

Figure S1

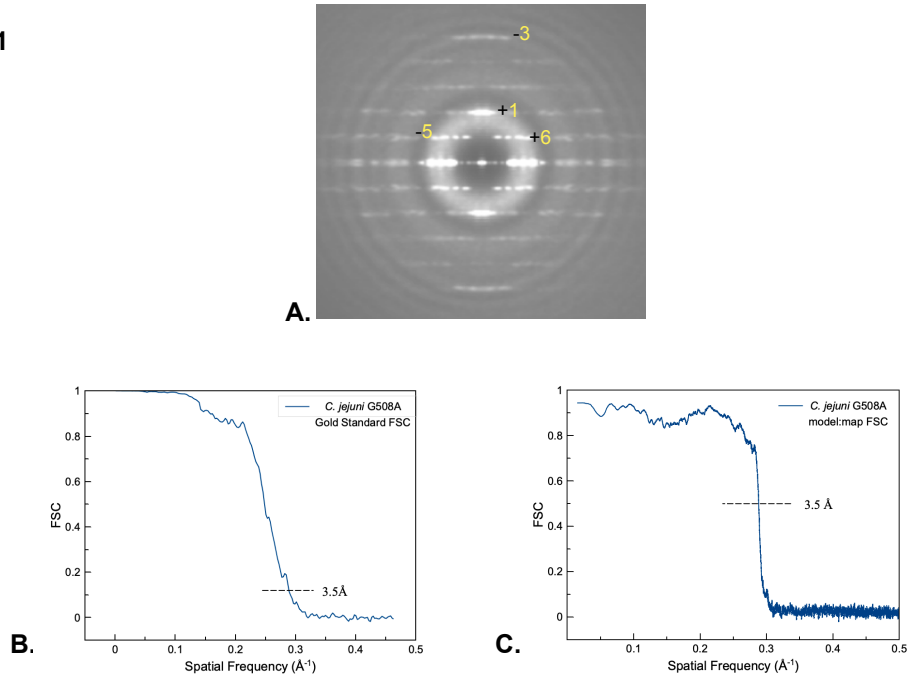


Figure S1. (A) The indexed power spectrum of the *C. jejuni* G508A flagellar filament. (B) FSC plot using the “gold-standard” map:map method. (C) FSC plot using the model:map method with a cutoff of 0.5.

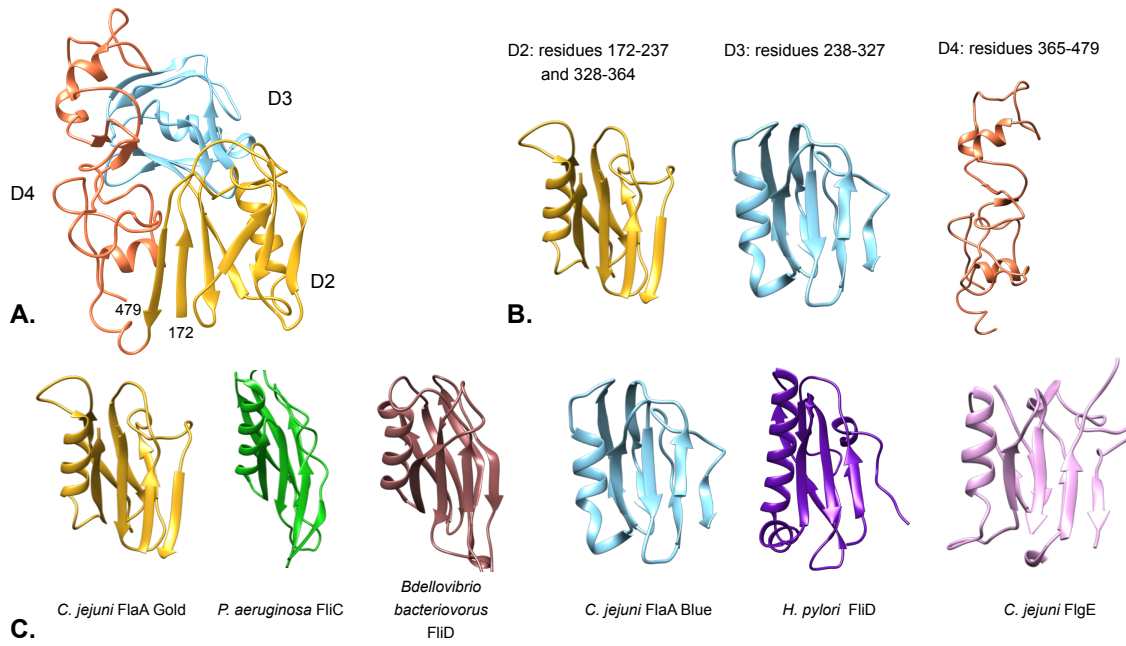


Figure S2

Figure S2. Domain duplication and structural homologs of the *C. jejuni* outer domain D2. (A) The outer domains D2 (gold), D3 (blue) and D4 (orange) of the *C. jejuni* flagellin). (B) The three outer domains shown separately. (C) Structural homology between the domain duplicated D2/D3 and domains from various flagella proteins.

<i>C. jejuni</i> FlaA D2 Homologues	<i>C. jejuni</i> FlaA D3 Homologues
<i>P. aeruginosa</i> FlIC: 4NX9 z=7.5	<i>H. pylori</i> FlID: 6IWY z=6.7
<i>E. coli</i> FlID: 5H5V z=7.3	<i>E. coli</i> FlID: 5H5V z=5.9
<i>B. bacteriovorus</i> FlID: 6KTY z=7.3	<i>P. aeruginosa</i> FlIC: 4NX9 z=5.4
<i>H. pylori</i> FlID: 6IWY z=6.0	<i>B. bacteriovorus</i> FlID: 6KTY z=5.4
<i>C. jejuni</i> FlgE: 5JXL z=5.0	<i>C. jejuni</i> FlgE: 5JXL z=5.1
<i>C. jejuni</i> FlgK: 5XBJ z=4.8	<i>C. jejuni</i> FlgK: 5XBJ z=4.1

Table S1

Table S1: Structural homologs of *C. jejuni* FlaA D2 and D3.

Amino Acid residue	
S343	1 MGFR I N T N V A A L N A K A N S D L N A K S L D A S L S R L S S G L R I N S A A D 43
S348	44 D A S G M A I A D S L R S Q A N T L G Q A I S N G N D A L G I L Q T A D K A M D E Q L 86
T394	87 K I L D T I K T K A T Q A A Q D G Q S L K T R T M L Q A D I N K L M E E L D N I A N T 129
S398	130 T S F N G K Q L L S G N F T N Q E F Q I G A S S N Q T V K A T I G A T Q S S K I G V T 172
S401	173 R F E T G A Q S F T S G V V G L T I K N Y N G I E D F K F D N V V I S T S V G T G L G 215
S405	216 A L A E E I N K S A D K T G V R A T Y D V K T T G V Y A I K E G T T S Q E F A I N G V 258
S412	259 T I G K I E Y K D G D G N G S L I S A I N A V K D T T G V Q A S K D E N G K L V L T S 301
S418	302 A D G R G I K I T G D I G V G S G I L A N Q K E N Y G R L S L V K N D G R D I N I S G 344
S426	345 T N L S A I G M G T T D M I S Q S S V S L R E S K G Q I S A T N A D A M G F N S Y K G 387
S430	388 G G K F V F T Q N V S S I S A F M S A Q G S G F S R G S G F S V G S G K N L S V G L S 430
S437	431 Q G I Q I I S S A A S M S N T Y V V S A G S G F S S G S G N S Q F A A L K T T A A N T 473
S441	474 T D E T A G V T T L K G A M A V M D I A E T A I T N L D Q I R A D I G S I Q N Q V T S 516
S443	517 T I N N I T V T Q V N V K A A E S Q I R D V D F A S E S A N Y S K A N I L A Q S G S Y 559
S449	560 A M A Q A N S S Q Q N V L R L L Q 576
S455 *	
S461 *	
T469	

A.

B.

Figure S3

Figure S3: Glycosylation sites detected in the *C. jejuni* FlaA Flagellin. (A) List of glycosylated residues seen in the *C. jejuni* FlaA density map. (B) FlaA sequence showing each of the observed glycosylated residues in red

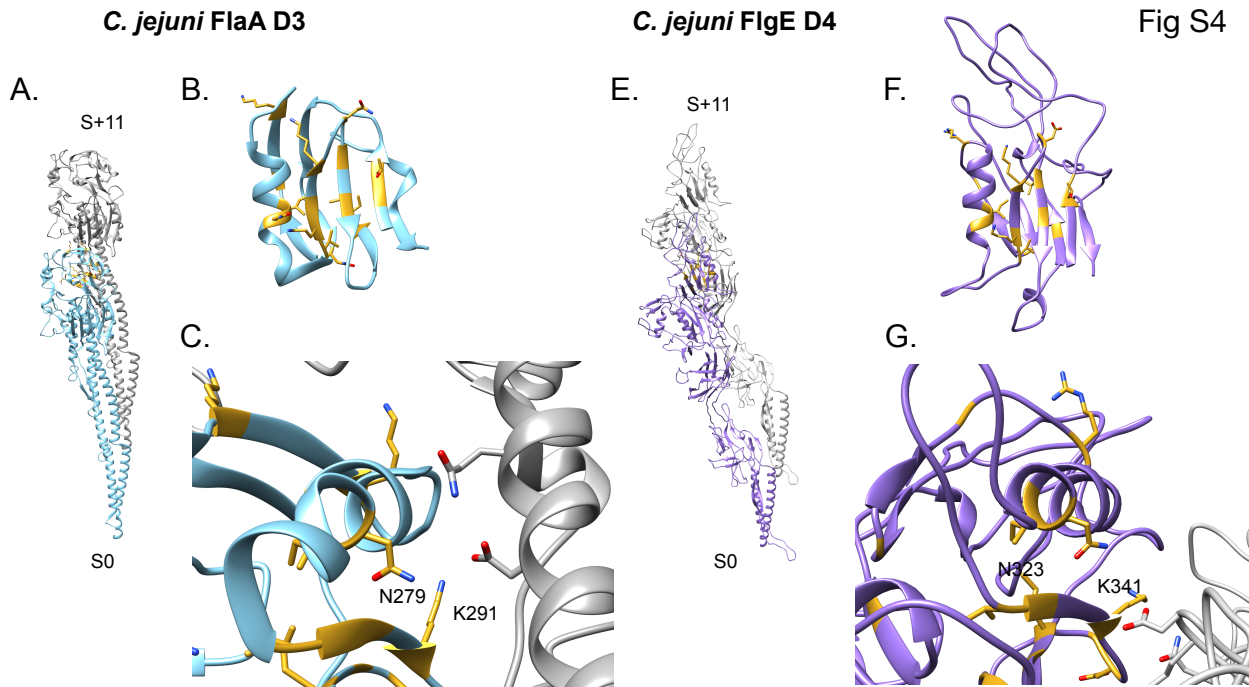


Figure S4: Comparison of *C. jejuni* FlaA D3 (A-C) and FlgE D4 (D-F) along their 11-start interfaces. (A) Two flagellins along the same protofilament are shown. (B) Residues that are conserved or similar in *C. jejuni* FlaA to *C. jejuni* FlgE are colored in gold. (C) A close up of the FlaA D3 11-start interface shows two key conserved residues (N279 and K291) between FlaA and FlgE. (D-F) As with A-C, two flagellar hook proteins along the same protofilament are shown. (E) Residues that are conserved or similar in *C. jejuni* FlgE to *C. jejuni* FlaA are colored in gold. (F) Two conserved residues along the 11-start interface in FlgE domain D4 are N323 and K341.

```

AA 59-60 AA 90-97
S. typhimurium_FliC/1-495 1 MGVINTRSLSELTQNNLNSSBSALGTAIERLSSGLRINSAKDDAKGQIANRFTANIKGELQASRNDGDISFADTIEGALNEINNNLGRVRELAVGSNST--NSQSDLSIQAEITQRLNEIBRVGCG 129
B. subtilis_Hag/1-304 1 --MRINHNIAALNTLNRELSNNSASQNMKELSSGLRINRAQDDAAGLASEKMRQIRGEMASKNSQDGLSIQTAEGALTEHAIQORVRELVQACNTGTODKATDLOSIQDEISALTEIDGINSR 129
C. jejuni_FliA/1-576 1 MGRFINTNVAALNAKANSDELNAKSLDASLSEKSSGLRINSAQDDASGMAIADSLRSQANTLGGQISNGNDALGILQADKAMDEQLKLDLTIKTKATQAAGDG--QSLKTRTMLQADINKLMELDNIAINT 129
H. pylori_FliA/1-510 1 MAFQVNTNINAMNAHVQSAUHQNALKTSLEKSSGLRINKAADDASGMTVADSLRSQASLGGQIANNDGMIQVADKAMDEQLKLDLTVKVKATQAAGDG--QTTESRKAIQSDIIVRLIQGLDNIGNT 129

S. typhimurium_FliC/1-495 130 TQFNGVKKVLAQDNLTIT-----RVCANDGETIDIDLKQINSQTLGLDLNVAQKQYKVS-DTAAIT--VTGYADTTIALDNSTF-KASATGLGGTDQKIDCG----- 220
B. subtilis_Hag/1-304 130 TEFNGKRLDQTYKVDATPANGKLVFQICANATQQLSNIIEBMDADLGIK----- 220
C. jejuni_FliA/1-576 130 TSFNGKQLLSQFNT-----DEFQIGASNSQTVKATIGATQSRIIGVTRFEETGAGSFSGVGLGTLINNGIIDE--RFBVWVISTSVGTGLGALKEEINKSADTGVKATVQVKTGYYAIKEGT 248
H. pylori_FliA/1-510 130 TTYNGALLSQFETN-----KEFQVGAYSNQSIIKASIGSTTSDKIQQVRIATGALITASGDISLTFKQVGVNDV--TLESVKVSSSAGTIGVLAIEINKNSRRTGVKAYASVITTSQVAVGSGS 248

S. typhimurium_FliC/1-495 221 -----LKFDDTTGKYFAKVT-VTGGTEKCYEYSVDKTNGEVTLA--CGATSPLTGC-----LPATATEDVKNVQVAN--ADLTEAKAALTAACVGTGA-SVVKH 310
183 ----- 310
B. subtilis_Hag/1-304 221 TSQEFAINCVTIGKI-EYKDDGNGSLISAINAVKDTTCVQASKD-----FNGKLVLSADGRGIIKITDITGV-----GSGILANQENYRSLVKNDRDINISGTLNSAIGMCTDMISSQSV 363
C. jejuni_FliA/1-576 249 L-SNLTLLNGIHLGNLADIKKNDSDGRLVAAINAVTSETGVAEAYTD-----QGRLLNLSIDGRGIEIKTDSVSNGPSALTMVNGQDLTKGSTNYGRSLTRLDAKSIINVVAS 363
H. pylori_FliA/1-510 357 ----- 356

S. typhimurium_FliC/1-495 311 SVYTONNGKT-----IDGLAVKVGDDYSAATONKQGS---ISINTTKYTADDGTSKALN--KLGADGKTEVVSII-GGTYAASK-----AEGHNFKAOPDLA-----E-AAAATT--ENPDAQI 412
184 -----ADESIAALHS-----NDLDVTFEA-----D-----NAA-----D-TADIGF--DRLQKVV 221
B. subtilis_Hag/1-304 364 SLRESKQGISATNADRMGFNSYKGGKKE-VITONVSSISAFMSADQSGESRSGSGFSGSGKNSLVGLSQCIISSAASMSNTFYVYAGSGFSSGSGNSQFPAALKTYAANTTDFAGVTLTKGMAVMDIR 493
C. jejuni_FliA/1-576 357 -----DSQHLGFTALICFGESQ-VAETT-----VNLRD-----VTGNFNA-----NVKSASGA-NYNA--VIASGNQSLDSGVTLLRGAMVVIDIA 427
H. pylori_FliA/1-510

S. typhimurium_FliC/1-495 413 DAALAQVDTLRSDLGAVQNRFNSAITNLNTVNNLTSARSRIEBSVYATEVSNMSRQILQAGTSVLAQANQPQNVLSLLR 412
B. subtilis_Hag/1-304 222 DEAINQVSSQRAKLGAVQNRLEHTINNLSSAGENLTAESRI RDVMAKEMS EFTKNNILSQASQAMLAQANQPQNVLQLLR 412
C. jejuni_FliA/1-576 494 ETAITNLDDI RADIGSIQNQVSTTINNITVTQVNVKAAESQIRVDVFAESANFNKNNILAQSGSYAMSQARTVQGNILRLLT 412
H. pylori_FliA/1-510 428 ESAMKMLDKVRSGLSDGVSQNGMISTVNNISITQVNVKAAESQIRVDVFAESANFNKNNILAQSGSYAMSQARTVQGNILRLLT 412

```

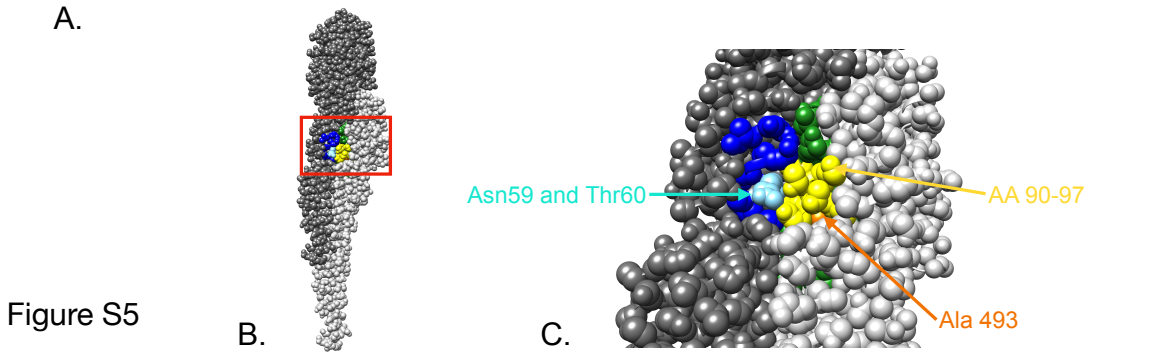


Figure S5: Sequence changes in the residues interfacing the TLR5 epitope previously suggested to allow for motility in *H. pylori* and *C. jejuni*. (A) Multiple sequence alignment of several key bacterial flagellins. (B) Space filling representation of two flagellins along the 11-start protofilament. The S0 flagellin is shown in light gray while the S+11 is in dark grey. (C) A close up of the interface site between the two flagellins confirming the previously reported predictions about the *H. pylori* and *C. jejuni* flagellins.

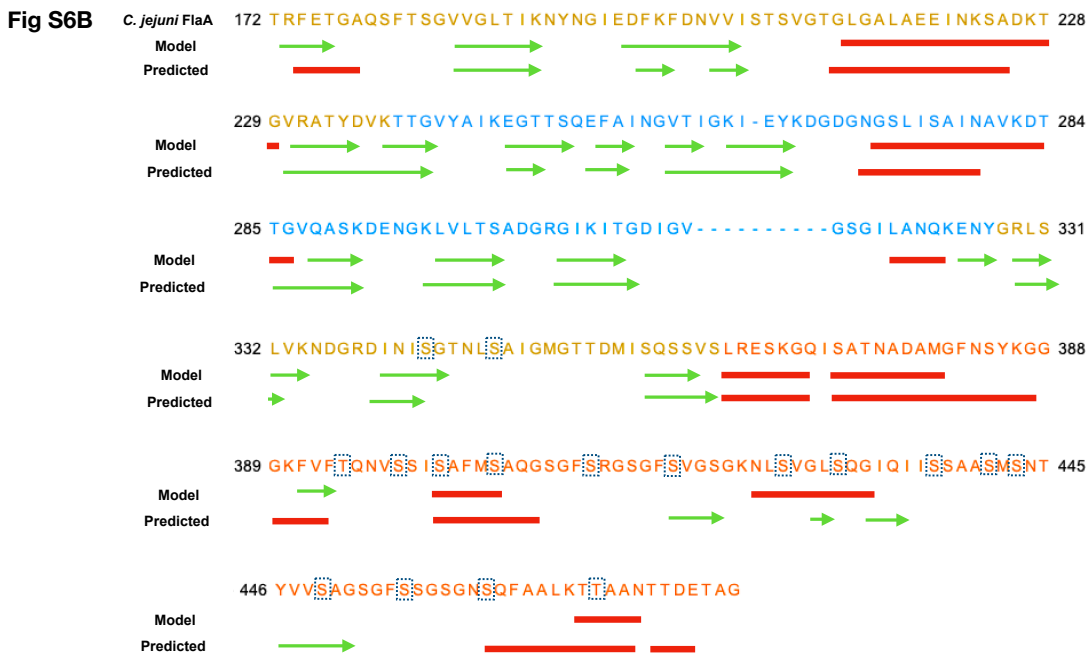
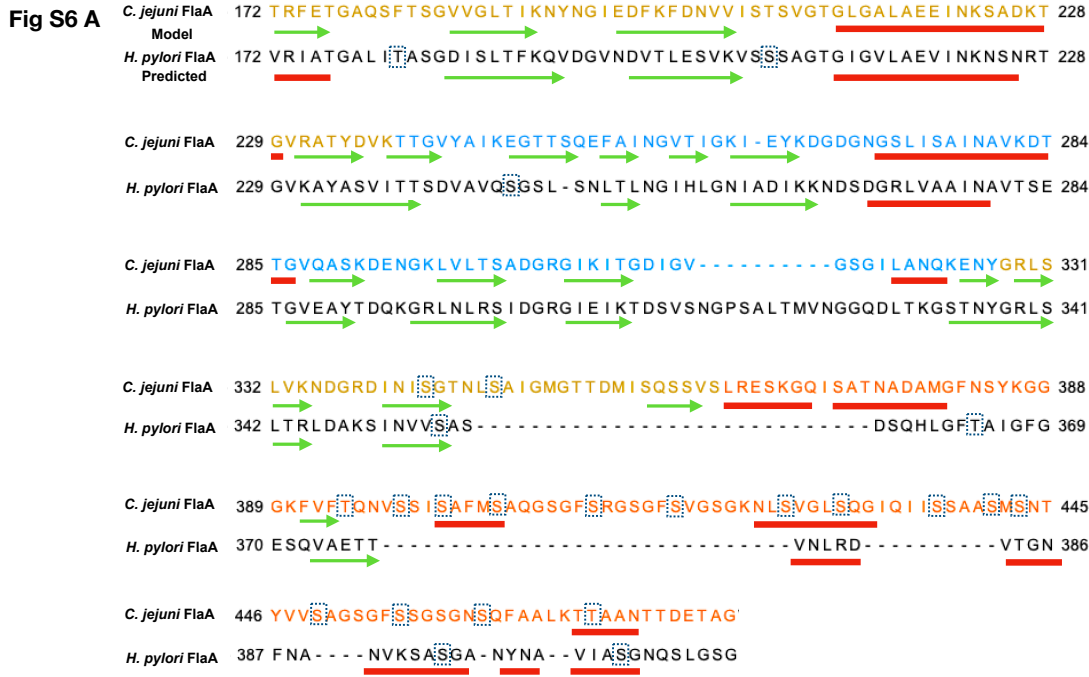


Figure S6: Sequence alignment and secondary structure of the *C. jejuni* and *H. pylori* FlaA flagellins. (A) Sequence alignment showing the observed secondary structure in *C. jejuni* FlaA and the predicted *H. pylori* FlaA secondary structure. (B) A comparison between the observed and predicted secondary structure of *C. jejuni* G508A.