	0	0	1

43	DLHSVCGFS ACGTCGLEG TCLICEDT	26	1	1	1	3	0	1	0	0	0	4	5	2	3	0	0	0	0	1	2	2	-4
44	LAWGAGGS RVPIN	13	2	1	1	1	0	0	1	0	1	3	0	1	0	1	0	1	0	0	0	0	1
45	ANQSFEYGA IGQCLPPCP MSH	21	2	1	0	1	1	1	0	1	3	2	2	2	0	1	2	0	0	1	0	1	-1
46	ANSCDILTAJ VWDSYMG CFICNKH	25	2	3	1	1	1	1	1	1	0	1	3	2	2	2	0	0	1	1	2	0	-1
47	SETNCGYPT KFCMVCA EHRVVTQC Q	28	1	0	3	0	1	1	0	2	1	1	5	1	4	1	2	1	1	1	0	2	0
48	GHCLTNSPL AGGCTGWL RI	16	1	1	0	3	0	0	1	0	1	4	1	2	0	1	0	0	1	0	1	0	1
49	NSDNKHCYY YTSGIYTRCD D	20	0	1	0	0	0	0	0	4	0	1	2	2	2	2	0	1	1	1	3	0	-1
5	DITWDFVSTL VTACADR HCCKK	24	2	1	2	1	1	1	1	0	0	0	3	1	4	0	0	1	2	1	3	0	0
51	ALQSTIQSEN CTFRGAN CQL	20	2	1	0	2	0	1	0	0	0	1	2	2	2	2	3	1	0	0	0	1	0
52	KDGTCTKCV TECKGRYC	17	0	0	1	0	0	0	0	1	0	2	4	0	3	0	0	1	3	0	1	1	2
53	KKPKLEYSN TSLACGC	16	1	0	0	2	0	0	0	1	1	1	2	2	1	1	0	0	3	0	0	1	2
SA15	VTLKYKNWC YCTAL	14	1	0	1	2	0	0	1	2	0	0	2	0	2	1	0	0	2	0	0	0	2
55	RGFSYLPQE CVTDYLCG	17	0	0	1	2	0	1	0	2	1	2	2	1	1	0	1	1	0	0	1	1	-1
SA6	GCSFEYGKM GKDKCSR	16	0	0	0	0	1	1	0	1	0	3	2	2	0	0	0	1	3	0	1	1	2
SA16	RIVCVSFGSL FIRRGKLS	18	0	2	2	2	0	2	0	0	0	2	1	3	0	0	0	3	1	0	0	0	4
SA11	CDIELVSLCS KTHNVLC	24	0	1	2	3	0	0	0	0	0	0	3	1	2	0	1	2	2	0	1	0	-1
59	CYNWKSAR DY	10	1	0	0	0	0	0	1	2	0	0	1	1	0	1	0	1	1	0	1	0	1
6	FECSPCKL SIGGPG	15	0	1	0	1	0	2	0	0	2	3	2	2	0	0	0	0	1	0	0	1	0
61	LGPKVSAGS LYCLCPG	16	1	0	1	3	0	0	0	1	2	3	2	2	0	0	0	0	1	0	0	0	1
62	TCFCFSVAC RLDTGITFR	18	1	1	1	1	0	3	0	0	0	1	3	1	3	0	0	2	0	0	1	0	1

63	WRCSVGPQ TNKQNWTA LCCQKGQI	25	1	1	1	1	0	0	2	0	1	2	3	1	2	2	5	1	2	0	0	0	3
SA7	YQSWDVWD GVGYNC	14	0	0	2	0	0	0	2	2	0	2	1	1	0	1	1	0	0	0	2	0	-2
65	ADTLCCPVR CGQTFSCIA	18	2	1	1	1	0	1	0	0	1	1	4	1	2	0	1	1	0	0	1	0	0
66	GAETACLTN NTCFEAQAC CYFTL	23	4	0	0	2	0	2	0	1	0	1	4	0	4	2	1	0	0	0	0	2	-2
67	KDYVGRILT QGKCGC	15	0	0	1	1	0	0	0	1	0	3	2	0	2	0	1	1	2	0	1	0	2
68	NCQRCNHKS ACSATYVPC VVLTEI	96	2	1	3	1	0	0	0	1	1	0	2	10	11	5	7	3	5	1	6	1	1
69	ECIGGGRGR CSFVSPQSE RGGVGDEK	26	0	1	2	0	0	1	0	0	1	7	2	3	0	0	1	3	1	0	1	3	0
70	CACFKKTEI WFIR	13	1	2	0	0	0	2	1	0	0	0	2	0	1	0	0	1	2	0	0	1	2
71	FGTCFIGRNT TDGKV ^U RITW YW ^U	22	0	2	2	0	0	2	2	1	0	3	1	0	4	1	0	2	1	0	1	0	2
72	ACIDCFTRYG TDEEVTLIDD AGSANPQGE	20	1	2	1	1	0	1	0	1	0	1	2	0	3	0	0	1	0	0	4	2	-5
SA1	DPWCTWDY PICINHK GHGVTFYNP CSTLIMTLKC CTKMLA ^U CP K	24	2	2	0	0	0	0	2	1	3	2	2	1	1	2	1	0	1	1	2	1	-2
74	GQAKQSIRV CRRTLKS	16	1	1	1	1	0	0	0	0	0	1	1	2	1	0	2	3	2	0	0	0	5
76	ESCPTYPICG NMNFGCCTS TGV	22	0	1	2	0	1	1	0	0	2	3	4	2	3	2	0	0	0	0	0	1	-1
77	QFGSYCMCH HKTLC ^U KNDS VDL	21	0	0	1	2	1	1	0	1	0	1	3	2	1	1	1	0	2	2	2	0	0
78	ACPSTFTIDA CAATGCNPK DL	22	4	1	0	1	0	1	0	0	2	1	2	2	0	0	1	2	2	0	1	0	-1
SA3	WCGNACTN WKWSNGAG TGC	19	2	0	0	0	0	0	3	0	0	4	3	1	2	3	0	0	1	0	0	0	1
	Total of AA's	178 3	102	75	80	94	18	56	57	66	86	178	178	131	149	82	55	66	87	25	89	59	Charge^c %

Percentage %		5,9	4,3	4,6	5,4	1,0	3,2	3,3	3,8	4,9	10	10	7,6	8,6	4,7	3,2	3,8	5,0	1,5	5,1	3,4	-	43
Aminoacid presence in core peptides^b		55	50	48	49	16	42	36	45	43	64	76	66	59	50	30	40	cor rec t or not	23	50	40	+	37
Percentage %		70	63	61	62	20	54	46	57	54	81	96	84	75	63	38	51	65	29	63	51	N ^d	20
		A	I	V	L	M	F	W	Y	P	G	C	S	T	N	Q	R	K	H	D	E		

87 ^a Total aminoacid per core sequence

88 ^b Count of times an amino acid is observed in SyncA's core.

89 ^c Summary of net charge² found in SyncA's. Percentage

90 ^d Neutral charge (N)

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100 **Supplementary Table S2.** Summary of plasmids and strains used in this study. All the used plasmids were cloned into *L. lactis*
 101 NZ9000.

Strain	Mutations	Characteristic	References
<i>Micrococcus flavus</i>		Sensitive strain	3
<i>Lactococcus lactis</i> NZ9000	<i>pepN:nisRK</i>	Nisin inducible strain used in cloning and peptides expression	4
pNZ-nisP, pIL253		NisP soluble producer strain, Cm ^R , Ery ^R	3
pNZe-NisP8H		Ery ^R , Cm ^R . NisP producer strain	3
pTLR-SyncM		SyncM lanthipeptide synthase cloned under nisin inducible promoter (<i>P_{nis}</i> promoter), Ery ^R	6
pNZ8048		Nisin inducible expression vector, Cm ^R ,	5
pNZ8048-SyncA2		SyncA2 cloned under <i>P_{nis}</i> promoter in pNZ8048 Cm ^R	6
pNZ8048-SA2 -S12A	S12A	SA2 -S12A cloned under <i>P_{nis}</i> promoter, Cm ^R	
pNZ8048-SA2-SWAP	Ring(C2S/S12C)	SA2-SWAP cloned under <i>P_{nis}</i> promoter, Cm ^R	This work
pNZ8048-SA2-+1A	+1A (P4_F5insA)	under <i>P_{nis}</i> promoter, Cm ^R	This work

pNZ8048- SA2-+2A	+2A (P4_F5insAA)	under P_{nis} promoter, Cm ^R	This work
pNZ8048- SA2-+3A	+3A (P4_F5insAAA)	under P_{nis} promoter, Cm ^R	This work
pNZ8048- SA2-+4A	+4A (P4_F5insAAAA)	under P_{nis} promoter, Cm ^R	This work
pNZ8048-SyncA6		SyncA6 cloned under under P_{nis} promoter, Cm ^R	5
pNZ8048-SyncA6- SA6-SC	Ring1(C2S/S15C)-Ring2(S3C /C14S)	SA6-SC cloned under P_{nis} promoter, Cm ^R	This work
pNZ8048-SyncA6- SA6-AS	Δ Ring1(C2A/S15A)	SA6-AS cloned under P_{nis} promoter, Cm ^R	This work
pNZ8048-SyncA6- SA6-AC	Δ Ring1 (C2A/S15A)- Ring2(S2C /C14S)	SA6-AC cloned under P_{nis} promoter Cm ^R	This work
pNZ8048-SyncA6- SA6-CA	Δ Ring2(S2A/C14S)	SA6-CA cloned under P_{nis} promoter Cm ^R	This work
pNZ8048-SyncA6- SA6-SA	Ring1(C2S/S15) - Δ Ring2(S2A/C14S)	SA6-SA cloned under P_{nis} promoter Cm ^R	This work
pNZ8048-SyncA2LE- SA2.1	F5K	SA2.1 cloned after SA2- LEADER -ASPR under P_{nis} promoter, Cm ^R	This work
pNZ8048-SyncA2LE- SA2.2	F5K_D9K	SA2.2 cloned after SA2- LEADER -ASPR under P_{nis} promoter, Cm ^R	This work
pNZ8048-SyncA2LE- SA-2.3	F5W_Y8W_D9R_L13R_L14R- Δ S15- Δ P16	SA-2.3 cloned after SA2-LEADER-ASPR under P_{nis} promoter, Cm ^R	This work
pNZ8048-SyncA2LE- SA-2.4	Most of the structure change	SA-2.4 cloned after SA2- LEADER -ASPR pNZ8048, under P_{nis} promoter, Cm ^R	This work
pNZ8048-SyncA2LE- SA-2.5	Most of the structure change	SA-2.5 cloned after SA2-LEADER ASPR pNZ8048, under P_{nis} promoter, Cm ^R	This work
pNZ8048-SyncA2LE- SAUW.1	Q1R_N7R	SAUW.1 cloned after SA2- LEADER -ASPR under P_{nis} promoter, Cm ^R	This work
pNZ8048-LACM	insS15 ⁷	LACM cloned after SA2- LEADER -ASPR pNZ8048, under P_{nis} promoter, Cm ^R Ery ^R , syncM cloned in pTLR under P_{nis} promoter	This work

pNZ8048- LACPINM	S16C ⁷	LACPINM cloned after SA2- LEADER -ASPR pNZ8048, under P_{nis} promoter, Cm ^R	This work
pNZ8048- -BACM	C3S ⁸	BACM cloned after SA2- LEADER -ASPR pNZ8048, under P_{nis} promoter, Cm ^R	This work
pNZ8048 - SUB3M	insS3_insC14 ⁹	SUB3M cloned after SA2- LEADER -ASPR pNZ8048, under P_{nis} promoter, Cm ^R	This work
pNZ8048 - M1M	Murepavadin mimic ¹	M1M cloned after SA2- LEADER -ASPR pNZ8048, under P_{nis} promoter, Cm ^R	This work
pNZ8048 - M2M	Murepavadin mimic	M2M cloned after SA2- LEADER -ASPR pNZ8048, under P_{nis} promoter, Cm ^R	This work
pNZ8048-SyncA7		under P_{nis} promoter Cm ^R	6
pNZ8048-SyncA7LE- SyncA7.1	D5K_D8K	Desired core peptide was cloned after SA7- LEADER GG pNZ8048, under P_{nis} promoter, Cm ^R Ery ^R , <i>syncM</i> cloned in pTLR under P_{nis} promoter	This work
pNZ8048-SyncA7LE- SyncA7.2	-Y1R_G2R_D5R_D8R_Y12R	Desired core peptide was cloned after SA7-LE LEADER GG pNZ8048, under P_{nis} promoter, Cm ^R Ery ^R , <i>syncM</i> cloned in pTLR under P_{nis} promoter	This work
pNZ8048-SyncA2LE- SA2.2, pTLR-SyncM	F5K_D9K	Desired core peptide was cloned after SA2- LEADER -ASPR pNZ8048, under P_{nis} promoter, Cm ^R Ery ^R , <i>syncM</i> cloned in pTLR under P_{nis} promoter	This work
pNZ8048-SyncA2LE- SA-2.3, pTLR-SyncM	F5W_Y8W_D9R_L13R_L14R- Δ S15- Δ P16	Desired core peptide was cloned after SA2- LEADER-ASPR pNZ8048, under P_{nis} promoter, Cm ^R Ery ^R , <i>syncM</i> cloned in pTLR under P_{nis} promoter	This work
pNZ8048-SyncA2LE- SA-2.4, pTLR-SyncM	Most of the structure change	Desired core peptide was cloned after SA2- LEADER -ASPR pNZ8048, under P_{nis} promoter, Cm ^R Ery ^R , <i>syncM</i> cloned in pTLR under P_{nis} promoter	This work

pNZ8048-SyncA2LE- SA-2.5, pTLR-SyncM	Most of the structure change	Desired core peptide was cloned after SA2-LEADER ASPR pNZ8048, under P_{nis} promoter, Cm^R Ery^R , <i>syncM</i> cloned in pTLR under P_{nis} promoter	This work
pNZ8048-SyncA2LE- SAUW.1, pTLR-SyncM	-Q1R_N7R	Desired core peptide was cloned after SA2-LEADER -ASPR pNZ8048, under P_{nis} promoter, Cm^R Ery^R , <i>syncM</i> cloned in pTLR under P_{nis} promoter	This work
pNZ8048-LACM_, pTLR- SyncM	_+S15 ⁷	Desired core peptide was cloned after SA2-LEADER -ASPR pNZ8048, under P_{nis} promoter, Cm^R Ery^R , <i>syncM</i> cloned in pTLR under P_{nis} promoter	This work
pNZ8048- LACPINM, pTLR- SyncM	S16C ⁷	Desired core peptide was cloned after SA2-LEADER -ASPR pNZ8048, under P_{nis} promoter, Cm^R Ery^R , <i>syncM</i> cloned in pTLR under P_{nis} promoter	This work
pNZ8048- -BACM, pTLR- SyncM	C3S ⁸	Desired core peptide was cloned after SA2-LEADER -ASPR pNZ8048, under P_{nis} promoter, Cm^R Ery^R , <i>syncM</i> cloned in pTLR under P_{nis} promoter	This work
pNZ8048-SUB3M, pTLR- SyncM	+S3+C14 ⁹	Desired core peptide was cloned after SA2-LEADER -ASPR pNZ8048, under P_{nis} promoter, Cm^R Ery^R , <i>syncM</i> cloned in pTLR under P_{nis} promoter	This work
pNZ8048- M1M, pTLR-SyncM	Murepavadin mimic ¹	Desired core peptide was cloned after SA2-LEADER -ASPR pNZ8048, under P_{nis} promoter, Cm^R Ery^R , <i>syncM</i> cloned in pTLR under P_{nis} promoter	This work
pNZ8048 - M2M, pTLR- SyncM	Murepavadin mimic	Desired core peptide was cloned after SA2-LEADER -ASPR pNZ8048, under P_{nis} promoter, Cm^R Ery^R , <i>syncM</i> cloned in pTLR under P_{nis} promoter	This work

pNZ8048-SyncA7		under P _{nis} promoter Cm ^R	6
pNZ8048-SyncA7LE-SyncA7.1	-D5K_D8K	Desired core peptide was cloned after SA7-LEADER GG pNZ8048, under P _{nis} promoter, Cm ^R Ery ^R , syncM cloned in pTLR under P _{nis} promoter	This work
pNZ8048-SyncA7LE-SyncA7.2	-Y1R_G2R_D5R_D8R_Y12R	Desired core peptide was cloned after SA7-LEADER GG pNZ8048, under P _{nis} promoter, Cm ^R Ery ^R , syncM cloned in pTLR under P _{nis} promoter	This work

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