Supporting Information

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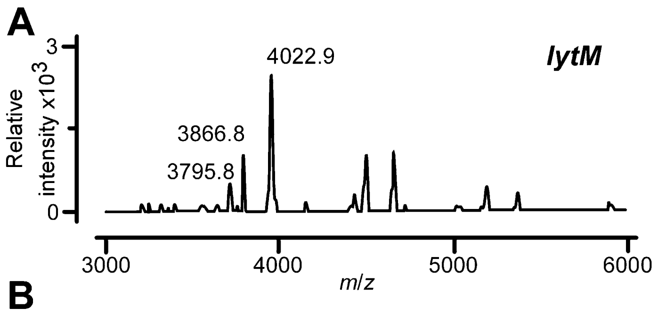

B

m/z	MW	Δ	Predicted structure
3795.8	3795.2	0.63	NH_2-Ala-iGln-(R-Gly$_5$)Lys-Ala
3866.8	3866.3	0.55	NH_2-Ala-iGln-(R-Gly$_5$)Lys-Ala-Ala
4022.9	4022.4	0.50	NH_2-Ala-iGln-(R-Gly$_5$)Lys-Ala-Gly$_4$

Fig. S1. Structure of protein A released by *lytM* mutant *Staphylococcus aureus*. (*A*) MALDI-TOF MS of C-terminal staphylococcal protein A (SpA) peptides released from the *S. aureus lytM* mutant. (*B*) Observed and predicted (MW) *m/z* ratios and their differentials (Δ) for SpA peptides released by the *S. aureus sle1* and *lytN* mutants with their predicted structures.

Table S1. Edman degradation of protein A released from *S. aureus* envelope

Cycle	Amino acid released	Predicted residue	Amino acid abundance (pmol)
1	A	A/A	39.82
2	Q	Q	9.85
3	Q	H	8.09
4	D	D	3.83
5	E	E	5.23
6	A	A	1.37
7	Q	Q	0.81
8	Q	Q	1.99

Table S2. Edman degradation of C-terminal peptide derived by cyanogen bromide cleavage of released protein A

Cycle	Amino acid released	Predicted residue	Amino acid abundance (pmol)
1	A/I	A/I	27.35/10.29
2	K	K	7.54
3	P	P	6.53
4	G	G	7.38
5	Q	Q	7.36
6	E	E	6.09
7	L	L	5.71
8	V	V	5.02
9	V	V	7.57
10	D	D	5.24