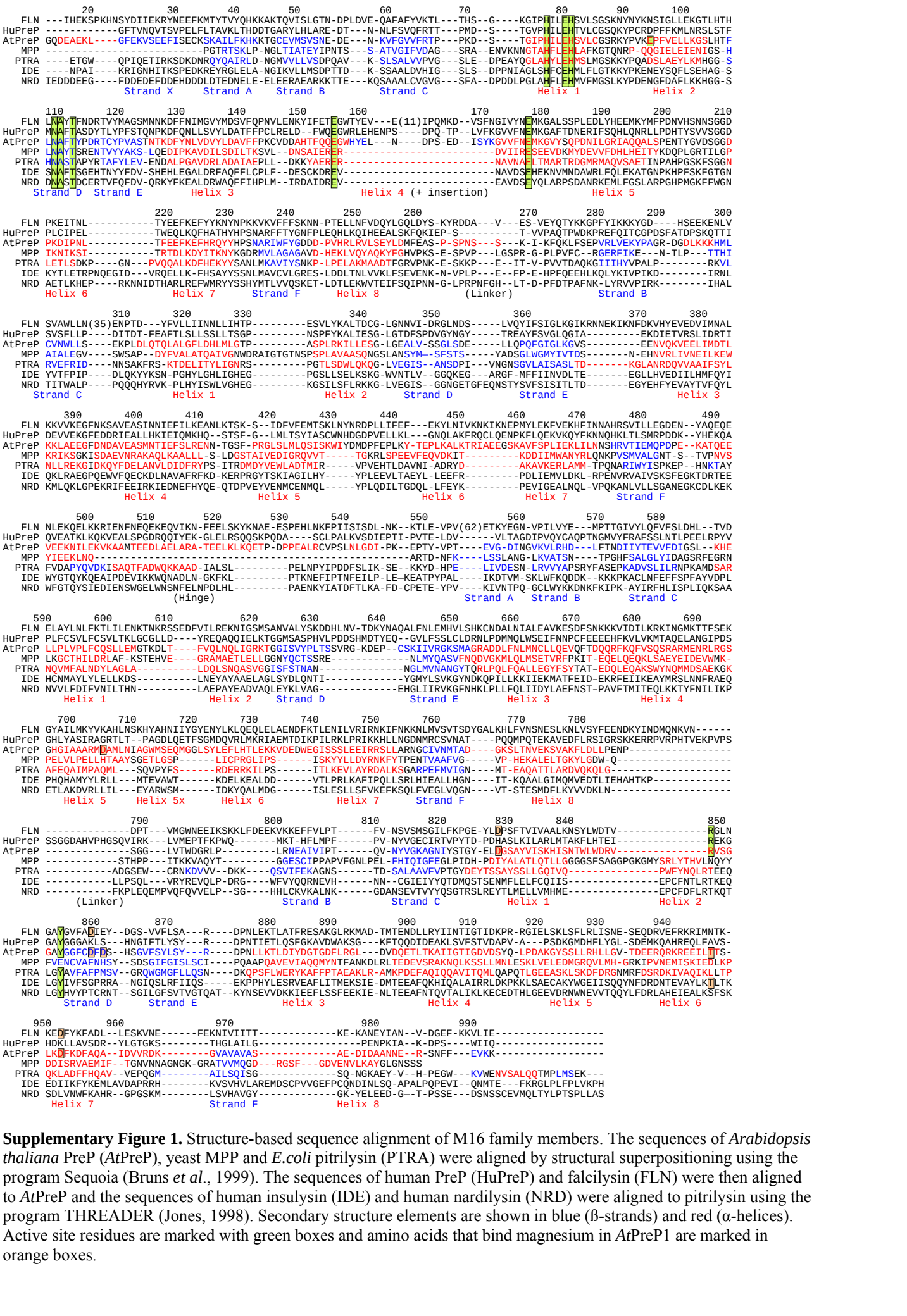

Supplementary Figure 1. Structure-based sequence alignment of M16 family members. The sequences of *Arabidopsis thaliana* PreP (*At*PreP), yeast MPP and *E.coli* pitrilysin (PTRA) were aligned by structural superpositioning using the program Sequoia (Bruns *et al*., 1999). The sequences of human PreP (HuPreP) and falcilysin (FLN) were then aligned to *At*PreP and the sequences of human insulysin (IDE) and human nardilysin (NRD) were aligned to pitrilysin using the program THREADER (Jones, 1998). Secondary structure elements are shown in blue (ß-strands) and red (α-helices). Active site residues are marked with green boxes and amino acids that bind magnesium in *At*PreP1 are marked in orange boxes.