

Supplementary Table S2

Table S2. Amino acid sequence comparison of the putative VWF binding site from different pathogenic bacteria and commensals.

	Acc. No. (UniProtKB)	identities [protein] in %	peptide sequence of putative VWF-binding site
<i>S. pneumoniae</i> serotype 2 (D39)	Q04KG2 (ENO_STRP2)		¹⁸⁵ G A P T F K E A L R Y G A E I F H A L K K I L K S R G L E T A V G D E G G P ²²³
<i>S. pneumoniae</i> (R6)	Q8DPS0 (ENO_STRR6)	100
<i>S. aureus</i> (NCTC 8325)	Q2G028 (ENO_STAA8)	94	. . T S . . W . . T N . . S . . S K
<i>L. plantarum</i> (CRL 1506)	KRU20356.1	50	E R T S . R D G F E K I V N T Y . T . . . V I E D A . Y I . G L
<i>B. animalis</i> subsp. <i>lactis</i> (AD011)	B8DTI9 (ENO_BIFA0)	56	. F Q . Y S . . . Q A . V . V Y . T . . N V . . K Q . . A . G L
<i>E. coli</i> (K12)	P0A6P9 (ENO_ECOLI)	59	. . K . V . . . I . M . S . V . . H . A . V . . A K . M N Y