

A.

FlpA 135-224	RLEAVP-FVQAVTNLPNRIKLIWR-PHPDFRVDSYIIERTKGDDKEFKKIAEVKNRLNAE	58
FN3-1	SSGPVEVFITETPSQPNSHPIQWNAQPSH-ISKYILRWRPKNSVGRWKEATIPGHLN-S	58
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FlpA 135-224	YIDSDLKPNENSSYRIIAVSFNGIKSGSSQVVSS	92
FN3-1	YTIKGLKPGVVYEGQLISIQQYGHQ-----	83
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B.

Campylobacter species	Percent homology with FlpA (cj1279c)
Campylobacter jejuni subsp. jejuni CG8486	99.51%
Campylobacter jejuni subsp. jejuni CG8421	99.51%
Campylobacter jejuni subsp. jejuni 81116	99.02%
Campylobacter jejuni RM1221	98.29%
Campylobacter jejuni subsp. jejuni 260.94	99.26%
Campylobacter jejuni subsp. jejuni 81-176	98.29%
Campylobacter jejuni subsp. jejuni 84-25	99.50%
Campylobacter jejuni subsp. jejuni HB93-13	99.00%
Campylobacter jejuni subsp. jejuni CF93-6	99.75%
Campylobacter jejuni subsp. doylei 269.97	94.63%
Campylobacter coli RM2228	78.05%
Campylobacter upsaliensis RM3195	71.22%
Campylobacter lari RM2100	56.16%
Campylobacter fetus subsp. fetus 82-40	45.16%
Campylobacter hominis ATCC BAA-381	42.21%



C. jejuni	81116	LRSEPS-SKVKAAQ
C. jejuni	81-176	LRSEPS-SKVKAAQ
C. jejuni	11168	LRSEPS-SKVKAAQ
C. doylei	269.97	LRSKPS-SKVKAAQ
C. fetus	82-40	INSNESKQAIIVVAK
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**Figure S3.** FlpA is a highly conserved lipoprotein with three domains homologous to FNIII repeats of Fn.

A. ClustalW alignment of FlpA-D2 (aa135-224) and 1FNIII amino acid sequences. The amino acid sequence of FlpA-D2 (aa135-224) was compared to the sequences of the 15 type three repeat domains of Fn (1-15FNIII). FlpA-D2 was most similar with 1FNIII, sharing 22.9% sequence identity with 15.7% conserved substitutions and 21.7% semi-conserved substitutions.

B. Percent homology of FlpA amino acids amongst Campylobacter species calculated using Microbes Online (<http://www.microbesonline.org>).

C. ClustalW alignment of FlpA amino acid sequences from divergent members of the Campylobacter genus. The FlpA FBLM is highlighted in bold letters.