

Figure S1. Multiple structure overlap of monomer subunits of bacterial M17 peptidases. *E. coli* PepB (PDB code 6oad, this study); *Y. pestis* PepB (6cxd, this study); *E. coli* PepA⁵ (1gyt); *P. putida* PepA⁶ (3h8e); *H. pylori* M17AP⁹ (4zla); *S. aureus* PepZ¹⁰ (3kzw) as aligned by the POSA server.³⁸

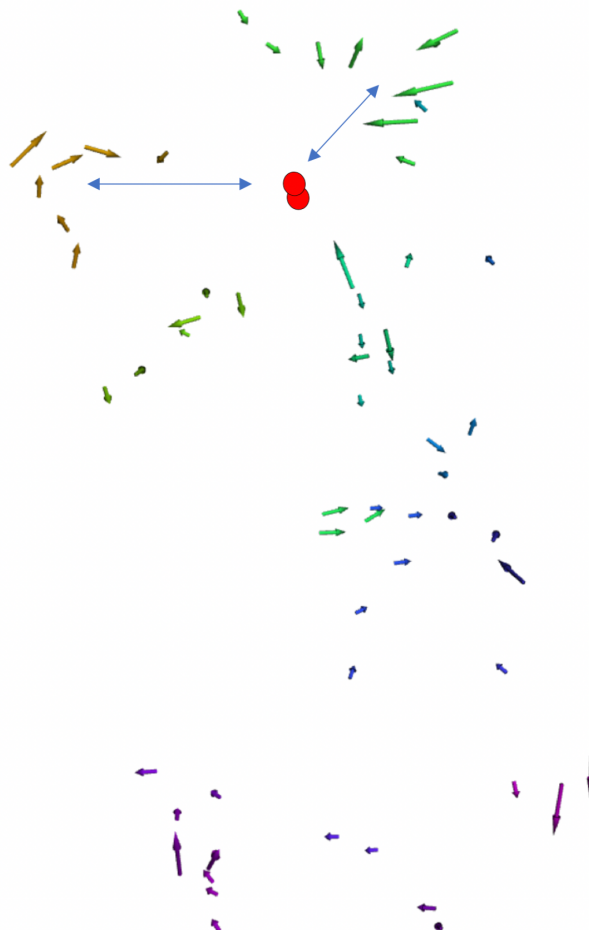


Figure S2. Displacement view of the structural changes in the PepB structure upon Zn²⁺ binding. Note the large changes in the loops, despite over 15Å distance between the ion binding sites and the center of the loops. Changes are also visible in the N-terminus. Figure was prepared using a new interface in the FATCAT structure alignment program.³⁹