

**S1 Fig. Alignments and secondary structure predictions of PG1058 domains predicted by Phyre2.** **A.** The TPR domain aligned to 412wA, the myosin chaperone unc-45 from *Caenorhabditis elegans* **B.** The β–propeller domain aligned to c2w8bB, *E. coli* TolB. Note the lack of homology in places, which results in fewer blades predicted in PG1058 than in the template molecule. **C.** The CRD domain aligned to cmn8A, *Drosophila melanogaster* carboxypeptidase d isoform 1b2 short. **D.** The OmpA\_C domain aligned to c1r1m1, the OmpA-like domain from RmpM of *Neisseria meningitidis*.