Supplementary Material

Supplementary Table S1 SpaA tryptic-peptide fragments generated by ESI Triple TOF mass analysis, and identified using the Mascot search engine.

A. Primary structure identity of SpaA tryptic-peptide fragments[a]

MKKTIAKKVL TLTSTILMTL LMVLGFNGTR VQADTNDTTT QNVVLTKYGF **50**

DKDVTAIDRA TDQIWTGDGA KPLQGVDFTI YNVTANYWAS PK**DYKGSFDS** **100**

APVAATGTTN DKGQLTQALP IQSKDASGKT RAAVYLFHET NPR**AGYNTSA** **150**

DFWLTLPAKA AADGNVYVYP KNVQKTTYER TFVKKDAETK EVLEGAGFK**I** **200**

SNSDGKFLKL TDKDGQSVSI GEGFIDVLAN NYRLTWVAES DATVFTSDKS **250**

GKFGLNGFAD NTTTYTAVET NVPDGYDAAA NTDFKADNSS SDILDAPSGI **300**

LPHTGGTGTV IFAILGVALI AFGAVAYRKR RNGF **334**

B. Mascot search analysis of SpaA tryptic-peptide fragments

Start-End[b]	MW_{obs}[c]	MW_{pred}[d]	Miss[e]	Sequence[f]
93 – 112	2044.77	2044.92	1	K.DYKGSFDSAPVAATGTTNDK.G
96 – 124	2903.72	2903.45	1	K.GSFDSAPVAATGTTNDKGQLTQALPIQSK.D
144 – 159	1754.76	1754.85	0	R.AGYNTSADFWLTLPAK.A
200 - 209	1107.69	1107.59	1	K.ISNSDGKFLK.L
210 – 233	2611.30	2611.28	1	K.LTDKDGQSVSIGEGFIDVLANNYR.L

[a] Matched amino acids for SpaA protein in tryptic-peptide fragments generated by ESI Triple TOF mass analysis are shown in red bold-face type.

[b] Residue number of first and last amino acid in each tryptic-peptide fragment.

[c] MW of tryptic-peptide fragments as identified by ESI Triple TOF MS analysis.

[d] Predicted MW of tryptic-peptide fragments.

[e] Missed number of trypsin cleavage sites.

[f] Actual trypsin cleavage site (**.**) in peptide fragment sequences.