

A.

FlpA 135-224	RLEAVP-FVQAVTNLPNRIKLIWR-PHPDFRVD SYIIERTKGDDKEFKKIAEVKNRLNAE	58
FN3-1	SSGPVEVFITETPSQPNSHPIQWNAPQPSH-ISKYILRWRPKNSVGRWKEATIPGHLN-S	58
	. * * : ... ** : * . * : * .. : * : .. : * : .. : * * : .. : * * .	
FlpA 135-224	YIDSDLKPNENSSYRIIAVSFNGIKSGSSQVSS	92
FN3-1	YTIKGLKPGVVYEGQLISIQYGHQ-----	83
	* .. * * . . : * : .. * :	

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.

C. jejuni 81116 -MKRFRLGFYLSFLTLLSACSVSQMNSLASSKEPAVNESLPKVESLKSLSDMSNIAFEWEPELYNENIKGFYLYRSS-DE
C. jejuni 81-176 -MKRFRLGFYLSFLTLLSACSVSQMNSLASSKEPAVNESLPKVESLKSLSDMSNIAFEWESLYNENIKGFYLYRSS-DE
C. jejuni 11168 MMKRFRLSFYLSFLTLLSACSVSQMNSLASSKEPAVNESLPKVESLKSLSDMSNIAFEWEPELYNENIKGFYLYRSS-DE
C. doylei 269.97 -MKRFRLSFYLSFLTLLSACSVLQMNLSASSKELTVNESLPKVESLKSLSDMSNIAFEWESLYDENIKGFYLYRSS-DE
C. fetus 82-40 -----MSGCAY-----KVSQVNPNLPTINSLKTISDMTQIAFEWNPVNNDENIAGYYLYRSNPNE
:.: * ** .**.:****:****:*****: :*** *:****. :*

C. jejuni 81116 NPDKLVLGTTIKDKFQTHYVDTKLEPGTKYRYMMKSNEQGQISEDGVIEVSTAPRLEAVPFVQAVTNLPNRIKLI**WRPH**
C. jejuni 81-176 NPDKLVLGTTIKDKFQTHYVDTKLEPGTKYRYMMKSNEQGQISEDGVIEVSTAPRLEAVPFVQAVTNLPNRIKLI**WRPH**
C. jejuni 11168 NPDKLVLGTTIKDKFQTHYVDTKLEPGTKYRYMMKSNEQGQISEDGVIEVSTAPRLEAVPFVQAVTNLPNRIKLI**WRPH**
C. doylei 269.97 NPDKLVLGTTIKDKFQTHYVDTKLEPNTKYRYTMKSNEQGQISEDGVIEVSTAPRLEAVPFVQAVTNLPNRIKLI**WRPH**
C. fetus 82-40 DGKMSVVANIKDRFATHYVDTNLAPSTEYSYELRSYDNNNGDISNNGEITVSTSCLIESVSFAQAVYGLPNRIKIL**WRPH**
: .:.*.****: * *****: * .*: * * :*:****:****: ***: :*:*.*** .*****:****

C. jejuni 81116 **PDFRVDSYIIERTKGDDKEFKKIAEVKNRLNAEYIDSLLKPNENSSYRIIAVSFNGIKSEPSQVVSSTS**KALPPQVEHLS
C. jejuni 81-176 **PDFRVDSYIIERTKGDDKEFKKIAEVKNRLNAEYIDSLLKPNENSSYRIIAVSFNGIKSEPSQVVSSTS**KALPPQVEHLS
C. jejuni 11168 **PDFRVDSYIIERTKGDDKEFKKIAEVKNRLNAEYIDSLLKPNENSSYRIIAVSFNGIKSGSSQVVSSTS**KALPPQVEHLS
C. doylei 269.97 **PDFRVDSYIIERTKGDDKEFKKIAEVKNRLNAEYIDNDLKSNNENSSYRIIAVSFNGIKSEPSQVVSASKALPPQVEHLS**
C. fetus 82-40 **PDPRVASYIIERNNISSDKWYRIAEVKGRLNEYIDDGLDPNHHYRYRILVKTVDGITSGPSAIISAQTKALPNLVNLQ**
** * ****: . . : :****.***.****.. .: * : . : :**** * : :**** * : * :**** * : *

C. jejuni 81116 ASTDGSNKIILTWDADTYEDFSYYKVYSTSSSFLPFSVLAKTDKNSYEDIVEGAGSKYYKVTMVDKDGLESPMPKGVE
C. jejuni 81-176 ASTDGSNKIMLTWDADTYEDFSYYKVYSTSSSFLPFSVLAKTDKNSYEDIVEVGVKSKYYKVTMVDKDGLESPMPKGVE
C. jejuni 11168 ASTDGSSKIILTWDADTYEDFSYYKVYSTSSSFLPFSVLAKTDKNSYEDIVEGAGSKYYKVTMVDKDGLESPMPKGVE
C. doylei 269.97 ASTDGSNKIILTWDADTYEDFSYYKVYSTSLSFLPFSVLAKTDKNSYEDIVEGAGSKYYKVTMVDKDGLESPMPKGVE
C. fetus 82-40 ATTNLPKKITLTWEPNTNDDFSHYNIYRSSNEIFPLLKLTEETTSVQYDDLINENGAQMYKVTAVDKDGLESPQNNPVV
:..***.***: . * :****:***: * .:.*: * :.*: . .:.*: * . .:****.*****: : *

C. jejuni 81116 GKTGNPLAPSIILAOSTSEGINLEWSN-DTRAVEYEVRYYGGEQNAVFKGIKEKRLKDVKALPGVEYSYEVIAIDSAG
C. jejuni 81-176 GKTGNPLAPSIILAOSTSEGINLEWSN-DTRAVEYEVRYYGGEQNAVFKGIKEKRLKDVKALPGVEYSYEVIAIDSAG
C. jejuni 11168 GKTGNPLAPSIILAOSTSEGINLEWSN-DTRAVEYEVRYYGGEQNAVFKGIKEKRLKDVKALPGVEYSYEVIAIDSAG
C. doylei 269.97 GKTLSNPLAPSIILAOSTSEGINLEWSN-DTRAVEYEVRYYGGKQNAVFKGIKEKRLKDVKALPGVEYNYEVIAIDSVG
C. fetus 82-40 GNTLTSPKSPIITGASFNGISIELSWSSGSDNRSVKYKILKSSAAGEAAIEDIVGNSYNDDQIQFGLETYKIVGIDEYG
:..***.***: . * :****:***: * . .:.*: * . .:****.*****: : * : * :****.***: . * *

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
		:.*: * . : .*:

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.