Supporting Information

Kojima *et al.* 10.1073/pnas.0800308105

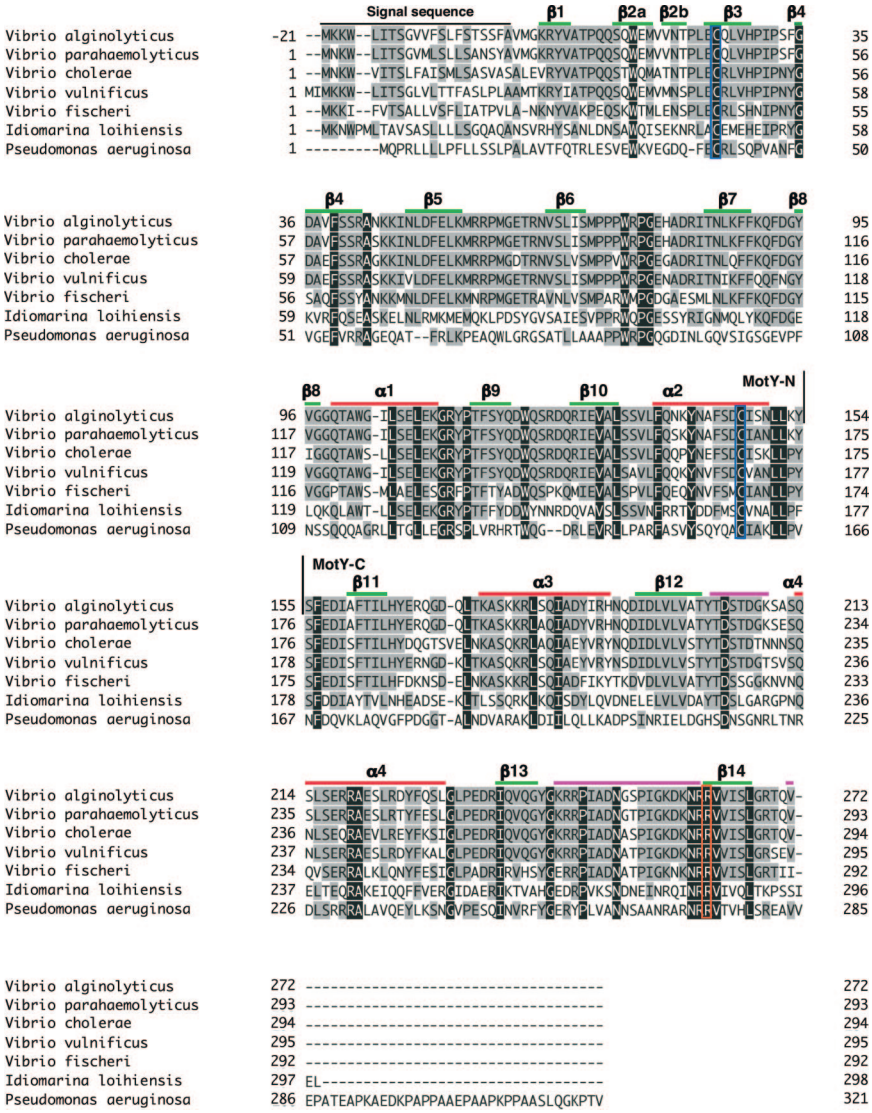

Fig. S1. Multiple alignments of the MotY proteins from bacterial species with polar flagellum. Various structural features revealed by this study are indicated on top of the amino acid sequence of *Vibrio alginolyticus* MotY: red line, α-helix; green line, β-structure. The secondary structural elements are labeled above the lines. The residues missing in the atomic model are indicated with magenta lines above the sequence. The blue boxes indicate the residues forming the intramolecular disulfide bridge. Arg-261, a well-conserved residue important for motility, is shown with the orange box. The N-terminal 21 signal-sequence residues of *V. alginolyticus* MotY are indicated with the black line above the sequence.

Table S1. X-ray refinement statistics

Measurement	Value
Resolution range, Å	41–2.85 (3.03–2.85)
Reflections working, no.	9,699 (1,323)
Reflections test, no.	953 (137)
R_w, %	29.0 (40.2)
R_{free}, %	31.2 (42.1)
rmsd bond length, Å	0.012
rmsd Bond angle, deg.	2.3
B-factors	
Protein atoms, no.	55.3
Solvent atoms, no.	45.6
Ramachandran plot, %	
Most favored	71.8
Additionally allowed	25.5
Generously allowed	2.8
Disallowed	0
Protein atoms, no.	2,003
Solvent atoms, no.	12

Values in parentheses are for the highest-resolution shell. $R_w = \Sigma \; ||Fo| - |Fc|| / \Sigma |Fo|$; $R_{free} = \Sigma \; ||Fo| - |Fc|| / \Sigma \; |Fo|$.