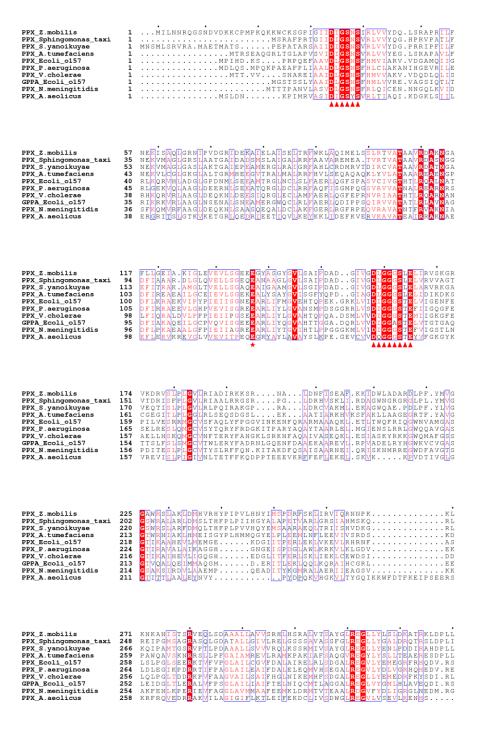


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Supporting information for article:

Purification, crystallization and X-ray crystallographic analysis of a putative exopolyphosphatase from Zymomonas mobilis

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PPX_substitis

PPX_synoixuyae

PPX_synoixuyae
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Supplementary Figure S1. Multiple sequence alignment of PPX proteins. Conserved residues are highlighted with red and similar residues colored with red respectively. Two conservative loops (highlighted by red triangles) form part of the active site. The catalytic residue Glu137 mutated in this work is labelled as red star. Key: *Z. mobilis* PPX (gi502556931), *Sphingomonas taxi* (gi758932120), *Sphingobium yanoikuyae* (gi893709514), *Agrobacterium tumefaciens* (gi499274033), *E. coli* O157:H7 PPX (gi666005157), *Pseudomonas aeruginosa* (gi4760367), *Vibrio cholerae* (gi446136634). *E. coli* O157:H7 GPPA (gi481023644), *Neisseria meningitidis* (gi488153892), *Aquifex aeolicus* (gi499183000). Sequence alignment was performed using ClustalW2 (Goujon *et al.*, 2010) and formatted using ESPript (Robert & Gouet, 2014).