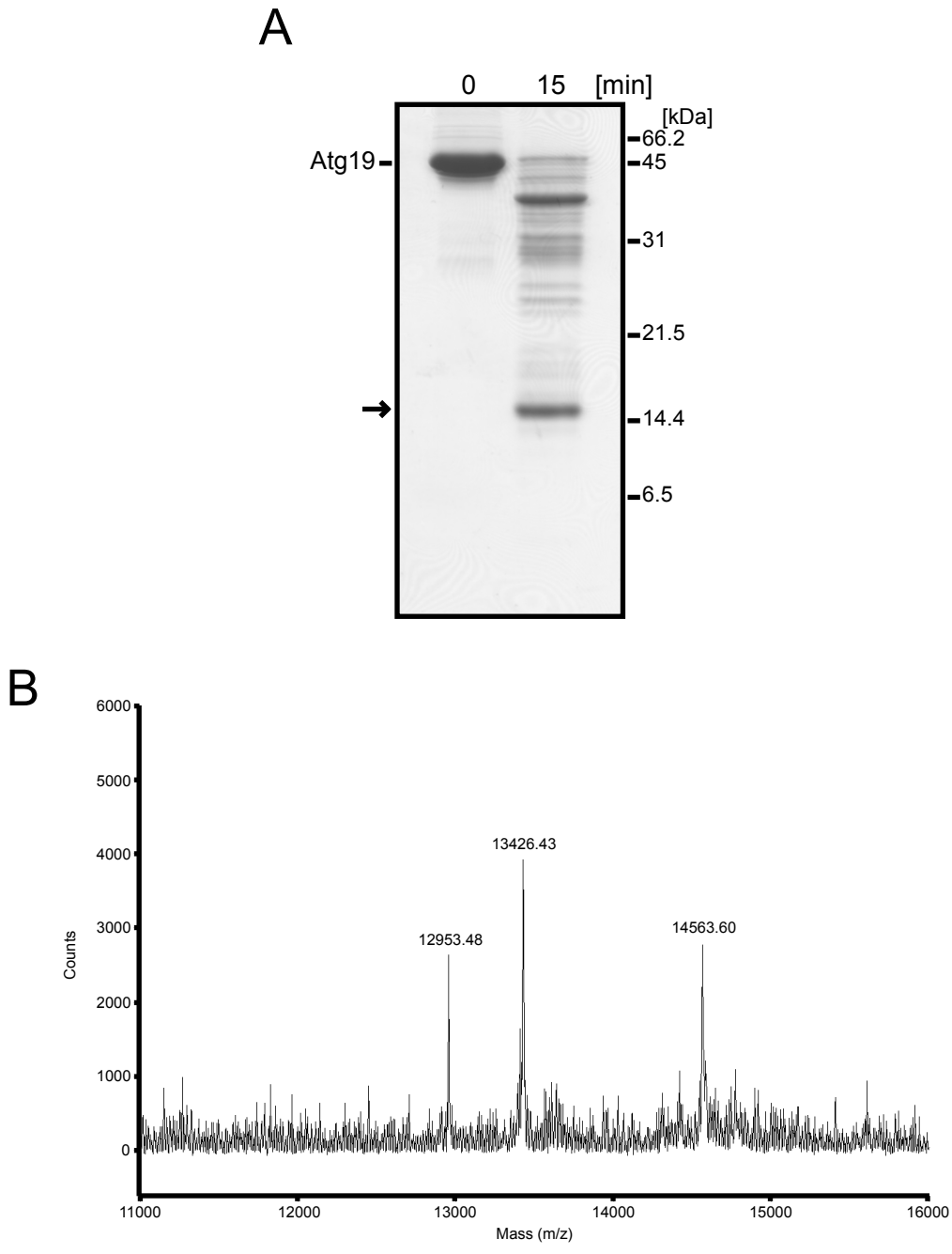
Supplemental Figure S1



Supplemental Fig. S1. A. Limited proteolysis of Atg19. The Atg19 before and after digestion were subjected to SDS-PAGE, and detected by Coomassie Brilliant Blue staining. Labels of 0 min and 15 min indicate the incubation time of Atg19 with V8 protease. The ~15 kDa product indicated with an arrow was sequenced by a protein sequencer. B. MALDI-TOF mass spectrometry. The 14563.60 m/z peak indicates the N-terminal domain (residues 1-123; calculated molecular mass is 14566.08). The 12953.48 m/z peak indicates the C-terminal domain (residues 254-367; calculated molecular mass is 12953.14). The 13426.43 m/z peak corresponds to the residues 250-367 (calculated molecular mass is 13424.67), which has additional four residues at the N-terminal side of the C-terminal domain.

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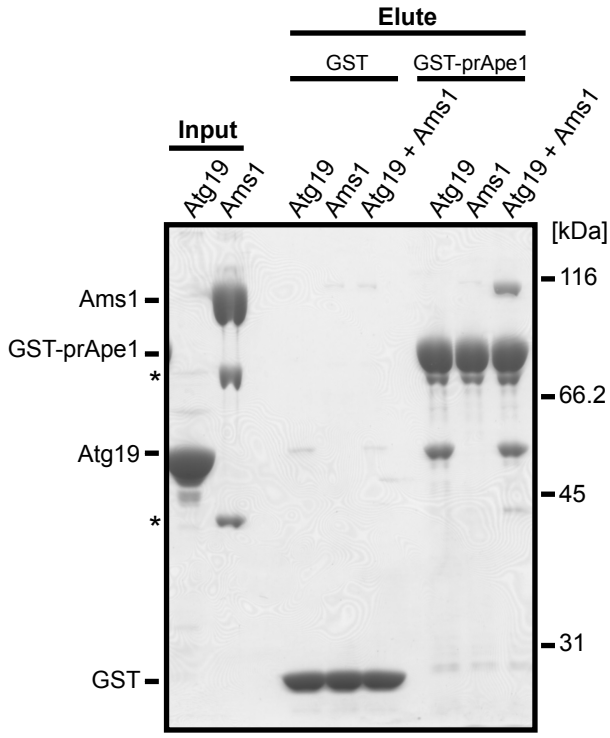
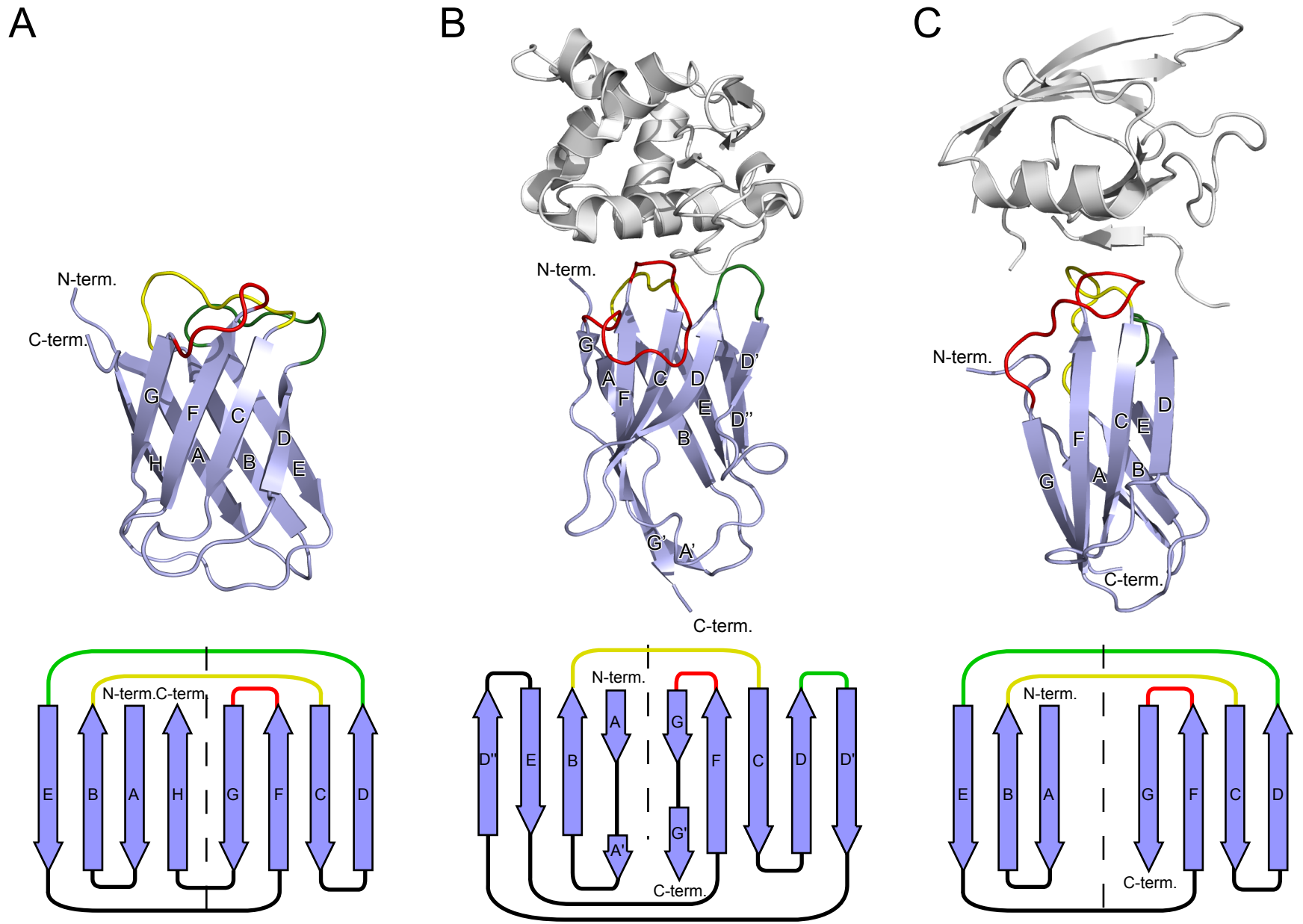
Supplemental Figure S2



Supplemental Fig. S2. *In vitro* pull-down assay between GST-fused prApe1, Atg19 and Ams1. The input and eluted proteins were subjected to SDS-PAGE and detected by Coomassie Brilliant Blue staining. Asterisks indicate degradation products of Ams1.

Supplemental Figure S3



Supplemental Fig. S3. Comparison of the structures of the Atg19 ABD (Left), the heavy chain fragment of the camelid antibody in complex with human lysozyme (Middle; PDB code 1OP9), and human 10th fibronectin type III domain in complex with the PDZ domain of Erbin and the ARVCF peptide (Right; PDB code 2QBW). The BC, DE and FG loops are colored yellow, green and red, respectively. Structures are represented in ribbon diagrams. Topology is shown below each model.