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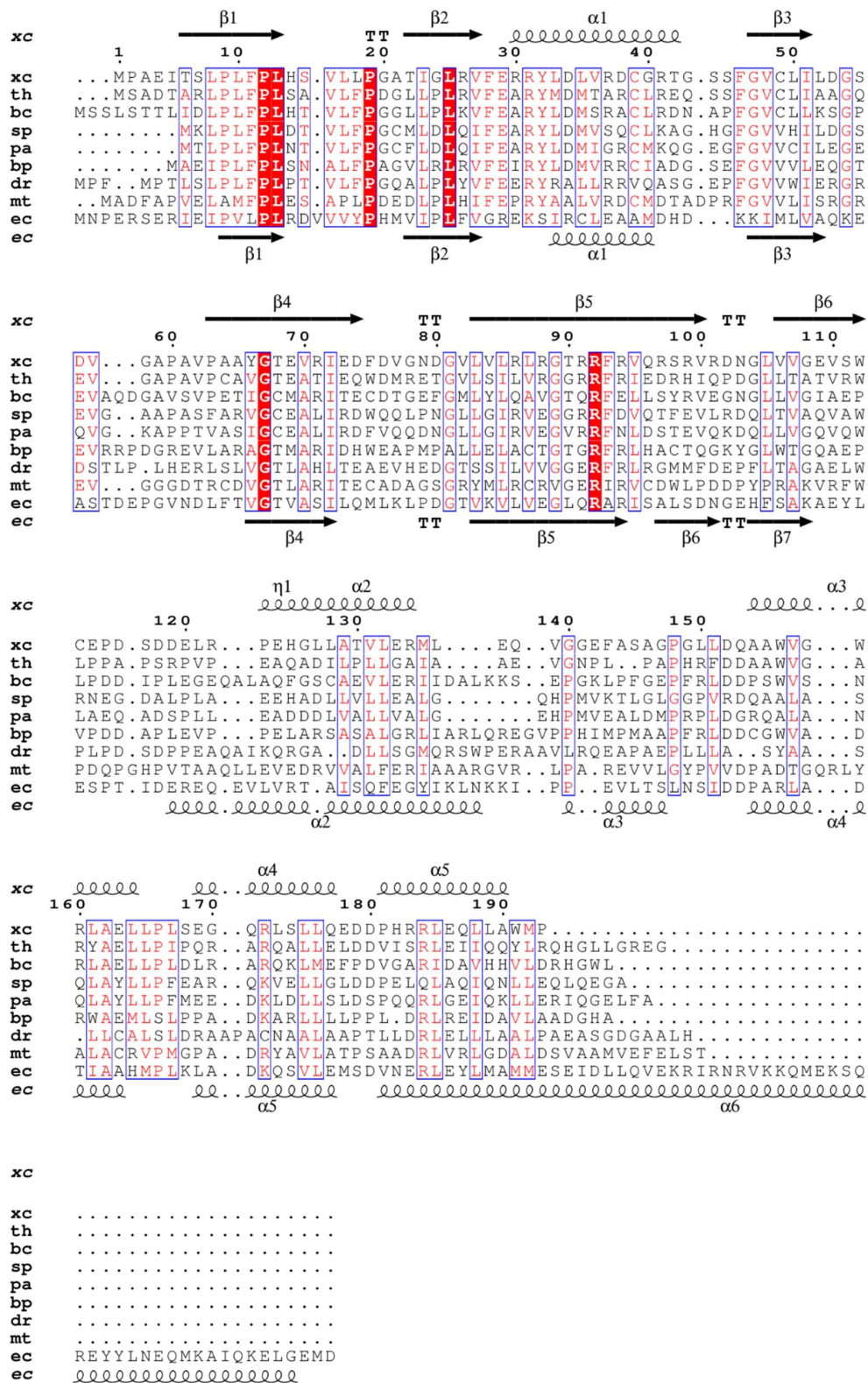
**Supporting information for article:**

**Crystal structure of XCC3289 from *Xanthomonas campestris*:  
homology with the N-terminal substrate-binding domain of Lon  
peptidase**

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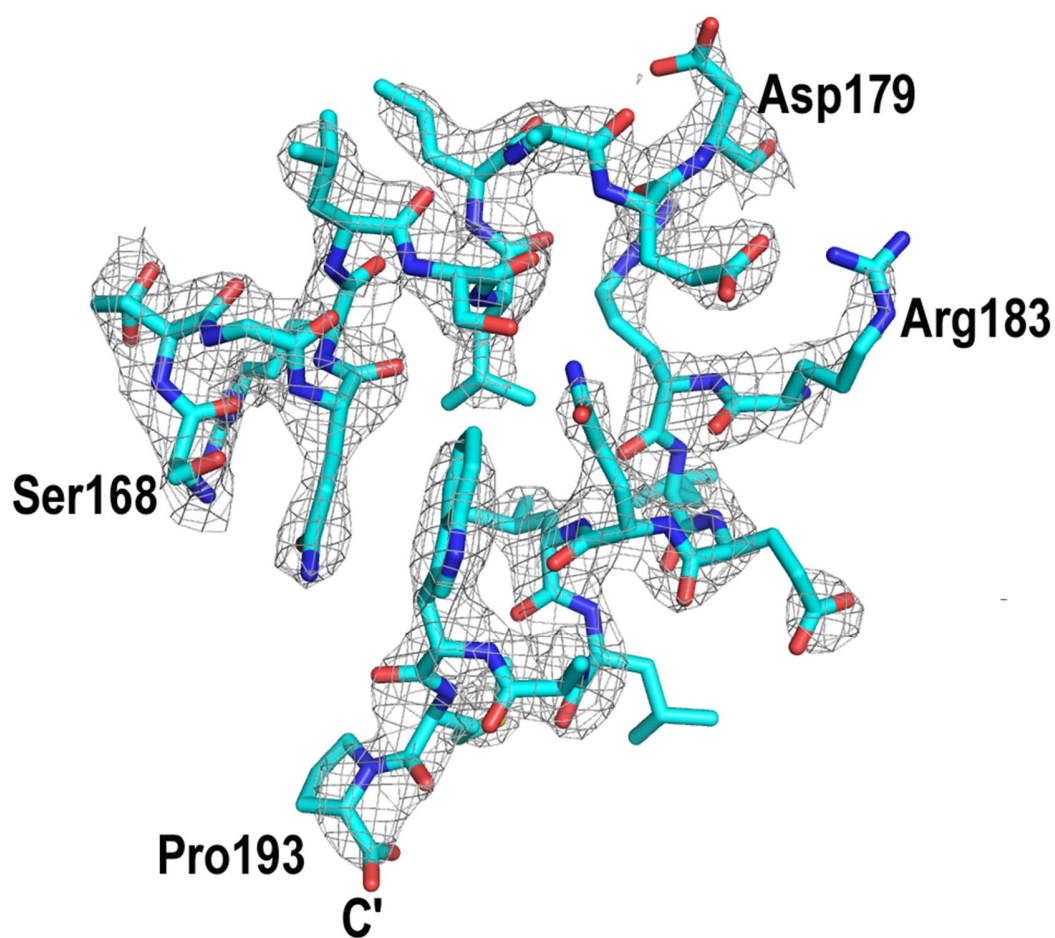


**Figure S1** Schematic representation of domain organization in LonA peptidase of *Escherichia coli* (upper) and XCC3289 proteins (lower).

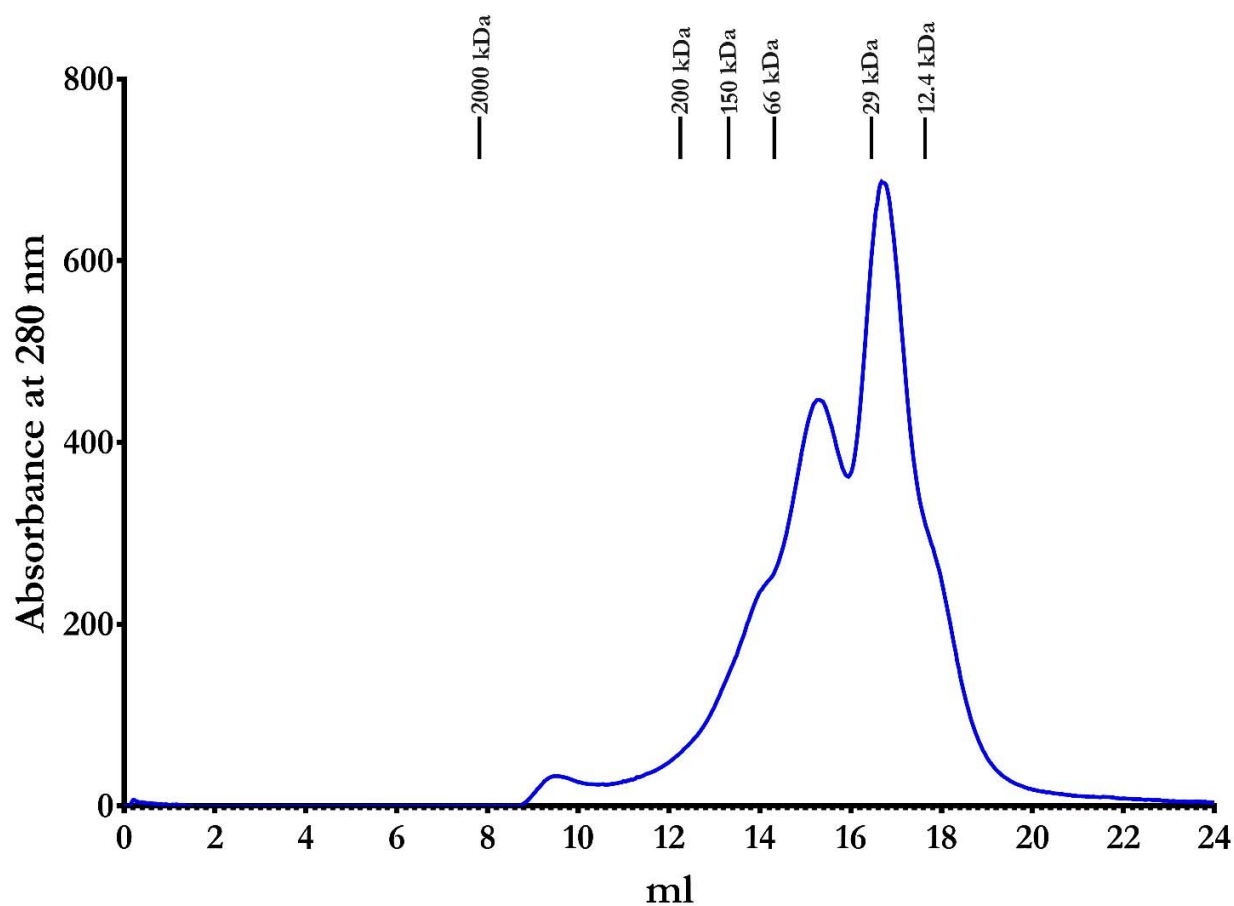


**Figure S2** Multiple sequence alignment (MSA) of LonNTD-like proteins from evolutionarily distinct prokaryotes. *Xanthomonas campestris* (present study; Q8P5P7), *Thauera hydrothermalis*

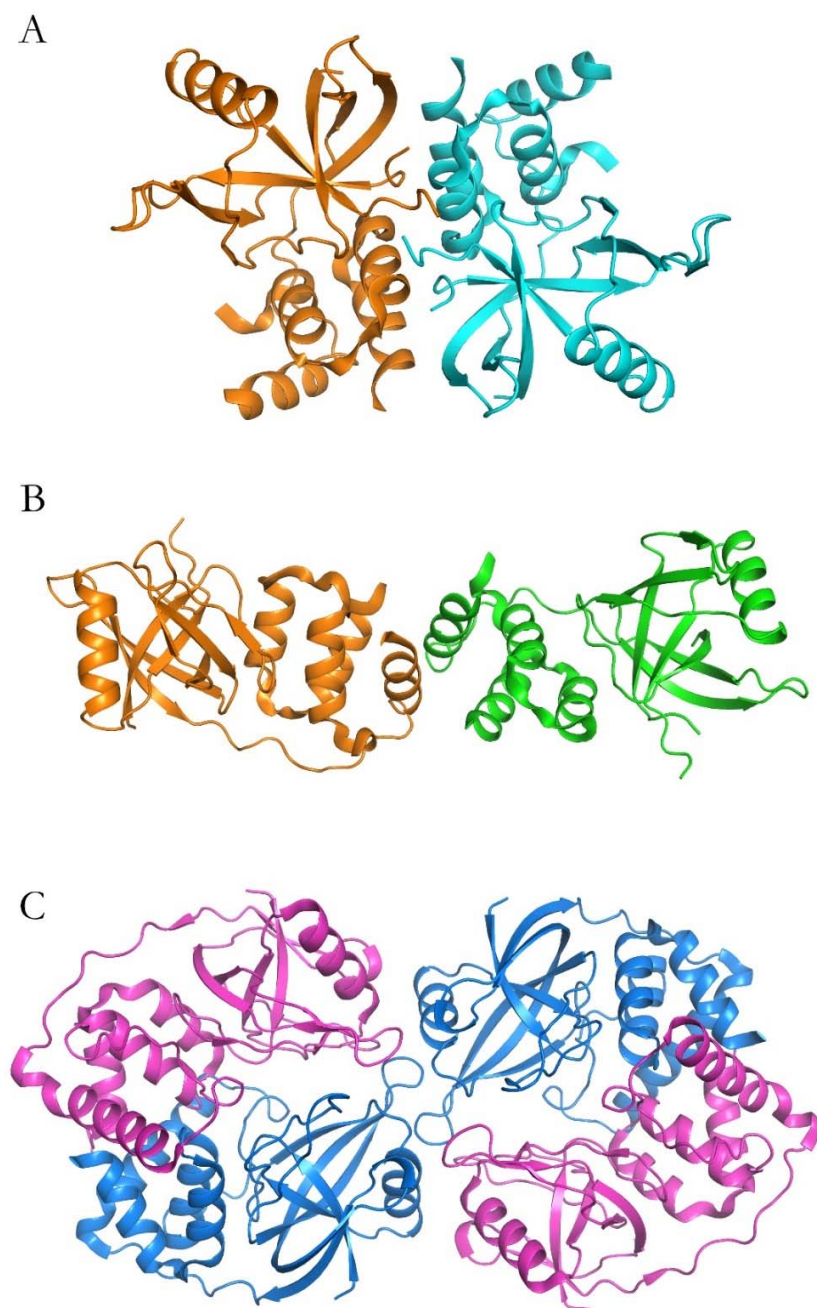
**Acta Cryst.** (2020). F76, doi:10.1107/S2053230X20011875 Supporting information, sup-3 (WP\_102042807), *Burkholderia cepacia* (WP\_034179063), *Streptococcus pneumoniae* (CJK92186), *Pseudomonas sp.* (WP\_009685818), *Bordetella parapertussis* (Q7WAM7), *Deinococcus radiodurans* (AAF11739), *Mycobacterium tuberculosis* (NP\_214948), and *Escherichia coli* (N-terminal region, P0A9M0). The secondary structure elements of the protein from *Xanthomonas campestris* are depicted on top of the alignments and those of the protein from *Escherichia coli* are depicted at the bottom of the alignment. The  $\beta$ -strands are represented using arrows and  $\alpha$ -helices are represented using curly lines.



**Figure S3** Electron density map overlapped on a portion which includes C' terminal helix of XCC3289 structure. 2mFo-DFc map is contoured at 1.5 sigma.



**Figure S4** Elution profile of XCC3289 on Superdex-200 size-exclusion column. (Molecular mass standards:  $\beta$ -Amylase-200 kDa, alcohol dehydrogenase-150 kDa, bovine serum albumin-66 kDa, carbonic anhydrase-29 kDa, cytochrome c-12.4 kDa).



**Figure S5** Oligomeric assemblies (Ribbon representation) predicted by PDBePISA (Proteins, Interfaces, Structures and Assemblies). (A) Dimeric assembly of XCC3289 with buried surface area of 1910 Å<sup>2</sup>. (B) Dimeric assembly of XCC3289 with buried surface area of 690 Å<sup>2</sup>. (C) Tetrameric assembly (dimer of dimer) of BPP1347 from *Bordetella parapertussis* (PDB: 1zbo) with buried surface area of 18070 Å<sup>2</sup> between the dimers of the tetramer.