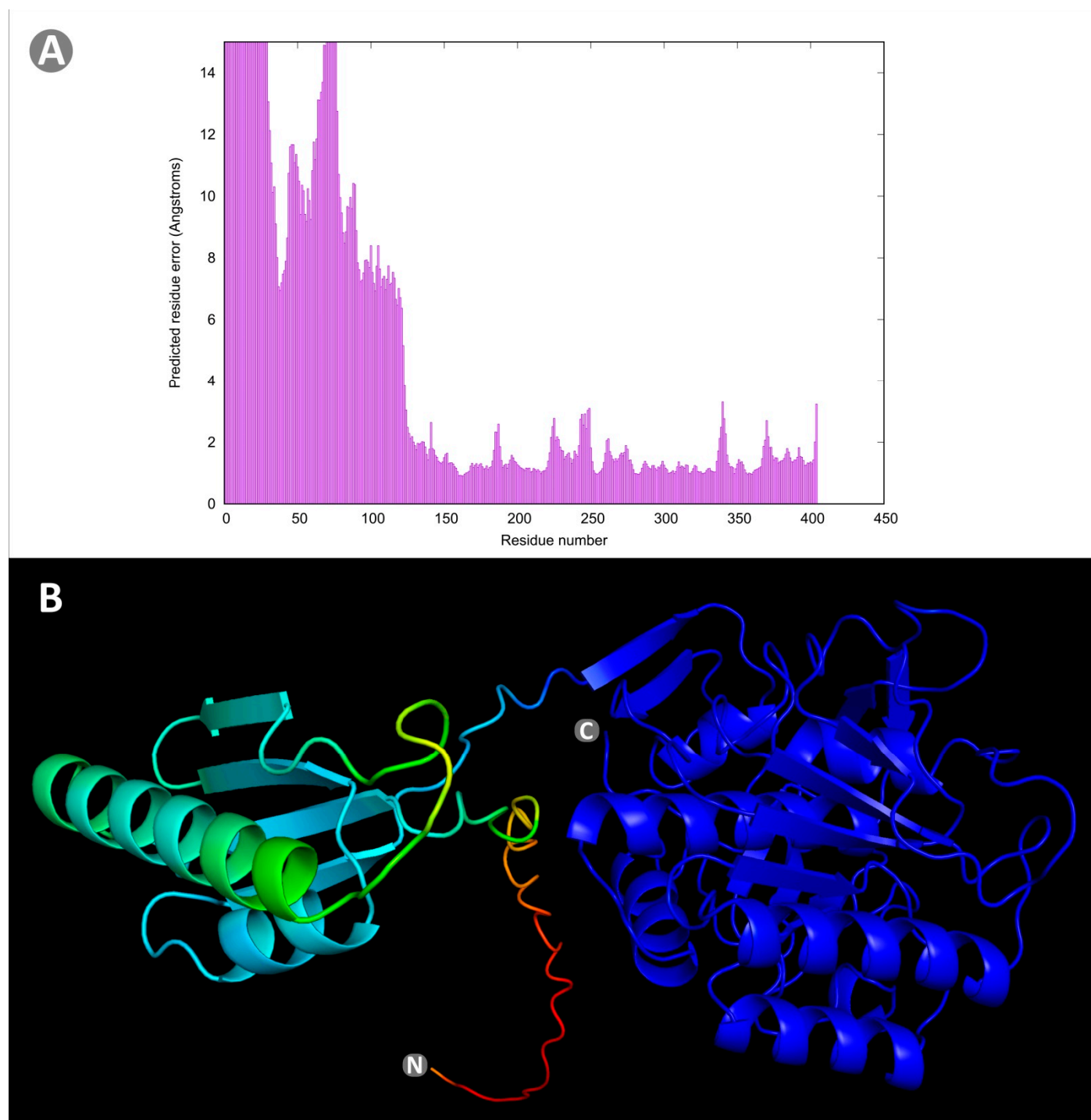
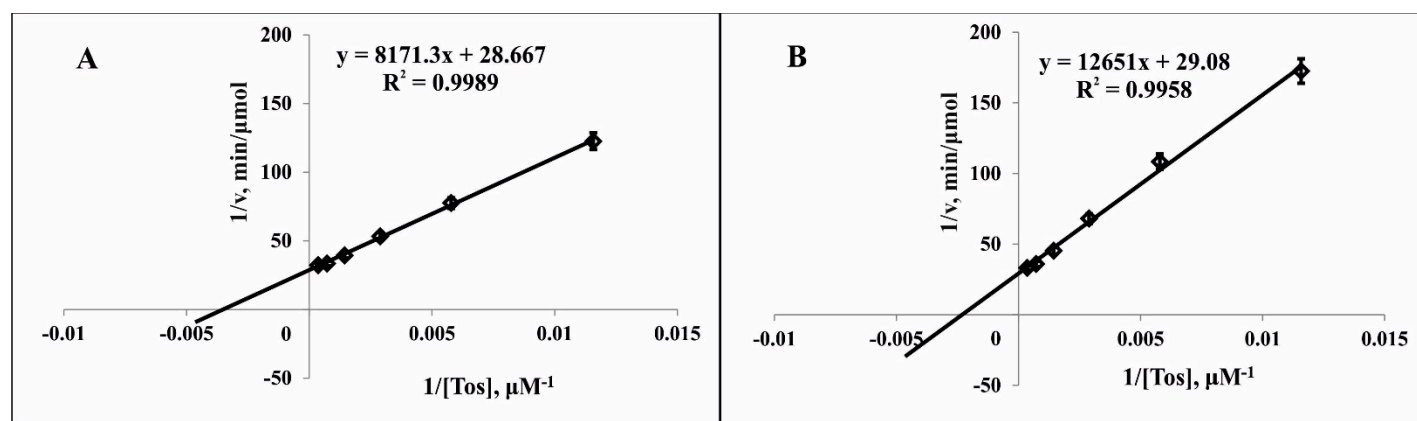


Supplementary Figure S1



Supplementary Figure S1. (A) ModFOLD8 residue error plot. (B) ModFOLD8 3D view of per-residue accuracy of the *Aspergillus ochraceus* protease model. The model is coloured based on a rainbow gradient scheme, where the residues with the lowest predicted residue errors are coloured blue and the residues with the highest predicted residue errors are coloured red. The N-terminus of the polypeptide chain is labeled “N” and the C-terminus is labeled “C”.

Supplementary Figure S2



Supplementary Figure S2. Lineweaver-Burk plot for native (A) and recombinant (B) form of PAPC-4104. [Tos] – concentration of chromogenic peptide substrate Tos-Gly-Pro-Arg-pNA. The error bars represent standard deviation.