# Supporting information

### S1.1. Experimental procedures for determination of ChiW-CD properties

The enzyme assays were performed according to the method used for ChiW-SLHd (Itoh *et al*., 2014) by monitoring the increasing in absorbance at 405 nm after the enzymatic reaction was terminated, which corresponds to the releasing *p*-nitro phenol (pNP) from pNP-*N*,*N*'-diacetyl-D-chitobiose [pNP-$(GlcNAc)_2$] (Seikagaku Kogyo, Tokyo, Japan). The reaction was performed at 310 K with 0.2 *M* of sodium acetate buffer at pH 5.5, 0.1 m*M* pNP-$(GlcNAc)_2$ and 10 n*M* enzyme, and was terminated by mixing the solution with 0.5 *M* NaOH. One unit of enzyme activity was equivalent to the amount of enzyme required to release 1 μmol of pNP in 1 min.

After the electrophoretic transfer to a PVDF membrane (Immobilon-PSQ; Millipore, Billerica, MA, USA), the N-terminal amino acid sequence of the recombinant ChiW-CD was determined by Edman degradation using the Procise 491HT protein sequencing system (Life Technologies, Carlsbad, CA, USA).

Structural conformation of purified ChiW-CD was also evaluated by far-UV circular dichroism spectroscopy using a Jasco J-805 spectropolarimeter at 190–250 nm with a quartz cell having a 1 mm path length. The enzyme (1 μ*M*) was prepared in a buffer containing 10 m*M* sodium phosphate at pH 7.4. The quadruplicate measurements were performed at room temperature under nitrogen flow. The results were expressed as ellipticity [$\theta$] (deg $cm^2$ $dmol^{-1}$) and were analyzed for assessing the secondary structure content of ChiW-CD by using the *CDPro* analysis software and the *SELCON3* program (Sreerama *et al.*, 1999).

### S1.2. Results of enzymatic activity, N-terminal sequencing analysis and secondary structural contents of ChiW-CD

The activity (0.74 U $mg^{-1}$) of ChiW-CD for pNP-$(GlcNAc)_2$ was nearly equivalent to that of ChiW-SLHd (0.71 U $mg^{-1}$) (Itoh *et al.*, 2014). The molecular mass of the enzyme was estimated at approximately 95 kDa (Fig. 1*b*), which was a little smaller than the calculated molecular mass based on its deduced amino acid sequence (98 kDa). The N-terminal amino acid sequence of the protein was determined to be $NH_2$-MNHKVH, which matched to the predicted sequence. The circular dichroism spectrum (Fig. S1) exhibited a negative peak around 220 nm, indicating that the recombinant ChiW was folded with some α-helix and β-strand structures. The estimated of α-helix and β-strand content of ChiW-CD was 21.4 and 27.0%, respectively. The amino acid sequences of ChiW-CD catalytic

domains were similar to that of chitinase A1 from *Bacillus circulans* WL-12 with approximately 42% identity (PDB: 1ITX; Matsumoto *et al*., 1999). The chitinase A1 TIM-fold consisted of approximately 35% α-helix and 18% β-strand structures. Therefore, the remaining regions of ChiW-CD should be almost exclusively β-stranded structures.

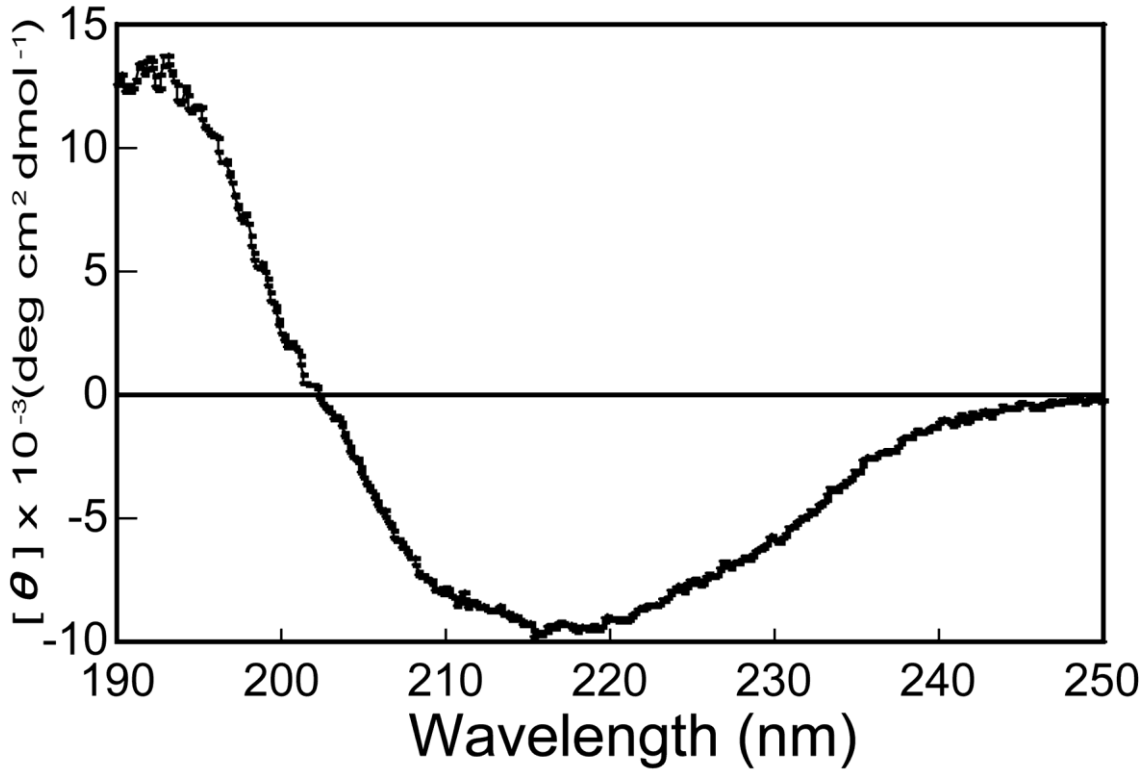


**Figure S1** Circular dichroism spectra of ChiW-CD. The path-length of the cell was 1 mm for measurements from 250 to 190 nm. The enzyme (1 μM protein concentration) was prepared in a buffer containing 10 m*M* sodium phosphate at pH 7.4.

#### References

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