



Supplementary Figure S2. Phylogenetic relationships for the AspS family of proteins.

Phylogenetic analysis of AspS sequences mirrors the relationships observed for Vibrio-type secretins. Phylogenetic tree reconstruction was performed with PhyML v3.0 [Guindon et al. 2003] using 500 bootstrap calculations and shown as percentage values, further details are described in the Methods. For a full list of the sequence accession numbers see Table S3.

Reference

Guindon S, Gascuel O (2003) A simple, fast, and accurate algorithm to estimate large phylogenies by maximum likelihood. *Syst Biol* **52**:696-704.