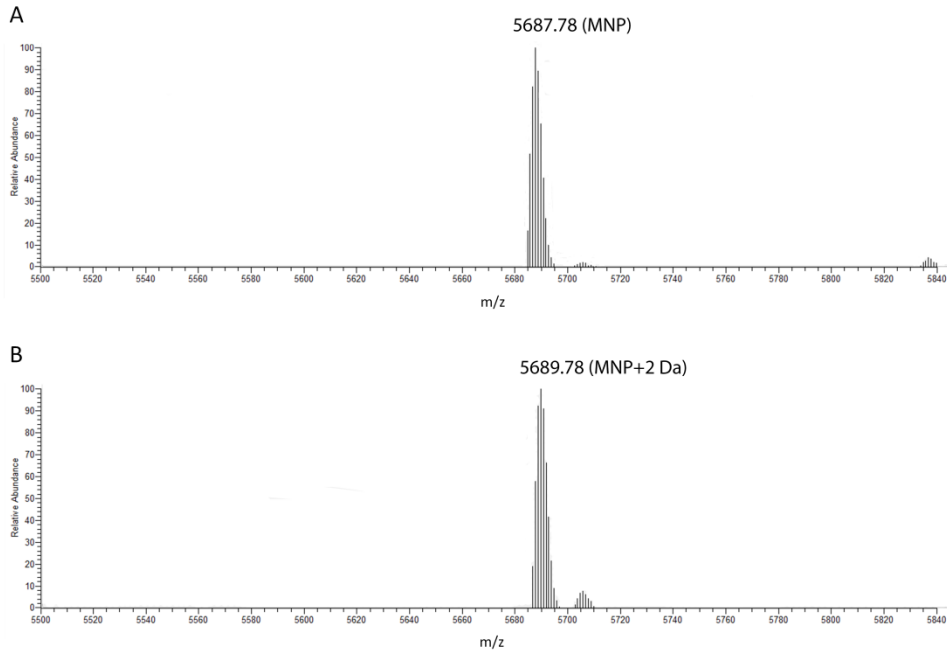


# Supplementary Information

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3

4 Figure S1

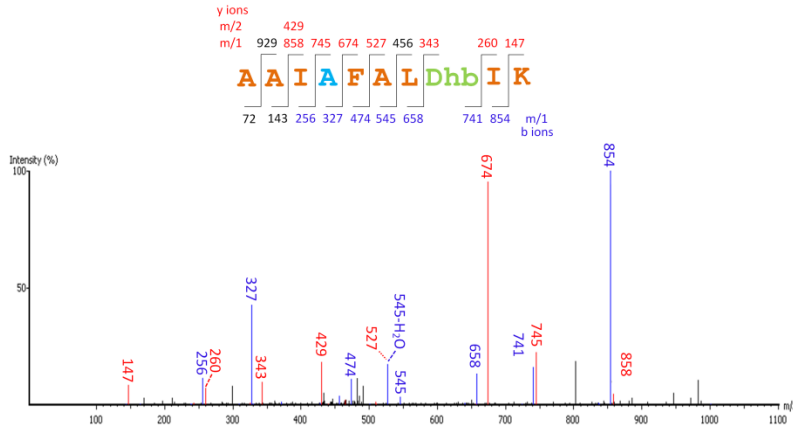
5 MS spectrum of peptide purified from NZ9000(pIL3EryBTC; pNZ-nisA-T-ltnJ) showing that

6 part of the peptide was modified by LtnJ. A, mature nisin precursor(MNP); B, mature nisin

7 precursor modified by LtnJ.

8

9

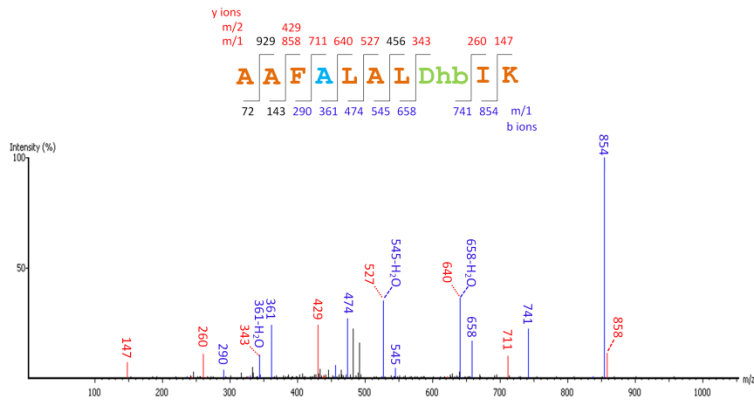


10

11 Figure S2

12 MS/MS spectrum and amino acid sequence of the C-terminus of L27F released after tryptic  
 13 digestion containing D-alanine. Expected masses for y and b ions are listed above and below the  
 14 peptide sequence respectively. Ions that were positively identified in the MS/MS spectrum are  
 15 highlighted in blue (b ions) or red (y ions). D-alanine converted from serine is colored in blue;  
 16 Dehydrated residues are labelled in green.

17



18

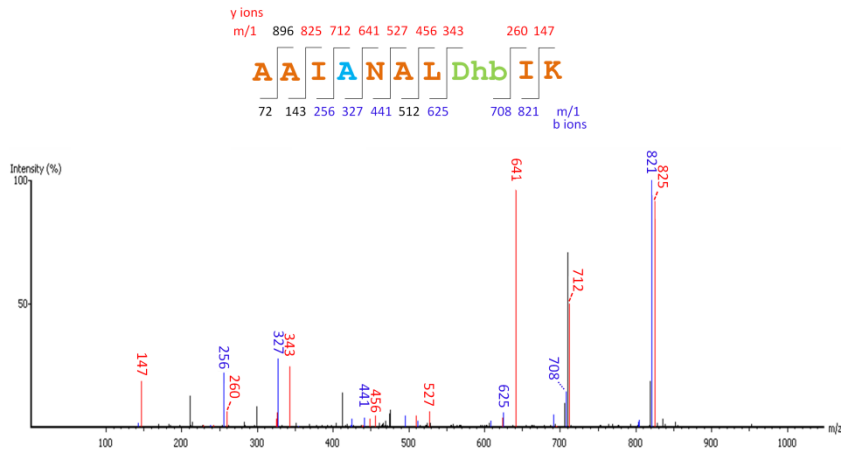
19 Figure S3

20 MS/MS spectrum and amino acid sequence of the C-terminus of I25F released after tryptic  
 21 digestion containing D-alanine. Expected masses for y and b ions are listed above and below the  
 22 peptide sequence respectively. Ions that were positively identified in the MS/MS spectrum are  
 23 highlighted in blue (b ions) or red (y ions). D-alanine converted from serine is colored in blue;  
 24 Dehydrated residues are labelled in green.

25

26

27



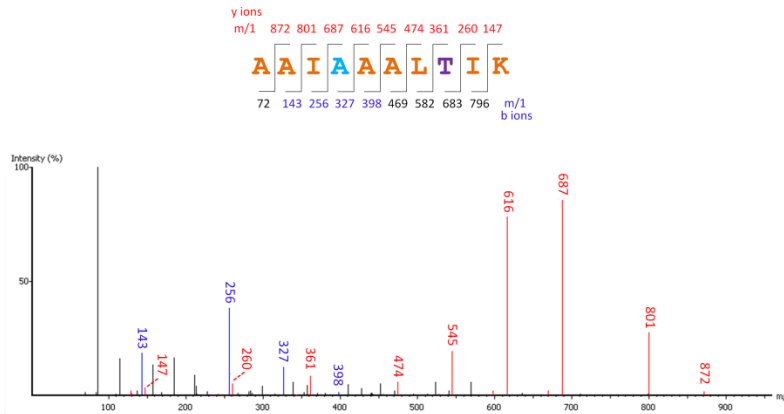
28

29 Figure S4

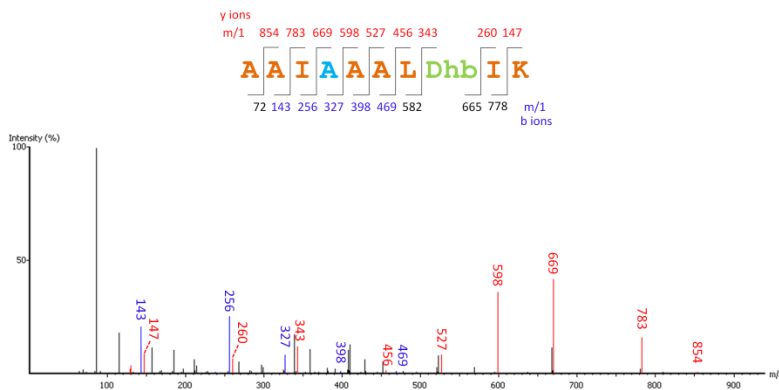
30 MS/MS spectrum and amino acid sequence of the C-terminus of L27N released after tryptic  
 31 digestion containing D-alanine. Expected masses for y and b ions are listed above and below the  
 32 peptide sequence respectively. Ions that were positively identified in the MS/MS spectrum are  
 33 highlighted in blue (b ions) or red (y ions). D-alanine converted from serine is colored in blue;  
 34 Dehydrated residues are labelled in green.

35

A



B

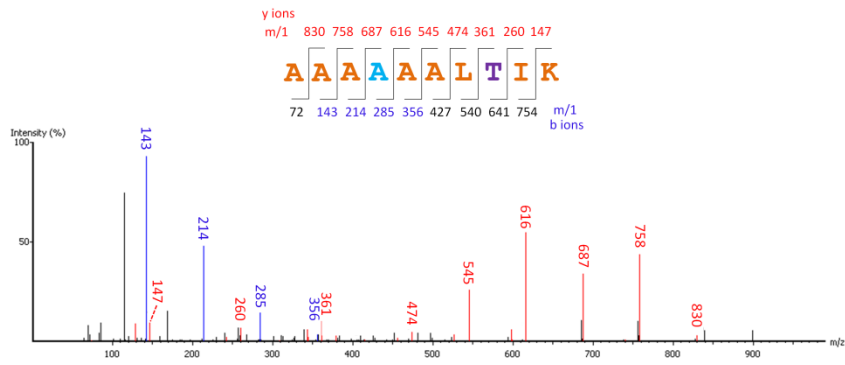


36

37 Figure S5

38 MS/MS spectrum and amino acid sequence of the C-terminus of L27A released after tryptic  
 39 digestion containing D-alanine. Expected masses for y and b ions are listed above and below the  
 40 peptide sequence respectively. Ions that were positively identified in the MS/MS spectrum are  
 41 highlighted in blue (b ions) or red (y ions). D-alanine converted from serine is colored in blue;  
 42 Threonine and dehydrated threonine are labelled in purple and green respectively. A, Partly  
 43 dehydrated peptide; B, Fully dehydrated peptide.

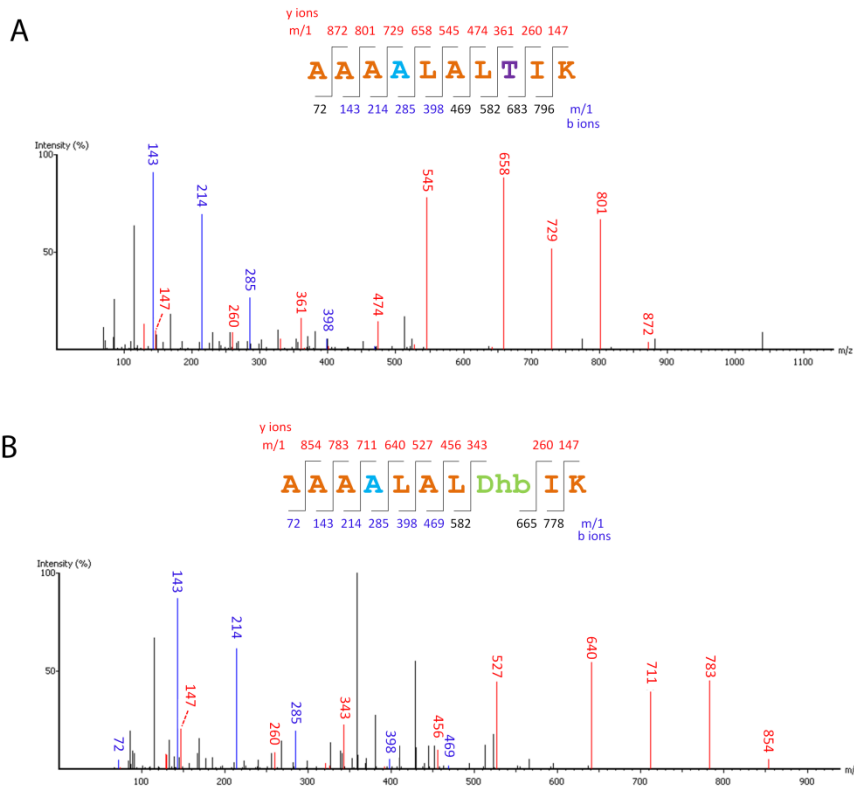
44



45

46 Figure S6

47 MS/MS spectrum and amino acid sequence of the C-terminus of I25A-L27A released after  
 48 tryptic digestion containing D-alanine. Expected masses for y and b ions are listed above and  
 49 below the peptide sequence respectively. Ions that were positively identified in the MS/MS  
 50 spectrum are highlighted in blue (b ions) or red (y ions). D-alanine converted from serine is  
 51 colored in blue; Threonine is labelled in purple.

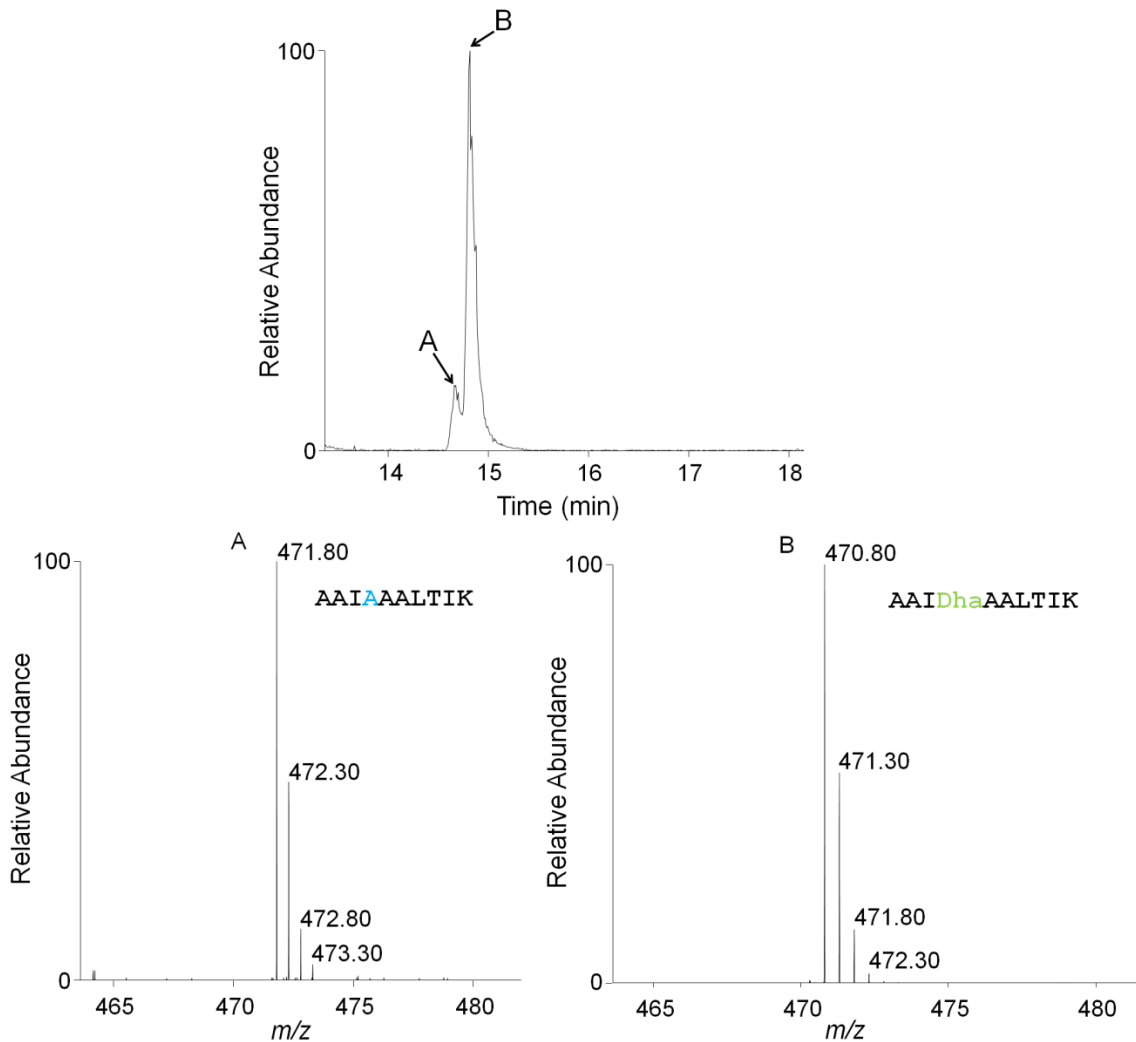


52

53 Figure S7

54 MS/MS spectrum and amino acid sequence of the C-terminus of I25A released after tryptic  
 55 digestion containing D-alanine. Expected masses for y and b ions are listed above and below the  
 56 peptide sequence respectively. Ions that were positively identified in the MS/MS spectrum are  
 57 highlighted in blue (b ions) or red (y ions). D-alanine converted from serine is colored in blue;  
 58 Threonine and dehydrated threonine are labelled in purple and green respectively. A, Partly  
 59 dehydrated peptide; B, Fully dehydrated peptide.

60



61

62 Figure S8. Comparison of the LC-MS profile of L27A tail (AAIS<sup>26</sup>AALT<sup>30</sup>IK) expressed  
 63 with/without LtnJ when threonine30 was not dehydrated. The M/H<sup>2+</sup> data showed 2 mass units  
 64 difference between fragments of the peaks. By dividing the arbitrary area of peak of modified tail  
 65 by the summed arbitrary area of two peaks representing either the modified or non-modified, the  
 66 conversion rate of LtnJ, in this case, was calculated to be 13% (see also figure 4).

67