

Supplementary Information

Bacterium	Phylum	Arrangement of flagella	Tilt-series showing flagella	Sub-tomograms averaged	Pixel size (nm)	Resolution (FSC 0.5) (nm)
<i>A. longum</i>	Firmicutes	>1, lateral	22	35	1.9	8.4
<i>B. burgdorferi</i>	Spirochetes	5 to 8 each tip	46	43	1.3	5.0
<i>T. primitia</i>	Spirochetes	1 each tip	19	20	1.9	7.7
<i>H. hepaticus</i>	Epsilon-proteobacteria	1 each tip	67	60	1.3	5.0
<i>C. jejuni</i>	Epsilon-proteobacteria	1 each tip	30	15	1.9	6.4
<i>H. gracilis</i>	Beta-proteobacteria	1 to 4 each tip	29	94	1.3	5.9
<i>V. cholerae</i>	Gamma-proteobacteria	1, polar	50	16	1.9	8.3
<i>S. enterica</i>	Gamma-proteobacteria	>1, lateral	72	83	1.3	4.8
<i>E. coli</i>	Gamma-proteobacteria	>1, lateral	61	46	1.3	5.9
<i>C. crescentus</i>	Alpha-proteobacteria	1, polar	82	30	1.3	5.9
<i>H. neptunium</i>	Alpha-proteobacteria	1, polar	31	27	1.5	6.8

Table S1. Summary of the 11 different bacterial flagellar motors.

FAMILY		<i>A. longum</i>	<i>B. burgdorferi</i>	<i>T. primitia</i>	<i>H. hepaticus</i>	<i>C. jejuni</i>
fliF	MS ring	ALO_14062	NP_212425.1	jcvi:TREPR_2558.1	NP_860142.1	YP_001481871.1
fliG	C ring	ALO_14067; ALO_11609	NP_212355.1; NP_212424.1	jcvi:TREPR_1015.1; jcvi:TREPR_2557.1	NP_860141.1	YP_001481872.1
fliM		ALO_14127	NP_212412.1	jcvi:TREPR_3134.1; jcvi:TREPR_2856.1; jcvi:TREPR_1885.1	NP_860678.1	YP_001481630.1
fliN		ALO_14202	NP_212411.1	-	NP_861108.1	YP_001481904.1
fliY	Occasional C ring component	ALO_14132	-	jcvi:TREPR_2855.1	NP_860679.1	YP_001481629.1
fliI	Soluble Export Apparatus	ALO_14077	NP_212422.1	jcvi:TREPR_2555.1	NP_860096.1	YP_001481760.1
fliH		ALO_14072	NP_212423.1	jcvi:TREPR_2556.1	NP_860140.1	YP_001481873.1
fliJ		ALO_14082	-	jcvi:TREPR_2554.1	-	-
flhA	Transmembrane Export Apparatus	ALO_14167	NP_212405.1	jcvi:TREPR_3866.1; jcvi:TREPR_2849.1	NP_859998.1	YP_001482396.1
flhB		ALO_14162	NP_212406.1	jcvi:TREPR_2850.1	NP_860549.1	YP_001481888.1
fliP		ALO_14147	NP_212409.1	jcvi:TREPR_2853.1	NP_860223.1	YP_001482343.1

Table S2. Hand-curated flagellar motor gene families for the 11 organisms.

fliR	Transmembrane Export Apparatus	ALO_14157	NP_212407.1	jcvi:TREPR_2851.1	NP_860235.1	YP_001482699.1
fliQ		ALO_14152	NP_212408.1	jcvi:TREPR_2852.1	NP_859969.1	YP_001483150.1
fliO		-	-	-	NP_861109.1	YP_001481905.1
fliE	Proximal Rod	ALO_14057	NP_212426.1	jcvi:TREPR_2559.1	NP_860940.1	YP_001482063.1
flgB		ALO_14047	NP_212428.1	jcvi:TREPR_2561.1	NP_860938.1	YP_001482065.1
flgC		ALO_14052	NP_212427.1	jcvi:TREPR_2560.1	NP_860939.1	YP_001482064.1
flgF		ALO_10009	NP_212909.1	jcvi:TREPR_3479.1	NP_860621.1	YP_001482240.1
flgG	Distal rod	ALO_10014	NP_212908.1	jcvi:TREPR_3480.1	NP_860612.1	YP_001482241.1
flgI	P-ring	ALO_10029	NP_212906.1	-	NP_859673.1	YP_001482943.1
flgH	L-ring	ALO_10024	-	-	NP_860430.1	YP_001482231.1
motA	Stator	ALO_08815	NP_212415.1	jcvi:TREPR_2861.1	NP_860032.1	YP_001481890.1
motB		ALO_08810	NP_212414.1	jcvi:TREPR_2860.1	NP_860033.1	YP_001482137.1; YP_001481889.1
motX		-	-	-	-	-
motY		-	-	-	-	-
flbB	Proposed Spirochaete P-collar component	-	NP_212420.1	jcvi:TREPR_2866.1	-	-

Table S2 (continued). Hand-curated flagellar motor gene families for the 11 organisms.

<i>H. gracilis</i>	<i>V. cholerae</i>	<i>S. enterica</i>	<i>E. coli</i>	<i>C. crescentus</i>	<i>H. neptunium</i>
HGR_14229	NP_231764.1	NP_460922.1	NP_416448.1	NP_419721.2	YP_758973.1
HGR_14234	NP_231763.1	NP_460923.1	NP_416449.1	NP_419722.1	YP_760109.1; YP_758977.1
HGR_14264	NP_231757.1	NP_460929.1	NP_416455.1	NP_420864.1	YP_758983.1
HGR_14269	NP_231756.1	NP_460930.1	NP_416456.1	NP_420978.1; NP_419724.1	YP_760111.1; YP_758975.1
-	-	-	-	-	-
HGR_14244	NP_231761.1	NP_460925.1	NP_416451.1	NP_421834.1	YP_758999.1
HGR_14239	NP_231762.1	NP_460924.1	NP_416450.2	NP_419723.1	-
HGR_14249	NP_231760.1	NP_460926.1	NP_416452.1	NP_421835.1	-
HGR_16580	NP_231701.1	NP_460870.1	NP_416393.1	NP_419726.1	YP_759004.1
HGR_16585	NP_231751.1	NP_460871.1	NP_416394.1	NP_419893.1	YP_759006.1
HGR_14279	NP_231754.1	NP_460932.1	NP_416458.1	NP_419767.1	YP_758976.1

Table S2 (continued). Hand-curated flagellar motor gene families for the 11 organisms.

HGR_14289	NP_231752.1	NP_460934.1	NP_416460.1	NP_419892.1	YP_759005.1
HGR_14284	NP_231753.1	NP_460933.1	NP_416459.1	NP_419891.1	YP_759003.1
HGR_14274	NP_231755.1	NP_460931.1	NP_416457.4	NP_419768.1	-
HGR_14224	NP_231765.2	NP_460921.1	NP_416447.1	NP_419771.1	YP_759002.1
HGR_16635	NP_231831.1; NP_231831.1	NP_460145.1	NP_415591.1	NP_419769.1	YP_759000.1
HGR_16640	NP_231830.1	NP_460146.1	NP_415592.1	NP_419770.1	YP_759001.1
HGR_16655	NP_231827.1	NP_460149.1	NP_415595.1	NP_420866.1	YP_758986.1
HGR_16660	NP_231826.1	NP_460150.1	NP_415596.1	NP_420867.1	YP_758987.1
HGR_16670	NP_231824.1	NP_460152.1	NP_415598.3	NP_421384.1	YP_758978.1
HGR_16665	NP_231825.1	NP_460151.1	NP_415597.1	NP_420869.1	YP_758989.1
HGR_16605	NP_230539.1	NP_460880.1	NP_416404.1	NP_419567.1	YP_762020.1; YP_758984.1
HGR_16600	NP_230540.1	NP_460879.1	NP_416403.1	NP_420384.1	YP_759621.1; YP_758982.1
-	NP_232229.1	-	-	-	-
-	NP_230654.1	-	-	-	-
-	-	-	-	-	-

Table S2 (continued). Hand-curated flagellar motor gene families for the 11 organisms.

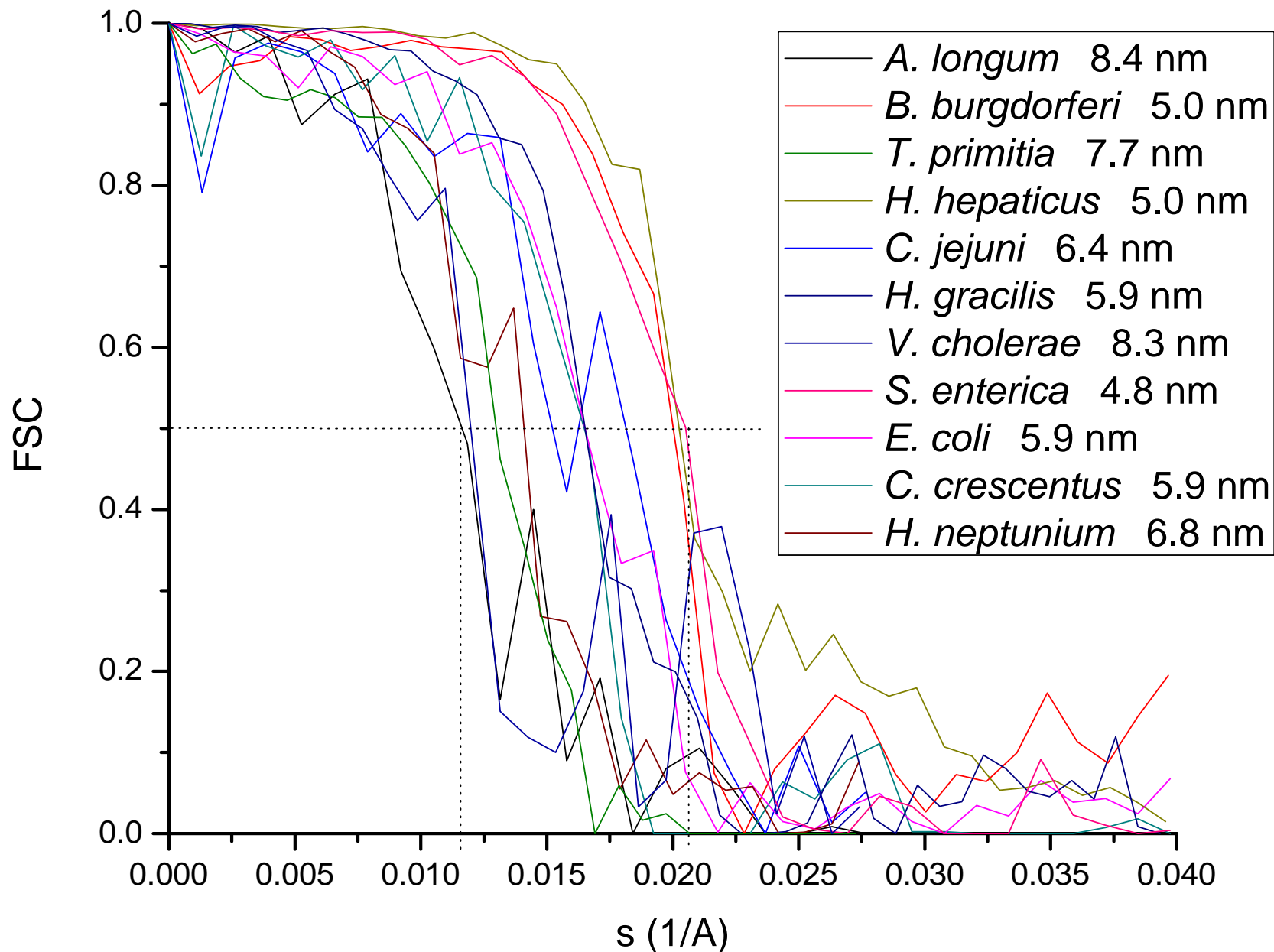


Figure S1. Fourier Shell Correlation (FSC) curves for the 11 flagellar motor subtomograms, calculated by comparing separately averaged and symmetrized halves of the data set.

Figure S2. Phylogenetic tree of 603 representative bacteria constructed by concatenation of multiple ribosomal protein genes as described previously (Briegel et al, 2009). Organisms imaged in this study are marked with red asterisks. The presence or absence of known flagellar motor genes (listed at top) is indicated by black or open cells, respectively, in concentric rings surrounding the tree. Note that this figure is enlargeable.

References

Briegel A, Ortega DR, Tocheva EI, Wuichet K, Li Z, Chen SY, Muller A, Iancu CV, Murphy GE, Dobro MJ, Zhulin IB, Jensen GJ (2009) Universal architecture of bacterial chemoreceptor arrays. *Proc Natl Acad Sci U S A* **106**: 17181-17186

