

Table S1. Closest FopA homologs identified by BLAST search ^a.

Organism	NCBI Reference Sequence	Order	Family	Query cover^b	E value^c	Identity ^d
<i>Fangia hongkongensis</i>	WP_018300465.1	Thiotrichales	Fastidiosibacteraceae	76%	4e-55	39.22%
<i>Caedibacter taeniospiralis</i>	WP_100550987.1	Thiotrichales	Fastidiosibacteraceae	82%	5e-52	36.28%
<i>Fastidiosibacter lacustris</i>	WP_116964154.1	Thiotrichales	Fastidiosibacteraceae	82%	6e-52	35.98%
<i>Cysteiniphilum</i> sp. JM-1	WP_151194100.1	Thiotrichales	Fastidiosibacteraceae	81%	6e-52	36.89%
<i>Geobacter bemidjensis</i>	WP_012529806.1	Desulfuromonadales	Geobacteraceae	75%	2e-13	25.94%
<i>Marinagarivorans algicola</i>	WP_053981259.1	Cellvibrionales	Cellvibrionaceae	75%	3e-12	26.28%
<i>Alishewanella jeotgali</i>	WP_008951022.1	Alteromonadales	Alteromonadaceae	86%	7e-12	26.46%
<i>Pseudomonas aeruginosa</i>	WP_134304455.1	Pseudomonadales	Pseudomonadaceae	64%	7e-11	28.09%
<i>Marinomonas piezotolerans</i>	WP_115468919.1	Oceanospirillales	Oceanospirillaceae	67%	1e-09	26.41%

^a Listed are all of the homologs with at least 25% sequence identity to FopA.

^b Percentage of query sequence residues that overlap with the reference sequence.

^c Expect value (E) is a parameter that describes the number of hits one can "expect" to see by chance when searching a database.

^d Quantitative measurement of the similarity between two sequences.