

Supplementary material

Therapeutic application of lantibiotics and other lanthipeptides: old and new findings

Anton Du Preez van Staden^{a,b*}, Winschau van Zyl^a, Marla Trindade^c, Leon M.T Dicks^a, Carine Smith^b

^a Department of Microbiology, Stellenbosch University, South Africa

^b Division of Clinical Pharmacology, Department Medicine, Stellenbosch University, South Africa

^c Institute for Microbial Biotechnology and Metagenomics, University of the Western Cape, South Africa

* Corresponding Author: AD van Staden (advstaden@outlook.com)

Classification of Lanthipeptides

For the purpose of this review, a combined classification system, based on amino acid sequence similarity of unmodified precursor peptides (without leader sequence) and biosynthetic machinery, was followed^{1,2}. According to this classification scheme, lanthipeptides are separated into four classes and 16 subgroups (Fig. S1-S4; Fig. 1 main text). It should be mentioned that the classification of lanthipeptides will evolve with the emergence of new methods for classifying lanthipeptides and the discovery of putative lanthipeptides from newly reported genome sequences³⁻⁵. The reader is referred to the review by Repka et al⁶ for an extensive overview on the mechanistic action of the modification enzymes involved in PTMs.

Sequence similarity network of lanthipeptide core peptides (Fig. 1 main text) were generated with the Enzyme Function Initiative-Enzyme Similarity Tool (<https://efi.igb.illinois.edu/efi-est/>) using an E-value cutoff of 10^{-3} and visualized using Cytoscape (v3.8.0). Core peptides used for analysis were selected based availability of experimental data and hypothetical peptides were excluded. Prediction of helical motifs in leader peptides were done using PEP2D (<http://crdd.osdd.net/raghava/pep2d/index.html>).

Figure S1

A

Nisin -----MSTKDFNLDL-----VSVSKKDSGASPR
 Epidermin -----MEAVKEKNDLENLDVK-----VNAKESNDSGAEP
 Planosporicin MGISSPALPQNTADLFQLDLE-----IGVEQSLAS---PA
 Pep5 -----MKNNKNLFDLEIK-----KETSQNTDE-LEPQ
 Paenibacillin -----MKVDQMFDDLRL-----KSYEASELSPQ*
 Streptin -----MNNTIKDFDLDLK-----TNKKDTA----TPY
 Pinensin MKDNQVTQIKLSIDDLKIDSFVTSIDSEMNMRLAGGLAGQ
 . . . : : :

B

NisinA ITSISL-CTPGCKTGALMG-CNMKTA-TCH-CSIHV-SK-7
 NisinF ITSISL-CTPGCKTGALMG-CNMKTA-TCN-CSVHV-SK-*8,9
 NisinH FTSISM-CTPGCKTGALMT-CNYKTA-TCH-CSIKV-SK-*10
 NisinJ ITSISL-CTPGCKTGALMT-CFAKTA-TCH-CSGHVHTK-*11
 NisinQ ITSISL-CTPGCKTGALMG-CNLKTA-TCN-CSVHV-SK-12
 NisinZ ITSISL-CTPGCKTGALMG-CNMKTA-TCN-CSIHV-SK-13
 NisinU ITSISL-CTPGCKTGILMT-CPLKTA-TCG-C--HFG---*14
 NisinP VTSKSL-CTPGCKTGILMT-CAIKTA-TCG-C--HFG---15
 NisinO1 YKS^USA-CTPGCPTGILMT-CPLKTA-TCG-C---HITGK**16
 NisinO4 ITSQHSFCTPNCLTGFL--CPPKTQLTCT-CKLKGQ---**16
 CMB001 WKSQSF-CTPGCVTGVLT-CFIQTA-TCN-C--HI-SK-17
 Subtilin WKSESL-CTPGCVTGVLT-CFLQTL-TCN-C--KI-SK-18
 EricinA VLSKSL-CTPGCITGVLQI-CYL^UCFP-TFAK-----19
 EricinS WKSESV-CTPGCVTGVLT-CFLQTI-TCN-C--HI-SK-19
 Entianin WKSESV-CTPGCVTGVLT-CFLQTI-TCN-C--KI-SK-20
 SalivaricinD FTSHSL-CTPGCITGVLMG-CHIQSIG-CNVHI-HISK--21
 GeobacillinI VTSKSL-CTPGCITGVLM--CL--TQNSCVS-CNSCIRC-22
 PaenicidinA VLSIVA-CSSGCGSGK--TAASCVE^UTCGNRCFTINVGSLC-23

C

Epidermin IASKFICTPGCA--KTGSFN^USYCC^U24
 Gallidermin IASKFLCTPGCA--KTGSFN^USYCC^U25
 StaphylococcinT IASKFLCTPGCA--KTGSFN^USYCC^U*26
 MutacinB-Ny266 FKSWSFCTPGCA--KTGSFN^USYCC^U27
 Mutacin1140 FKSWSLCTPGCA--RTGSFN^USYCC^U28
 Clausin FTSVSFCTPGCG--ETGSFN^USFCC^U29
 MutacinI FSSLSLCSLGCTGVKNPSFN^USYCC^U30
 BsaA2 ITS^USHSLCTPGCA--KTGSFN^USFCC^U*31

D

Planosporicin ITS^USVSWCTPGCTS^UEGGGSGCSHCC^U32
 Microbisporicin VTS^UWSLCTPGCTS^UEGGGSNCSFCC^U32

E

Pep5 ---TAGPAIRASV^UQ^UCQKTLKATRLFTVSC^UKGKNGCK-----33
 Epicidin280 ---SLGPAIKATRQVCPK---ATRFVTVSC^UKKSD-CQ-----34
 Epilancin15x SASIVKTTIKASKKLCRG-----FTLTCG---CHFTGKK35
 EpilancinK7 SASVLKTSIKVS^UKKY^UCKG-----VTLTCG---CNI^UTGGK36



Figure S1: Class I lanthipeptides. Where possible structural information is given and lines above letters indicate ring topology of prototypical lanthipeptide. Unless otherwise stated; Letters highlighted in corresponding colours indicates residues that participate in Lan/Melan formation. Bold letters in purple and green designate Thr/Ser that are dehydrated, respectively. Bold black letters indicate Thr/Ser that escapes dehydration. **A) Leader peptides of prototypical class I lanthipeptides.** Strongly- and weakly-conserved residues are indicated by (:) and (.), respectively. Bold letters indicate LanP (lanthipeptide protease) cleavage sites and bold double underlined letters indicates putative cleavage sites for pinensin. Highlighted grey letters indicate conserved residues. * Predicted from WP_080561132.1. Residues predicted to be involved in helical or coiled structures are underlined and italicized, respectively. Structure prediction performed using PEP2D (<http://crdd.osdd.net/raghava/pep2d/index.html>). **B) Nisin-like lanthipeptides.** * Dehydrated Ser/Thr residues predicted based on mass of modified peptide and sequence similarity. ** No accurate mass data reported, dehydratable residues coloured and underlined. **C) Epidermin-like lanthipeptides.** Blue line above letters represents C-terminal AviCys. * Dehydrated Ser/Thr residues predicted based on mass of modified peptide and sequence similarity. **D) Planosporicin-like lanthipeptides.** Red highlighted Trp and Pro are chlorinated to chlorotryptophan and hydroxylated to dihydroxyproline, respectively. Gold highlighted letters in microbisporicin indicate amino acids involved in AviCys formation. **E) Pep5-like lanthipeptides.** Grey highlighted Ser/Thr indicate residues that undergo hydration-deamination. **F) Paenibacillin-like lanthipeptides.** Grey highlighted letters represent Ala/Thr that undergo acetylation and hydration-deamination, respectively. **G) Streptin-like lanthipeptides.** Red lines indicate alternative ring C for streptin with dashed lines indicating possible bridging patterns. **H) Pinensin-like lanthipeptides.** Grey highlighted letters represent Ser that undergoes spontaneous hydration-deamination.

Figure S2

A

LactocinS -----MKTEKK-----VLDELSL-----H-ASA-----KMGARD-----VESSMNAD
 BovicinHJ50 MMN-----AT-EN-----QIFVE-----TVSDQE-----LEMLI GG
 Mersacidin MSQEAI IRSWK- DPFSRENS TQNP-- A-----GN- PFS-----ELKEAQ-----MDKLV GAGDMEAA
 Lacticin3147 MKE-----KN-MK-----KMDTIELQLGKYLEDDMI ELA EGDESHGG
 Lacticin481 -----MK-EQN-----S-----FN-LLQ-----EVTESE-----LDLIL GA
 CytolysinCLL -----ME-N-----LSV-----VP-SFE-----ELSVEE-----MEAIQ GS
 CytolysinCLs MLN-----KE-NQE-- NYYSNKLELV-----GP-SFE-----ELSLEE-----MEAIQ GS
 Cinnamycin MTASILQQSVV- DADFRAAL LENP--AAF GASAAALPT- PVE-----AQDQAS-----LD FWT KDIAATEAFA

B

Lacticin481 -KGGSGVIHTI SHECNMNSWQFVFTCCS⁴²
 MutacinII NRWWQGVVPTVSYECRMNSWQHVFVTC-⁴³
 NukacinISK-1 -KKKSGVIPTVSHDCHMNSFQFVFTCCS⁴⁴
 StreptococcinA-FF22 --GKNGVFKTISHECHLNTWAFLATCCS⁴⁵
 Macedocin --GKNGVFKTISHECHLNTWAFLATCCS⁴⁶
 ButyrivibriocinOR79 ---GNGVIKTI SHECHMNTWQFIFVTCSS^{**47}
 Salivaricin9 ---GNGVVLTLTHECNLATWTKKLKCC-⁴⁸
 SalivaricinB ---GGGVIQTI SHECRMNSWQFLFTCCS^{*49}
 SalivaricinG32 ---GNGVFKTISHECHLNTWAFLATCCS^{*50}
 Variacin ---GSGVIPTI SHECHMNSFQFVFTCCS^{*51}
 RuminococcinA ---GNGVLKTI SHECNMNTWQFLFTCC-⁵²
 SalivaricinA -KRGS GWIATITDDC- PNS---VFVCC-^{*53}
 SalivaricinA1 -KKGS GWFATITDDC- PNS---VFVCC-^{*54}
 SalivaricinA2 -KRGT GWFATITDDC- PNS---VFVCC-⁵⁵
 SalivaricinA3 -KKGPGWIATITDDC- PNS---IFVCC-^{*54}
 SalivaricinA5 -KRGPGWIATITDDC- PNS---VFVCC-^{*54}

C

Mersacidin -----CTFTLPGGGGV-----CTLTSEC-----IC-----56
 Actagardine -----SSGWV-----CTLTIEC-----GTV-----ICAC-----*57
 Nai-802 -----ASSGWV-----CTLTIEC-----GTV-----ICACR-----*58
 Michiganin -----SSSGWL-----CTLTIEC-----GTI-----ICACR-----59
 Amylolysin -----AEQRGISQGNDGKL-----CTLTWEC-----GLCPHTHCWC-----60
 PlantaricinC -----KKTKKNSSGDI-----CTLTSEC-----DHLATWVC-----C-----61
 Pseudomycoicidin -----GDCGGT-----CTWTKDCSICCPSSWSSWSSC-----62

Haloduracinα -----C-----AWYNI SCRLGNKGGAYCTLTVECMPS CN-----63
 PlantaricinWα -----KCKWWNI-----SCDLGNNGHVCTLSHECQVSCN-----64
 EnterocinWα -----KCPWWNL-----SCHLGNDGKI CTYSHECTAGCNA-----65
 Amyloliquecidinα -----C-----AWYDISCKLGNKGAWCTLTVE CQSSCN-----**66
 Lichenicidinα -----TITLSTC-----AILS SKPLGNNGYLCTVTKECMPS CN-----67
 Lacticin3147Aα -----CSTNTFSLSDYWGNGAWCTLTHECMAWCK-----68
 StaphylococcinC55α -----CSTNTFSLSDYWGNGKNWCTATHECMSWCK-----**69
 FlvAα.a GWKQTI VCTIAQGT VGC LVS YGLGNGGYCCTYTVTECSKTCNK-----70
 BhtAα -----IGTTVVNSTFSIVLGNKGYICTVTVCEMRNCQ-----***71
 SmbAα -----IGTTVVNSTFSIVLGNKGYICTVTVCEMRNC SK-----***72
 ThusinAα -----INTWNTTATSTSIIS ETFGNKGVCTYTVCEVNNCRG-----73

Roseocinα -----GSGVLGTLGCCSCLPWYSGWTVCGLACNPGKPCKN-----74
 Bicerucinα -----QRATPATPATPWLIKAS YVVS GAGVS FVAS YITVN-----75

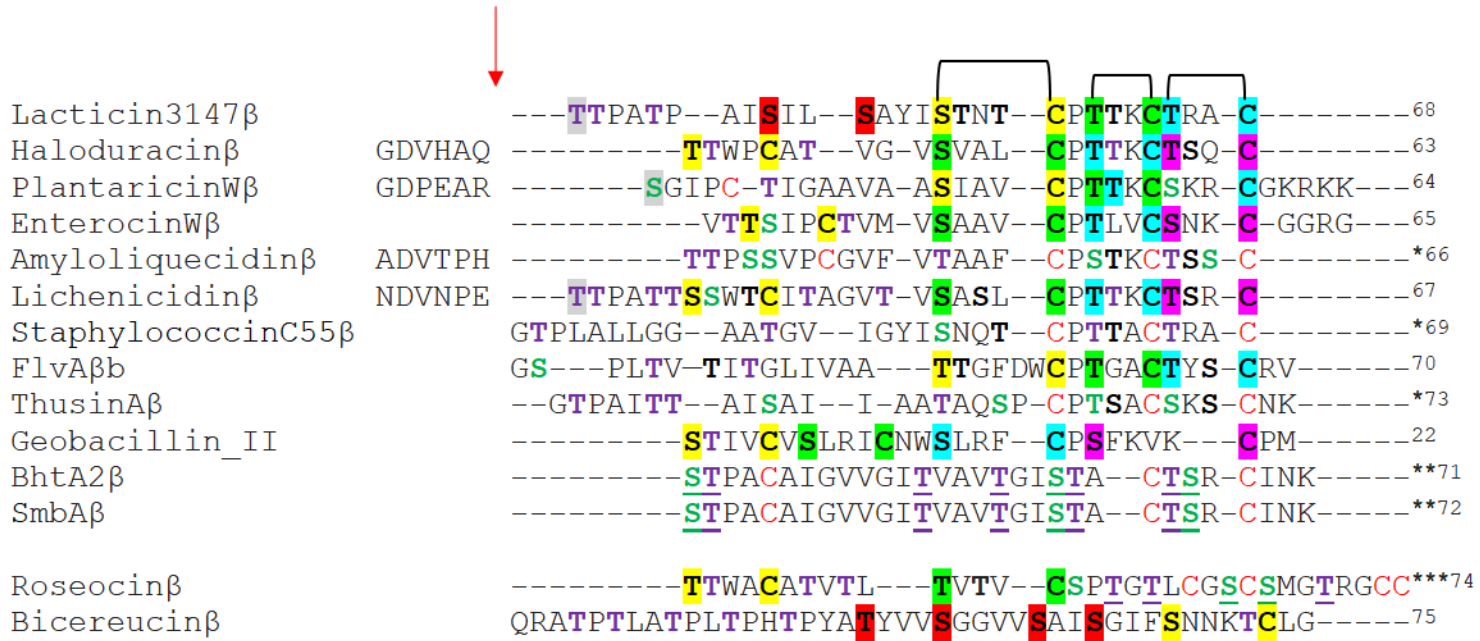
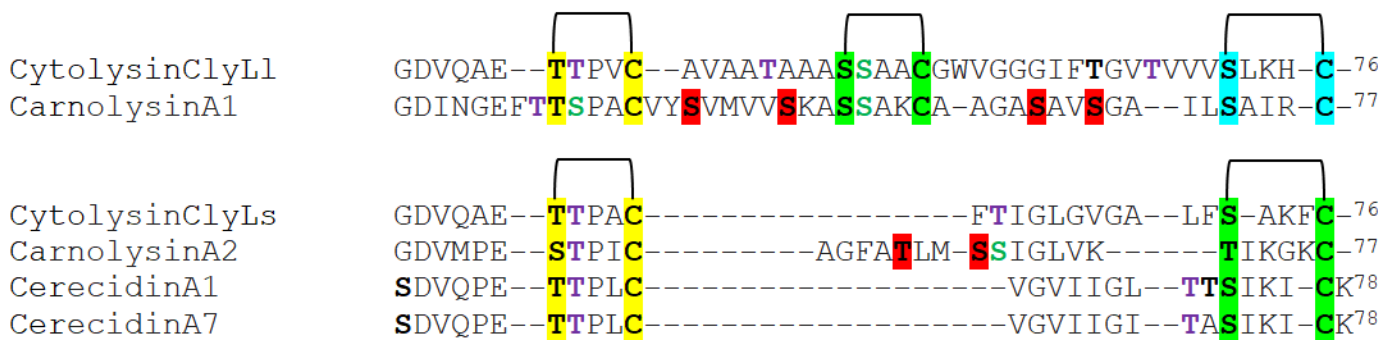
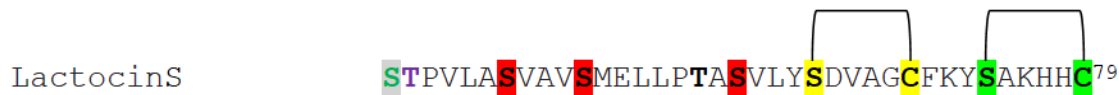
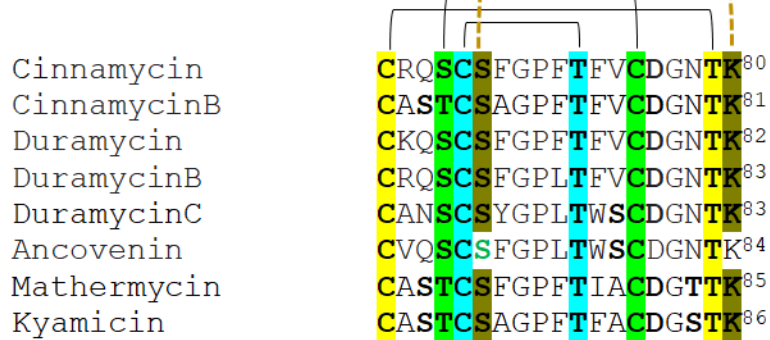
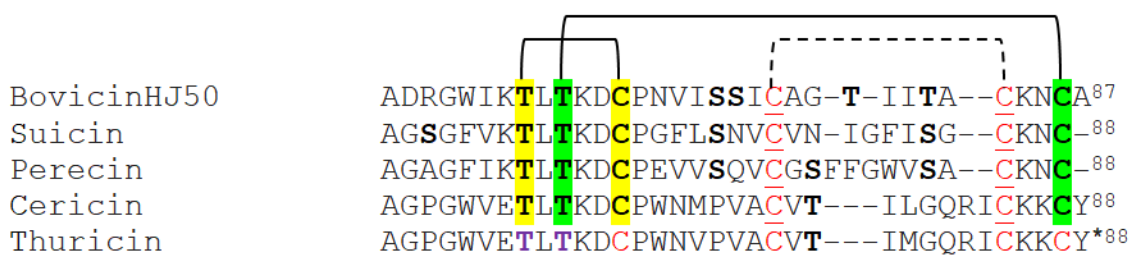
D**E****F****G****H**

Figure S2: Class II lanthipeptides. Where possible structural information is given and lines above letters indicate ring topology of prototypical lanthipeptide. Unless otherwise stated; Letters highlighted in corresponding colours indicates residues that participate in Lan/Melan formation. Bold letters in purple and green designate Thr/Ser that are dehydrated, respectively. Bold black letters indicate Thr/Ser that escapes dehydration. **A) Leader peptides of prototypical class II lanthipeptides.** Bold letters indicate site of leader cleavage. Residues predicted to be involved in helical or coiled structures are underlined and italicized, respectively. Structure prediction performed using PEP2D (<http://crdd.osdd.net/raghava/pep2d/index.html>). **B) Lacticin 481-like lanthipeptides.** Grey highlighted Gly is conserved throughout group. * Position of dehydrated Ser/Thr residues predicted based on mass of modified peptide and sequence similarity. ** No accurate mass data reported, dehydratable residues coloured and underlined. **C) Mersacidin-like lanthipeptides.** Lines above letters indicates the ring topology of mersacidin (blue line indicates AviMeCys) and haloduracin- α , respectively. Dashed line indicates a disulphide bridge in haloduracin- α , with underlined Cys residues taking part in disulphide bridge formation. Grey highlighted residues are conserved throughout group. Red highlighted Ser are converted to D -Ala. * Blue highlighted letters form methylanthionine sulfoxide. ** Position of dehydrated Ser/Thr residues predicted based on mass of modified peptide and sequence similarity. *** Exact position of dehydrated residues unknown, dehydratable residues coloured and underlined. **D) LtnA2-like lanthipeptides.** Grey highlighted Thr are converted to 2-oxobutyl. Red highlighted Ser/Thr are converted to D -Ala/ D -Abu, respectively. Red arrow indicates site of second proteolytic cleavage. * Position of dehydrated Ser/Thr residues predicted based on mass of modified peptide and sequence similarity. ** Exact position of dehydrated residues unknown, dehydratable residues coloured and underlined. *** Dehydration status of underlined letters unknown (six out of nine dehydrated Ser/Thr known). **E) Cytolysin-like lanthipeptides.** Lines above letters indicate the ring topology of cytolysin C_L and cytolysin C_S , respectively. Red highlighted Ser and Thr are converted to D -Ala and D -Abu, respectively. **F) Lactocin-like lanthipeptides.** Red highlighted Ser are converted to D -Ala. Grey highlighted letter represents Ser that undergoes hydration-deamination. **G) Cinnamycin-like lanthipeptides.** Bold black letters indicate Ser/Thr that escapes dehydration and Asp that undergoes hydroxylation, respectively. Dashed gold line and highlighted letters indicates lysinoalanine bridge and residues involved. **H) Bovicin HJ50-like lanthipeptides.** Dashed line indicates a disulphide bridge with underlined Cys residues taking part in disulphide bridge formation. * Position of dehydrated Ser/Thr residues predicted based on mass of modified peptide and sequence similarity.

Figure S3

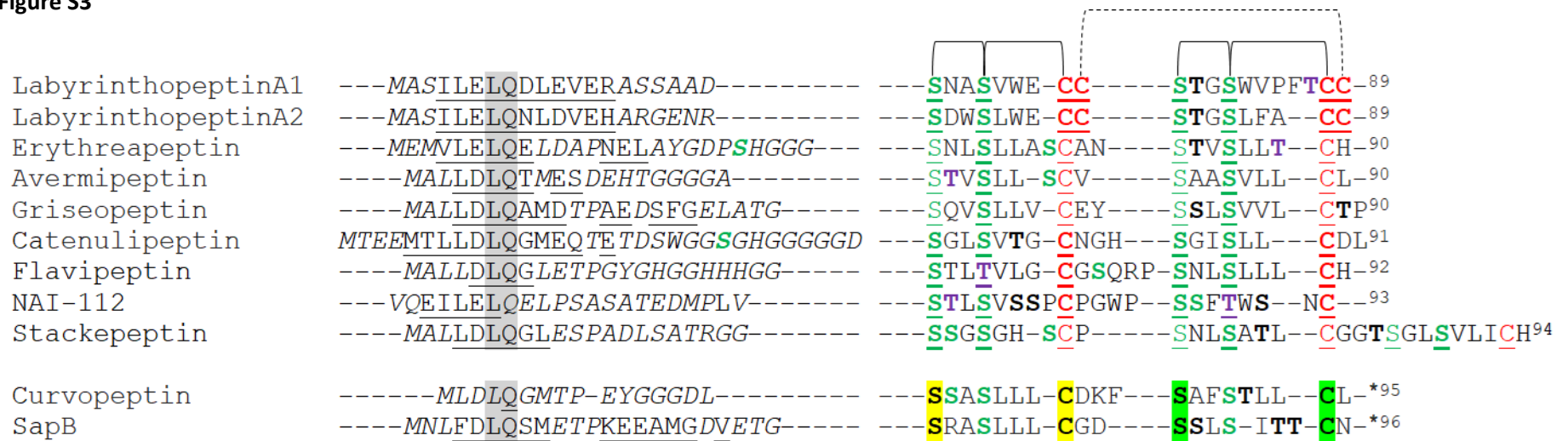


Figure S3: Labyrinthopeptin-like lanthipeptides (Class III). Precursor sequences are illustrated due to conflicting results regarding leader peptide processing. Residues predicted to be involved in helical or coiled structures are underlined and italicized, respectively. Structure prediction performed using PEP2D (<http://crdd.osdd.net/raghava/pep2d/index.html>). Lines above letters indicate the ring topology of labyrinthopeptinA1 (labionin rings) and dashed line indicates a disulphide bridge. Amino acids involved in lanthionine/labionin formation are indicated Cys residues are indicated in red. Purple and green letters indicate dehydrated Thr and Ser, respectively. Bold and underlined letters indicate residues that take part in labionin formation (Ser/Thr must be dehydrated). Letters underlined and not in bold indicate residues that can be involved in lanthionine or labionin formation. Bold black letters indicate Thr that escape dehydration. * Labionin residues only present in trace amounts, residues involved in Lan formation are highlighted in corresponding colours.

Figure S4

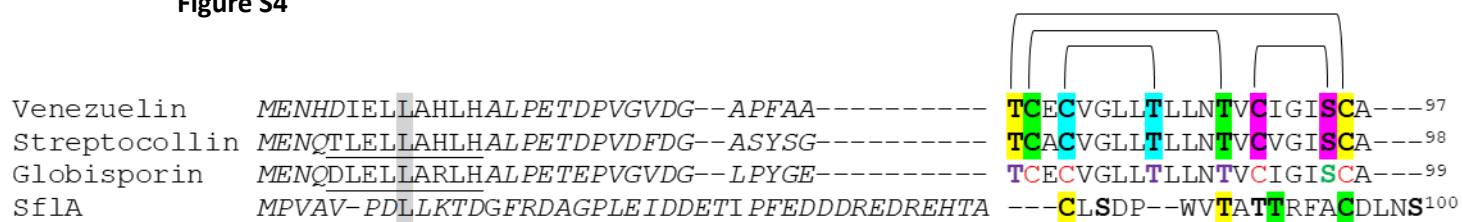


Figure S4: Venezuelin-like lanthipeptides (Class IV). Precursor sequences are illustrated due to conflicting results regarding leader peptide processing. Residues predicted to be involved in helical or coiled structures are underlined and italicized, respectively. Structure prediction performed using PEP2D (<http://crdd.osdd.net/raghava/pep2d/index.html>). Lines above letters indicates ring topology for venezuelin. Highlight letters indicate residue that participate in Lan/MeLan formation. Bold purple and green Thr/Ser are dehydrated and bold black Thr/Ser escapes dehydration.

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