

## *Supplementary Materials*

# **Characterization of the Specific Mode of Action of a Chitin Deacetylase and Separation of the Partially Acetylated Chitosan Oligosaccharides**

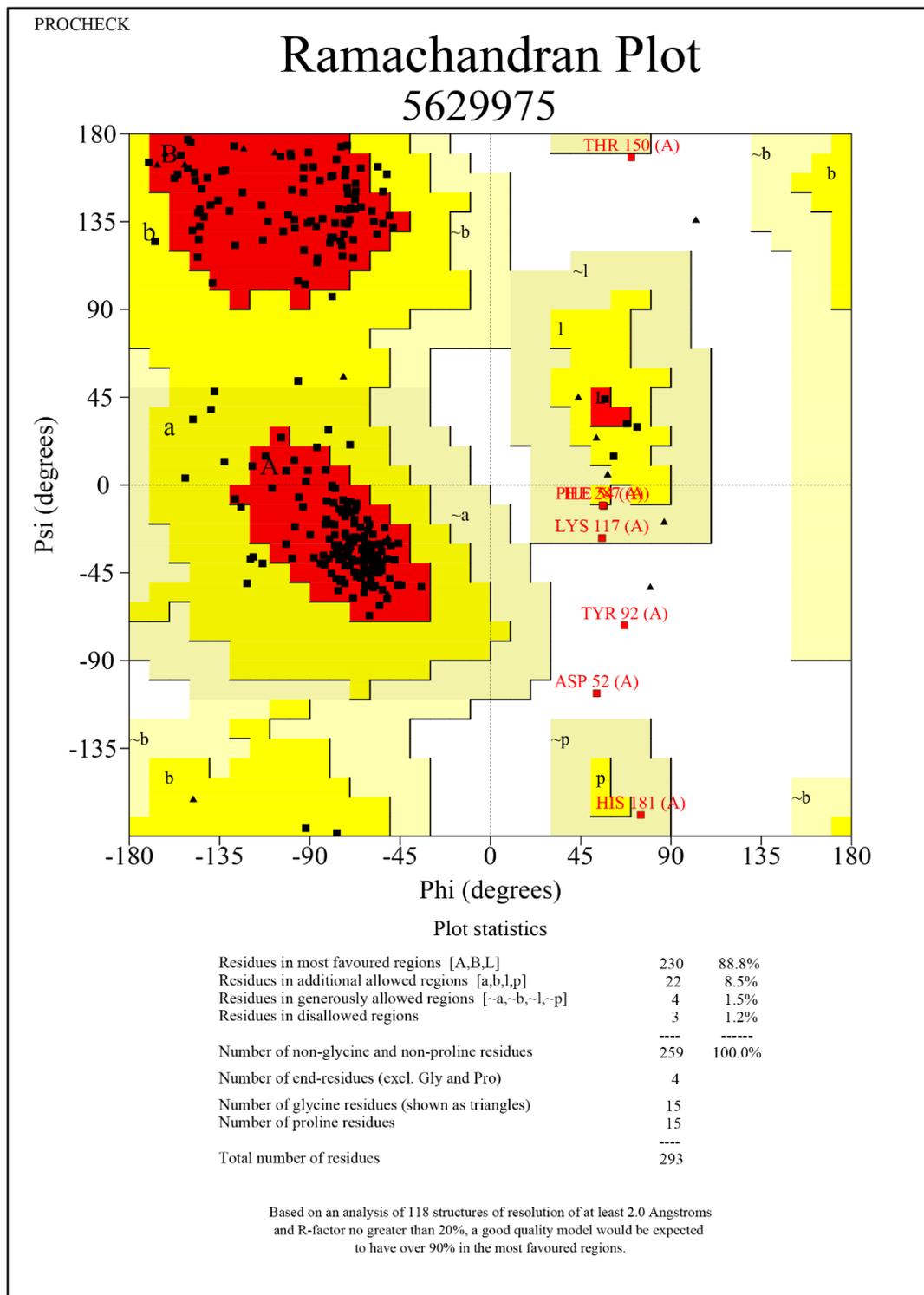
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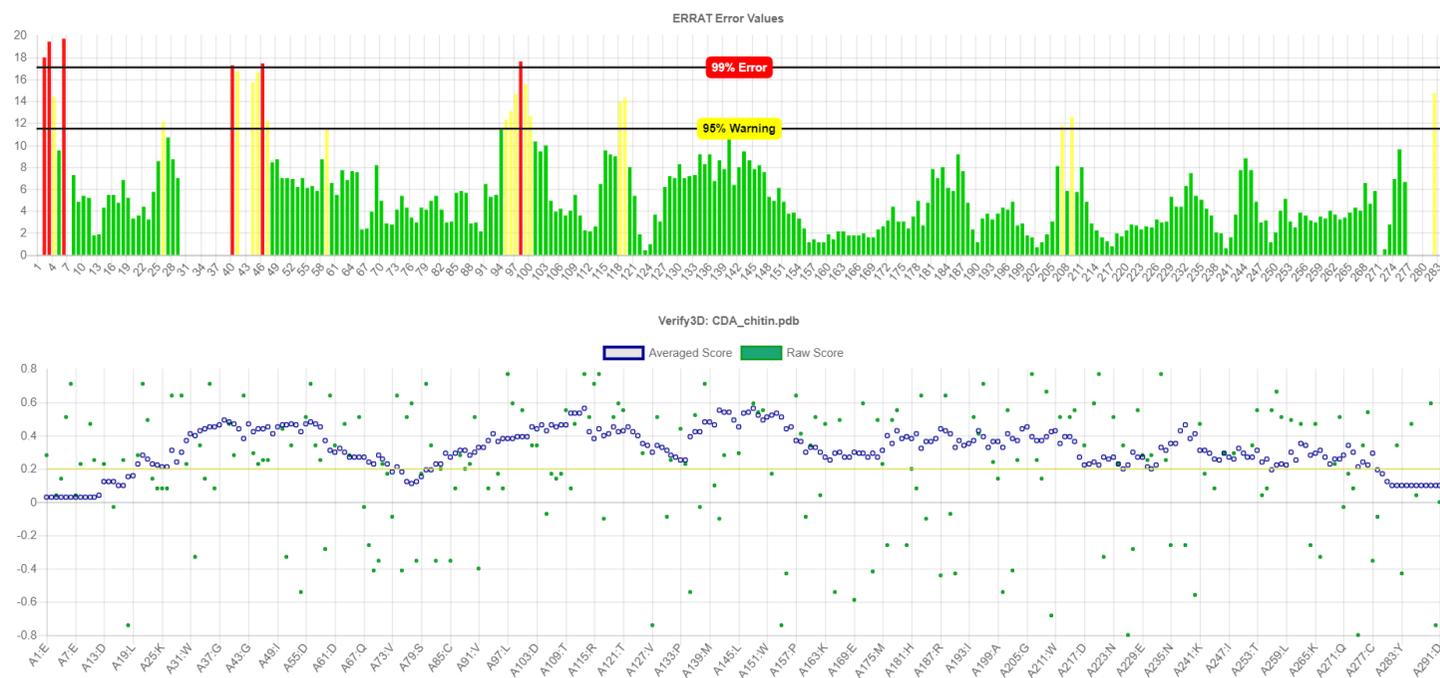
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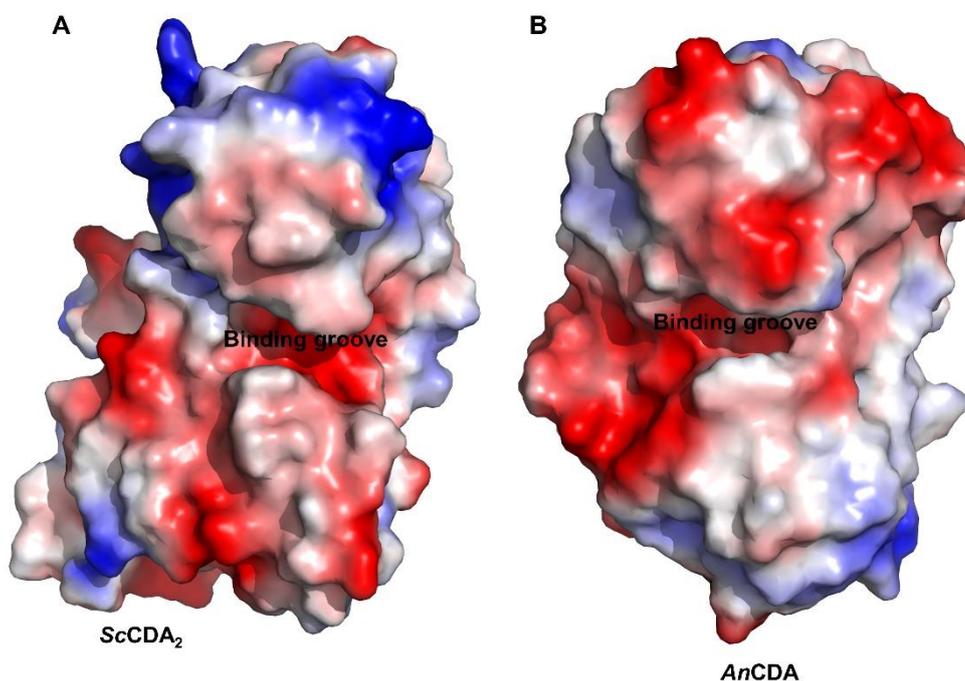
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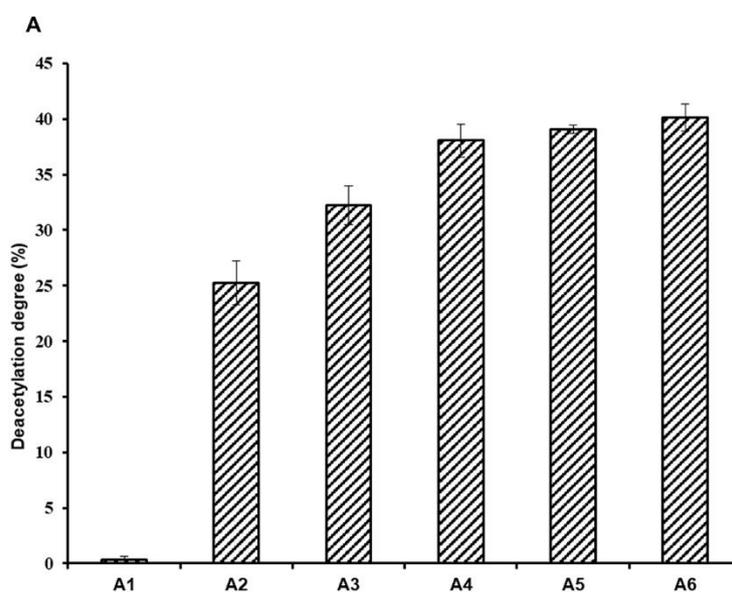
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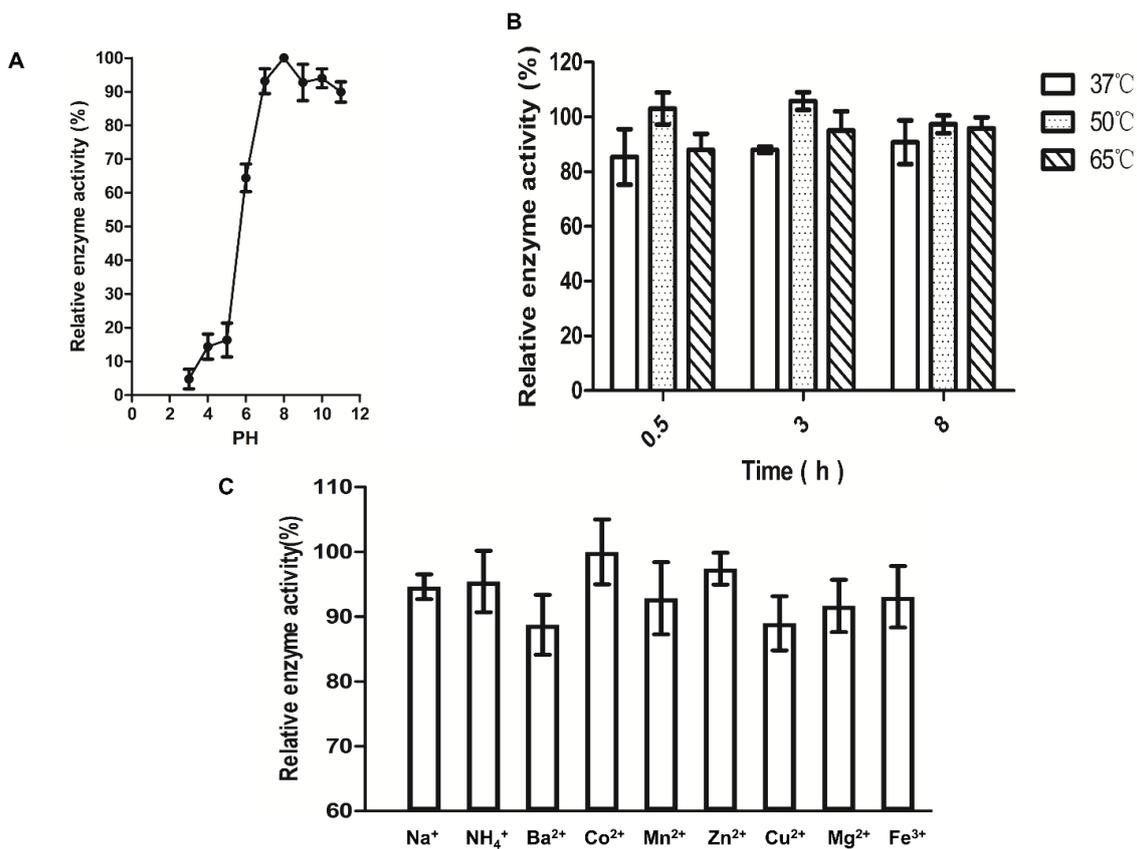
**Figure S1.** The model was further evaluated for protein geometry by SAVES (A comprehensive measurement website for the quality of a protein structure). 97.3% Residues in additional allowed regions and 85.57% of the residues have averaged 3D-1D score  $\geq 0.2$ , and the quality factor is 91.2214.



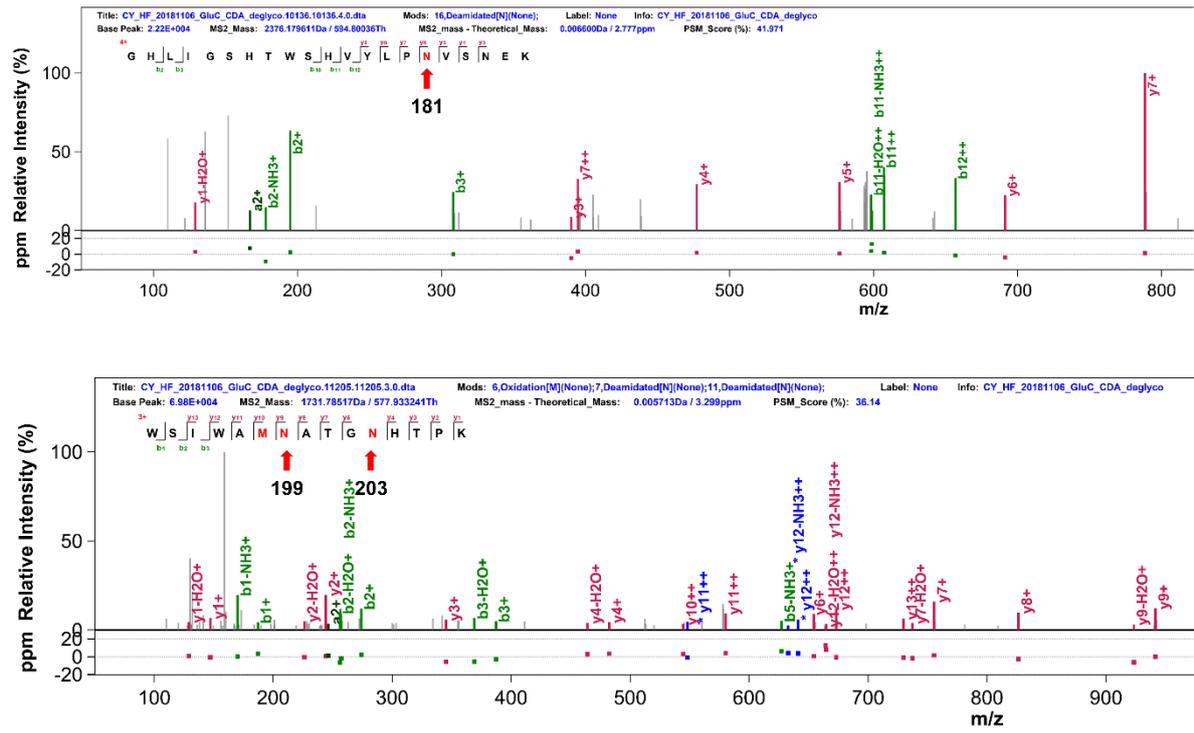
**Figure S2.** Compare deacetylase charge distribution. These pictures show the surface charge distributions of chitin deacetylase from *Saccharomyces cerevisiae* (ScCDA<sub>2</sub>) and chitin deacetylase from *Aspergillus Nidulans* (AnCDA, PDB ID: 2Y8U) calculated using ABPS (The Adaptive Poisson-Boltzmann Solver to generate electrostatic surface displayed) in VMD. Red represents a negative charge and blue represents a positive charge.



**Figure S3.** ScCDA<sub>2</sub> substrate specificity on chitin oligomers. 0.5mg/ml chitin oligomers as substrates were incubated with 0.75  $\mu$ M ScCDA<sub>2</sub> at 37  $^{\circ}$ C for 30 min. The data represents the mean SD values of the results from three independent experiments.



**Figure S4.** Effects of pH, temperature and metal ion on enzyme activity. (A) The optimum pH was determined by incubating the 0.75  $\mu$ M ScCDA<sub>2</sub> with A4 chitin oligomer (0.5 mg/mL) for 60 min at pH 3–11 in universal buffer. (B) To obtain the optimal temperature, the enzyme (075  $\mu$ mol) was incubated for 60 min at different temperatures in 50mM Tris-HCl buffer (pH 8.0) containing chitin oligomer mixture (0.5 mg/mL) as a substrate. (C) Relative activity with different metal cations. Proteins were incubated with 1 mm metallized cations, and activity was determined in 50 mM Tris-HCl buffer (pH 8.0) using 0.5 mg/mL A4 as a substrate.



**Figure S5.** Spectra of N-glycosylation of ScCDA<sub>2</sub>. Mass spectrometry showed that ScCDA<sub>2</sub> have N-glycosylation post-translational modification at Asn 181, Asn 199 and Asn 203.