Supplementary Fig.1 LEGEND

Amino acid sequence alignment of WfaP and WfgD. The sequences of WfaP (ABB29913) and WfgD (unpublished data) were compared using ClustalW. The lines connecting the two sequences show identity, and the dots show similarity. The conserved DxD motifs are highlighted. The hydrophobic region at the C terminus containing positively charged amino acids that may help to associate proteins with the inner membrane are underlined.

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WfaP          1 ME--LVSIIIAAYNCKDTIYATVESALSQTYKNIEIIICDDSSTDDTWDI     48
                |:  |||||:.:||.:.||.|::.|.|.|||.|.|:::|||.|:|:|...
WfgD          1 MDDYLVSIIMPSYNAEHTISASISSVLKQTYANWELLVCDDDSSDNTRFK     50

WfaP         49 INKIKDSRIICIKNNYCKGAAGARNCALKIAKGRYIAFLDSDDYWVTTKI     98
                :.:..||||..:.|.|.|||||||||.|||.|.||:||||||||.|:..|:
WfgD         51 VLEFSDSRIKLLTNEYAKGAAGARNTALKYASGRFIAFLDSDDIWIANKL    100

WfaP         99 SNQIHFMETEKVFFSYSNYYIEKDFVITGVFSSPPEINYGAMLKYCNIAC    148
                ..||..|....:.|.|.||.|..:..|.|.|.:|.:|.|..:||.|.|.|
WfgD        101 EMQISMMLKNNISFMYGNYEIINNNSIVGKFVAPQKITYNKLLKNCGIGC    150

WfaP        149 STVILDRTGVKNISFPYIDKEDYALWLNIL-SKGIKARNTNLVDTYYRVH    197
                .||:||||.:...|||::.||||.|||:|| ...|.|.|...:.:.||:.
WfgD        151 LTVVLDRTLLNPFSFPFVHKEDYYLWLSILKDNNISAINCGFICSKYRLS    200

WfaP        198 AGSVSANKFKELIRQSNVLKSIGIKAHHRIICLFYYAINGLIKHCFSYRD    247
                ..|:|:||||||.||.:||.........||..|..|.:.|:.||.|.|::
WfgD        201 QSSISSNKFKELKRQWDVLGDFVENPLARIYYLLNYIVIGIKKHAFDYKN    250

WfaP        248 KRNA    251
                .:.
WfgD        251 GKK     253
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Supplementary Fig. 1