Supplemental Materials

Mechanism for Controlling the Monomer-Dimer Conversion of SARS Coronavirus Main Protease

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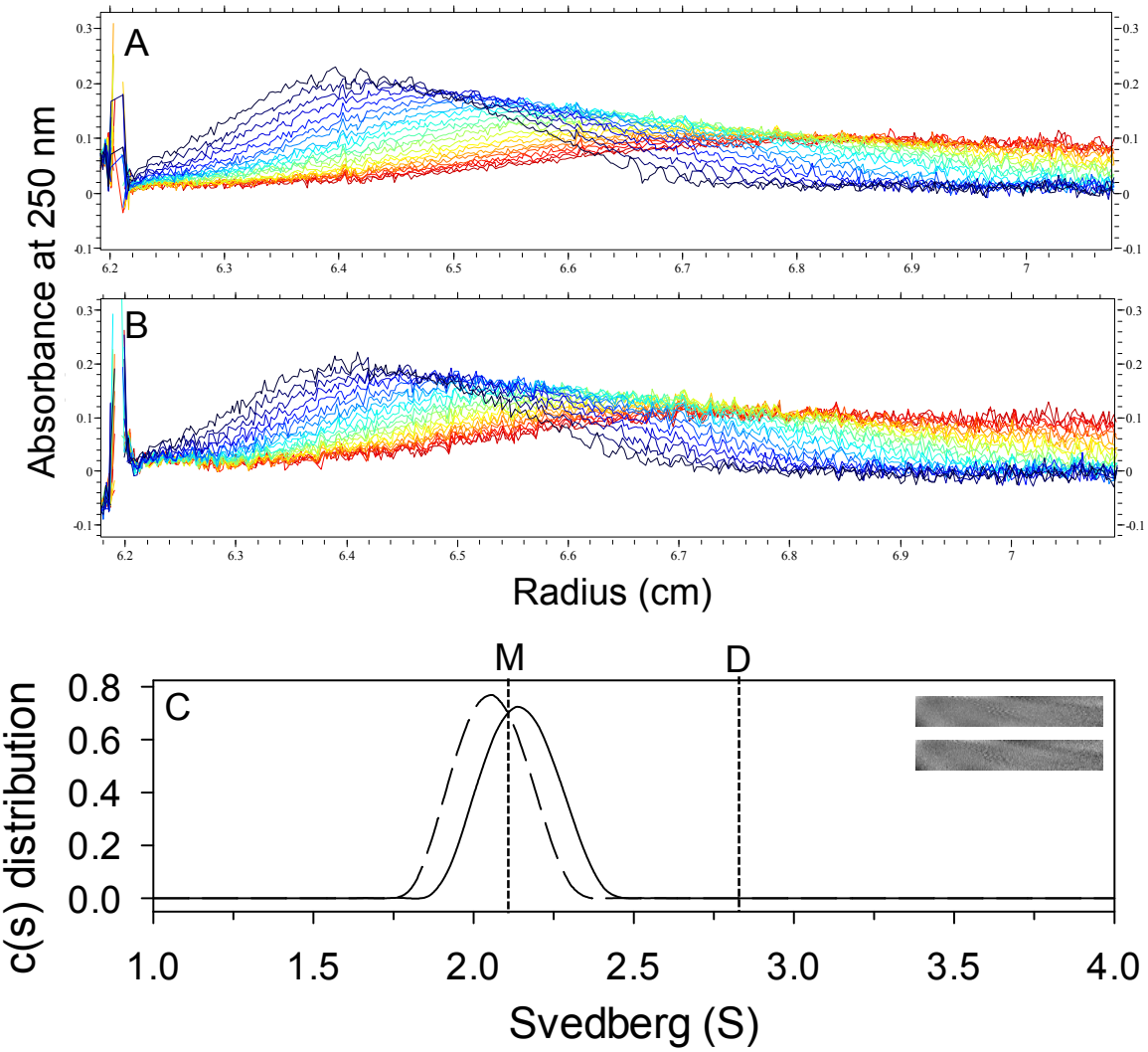
Containing 1 supplement figure



Supplemental Figure 1. AEC pattern of the N-strept tagged R298A mutant of SARS-CoV M^{pro}. The amount of protein used was 15 µl (2 mg/ml), and the total volume of the cell was 330 µl. A and B, show the trace of absorbance at 250 nm of the N-strept tagged R298A mutant during the experiments at phosphate buffer (pH 7.6) (A) and a substrate concentration of 200 µM (B), respectively. C, shows the continuous c(s) distributions of the proteins from the best-fit analysis of the 250 nm results. Solid and dashed lines show the results in phosphate buffer (pH 7.6) and in the substrate concentration of 200 µM, respectively. Two straight dotted lines indicate the positions of the monomer (M) and dimer (D). Insets show the residual bitmap of the raw data and the best-fit results.