Fig. S1

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                  10        20        30        40        50        60        70
S. caviae         MITLFLSPSCTSCRKARAWLNKHDVAFREHNIITSPLSRDDLLKILSYTENGTEDIISTRSKVFQKLDID
S. devriesei      MITLFLSPSCTSCRKARAWLNKHDVAFREHNIITSPLSRDDLLKILSYTENGTEDIISTRSKVFQKLDID
S. mutans         MVTLFLSPSCTSCRKARAWLNRHDVVFQEHNIMTSPLSRDELLKILSYTENGTEDIISTRSKVFQKLDID
S. orisasini      MITLFLSPSCTSCRKARAWLNKHDVAFKEHNIITSPLSRDDLLKILSYTENGTEDIISTRSKVFQKLDID
S. troglodytae    MVTLFLSPSCTSCRKARAWLNRHDVVFQEHNIMTSPLSRDELLKILSYTENGTEDIISTRSKVFQKLDID
S. ratti          MVTLFLSPSCTSCRKARAWLNKHDVAFREHNIITSPLNRDDLLKILSYTENGTEDIISTRSKVFQKLDID
S. agalactiae     MITLFLSPSCTSCRKARAWLSKHEVAFEEHNIITSPLNKEELLQILSFTENGTEDIISTRSKVFQKLAID
                  MITLFLSPSCTSCRKARAWLNKHDVAF.EHNIITSPLSRDDLLKILSYTENGTEDIISTRSKVFQKLDID

                  80        90        100       110       120       130
S. caviae         VDELSVSELINLISKNPSLLRRPIIMDDKRMQIGFNEDEIRAFLPRDYRKQELRQATIKAETEEEDE
S. devriesei      VDELSVSELINLISKNPSLLRRPIIMDDKRMQIGFNEDEIRAFLPRDYRKQELRQATIKAETEEEDD
S. mutans         VDELSVSELINLISKNPSLLRRPIIMDNKRMQIGFNEDEIRAFLPRDYRKQELRQATIRAEVEGEDD
S. orisasini      VDELSVSELINLISKNPSLLRRPIIMDDKRMQIGFNEDEIRAFLPRDYRKQELRQATIKAEIEGRNE
S. troglodytae    VDELSVSELINLISKNPGLLRRPIIMDDKRMQIGFNEDEIRAFLPRDYRKQELRQATIRAEVEGEDD
S. ratti          VDELSVSELINLISKNPSLLRRPIIMDDKRMQIGFNEDEIRAFLPRDYRKQELRQATIKAETEEEDE
S. agalactiae     VDELSTSSLMELISENPSLLRRPIILDKKRMQIGFNEDEIRAFLPRDYRKQELKQATIRAEIEGKHD
                  VDELSVSELINLISKNPSLLRRPIIMDDKRMQIGFNEDEIRAFLPRDYRKQELRQATIKAE.EGEDD
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Figure S1. ClustalW alignment of streptococcal SpxA1 proteins containing multiple acidic residues at the C-terminal tail. Location of the CXXC motif and conserved glycine 52 residue typical of bona fide Spx proteins are indicated inside black boxes. Acidic residues within the last 10 amino acids are shown inside red boxes.