**Table S1** Sequence identities of *Of*ChtI-CAD with other structure-known chitinases from different species.

| Species | PDB | Identity (%) | RMSD |
|---|---|---|---|
| *Homo sapiens* | 3fxy | 43 | 0.90 |
| | 1guv | 40 | 1.07 |
| *Nicotiana tabacum* | 3alf | 30 | 1.79 |
| *Bacillus circulans* | 1itx | 29 | 1.07 |
| *Arabidopsis thaliana* | 3aqu | 27 | 1.56 |
| *Serratia marcescens* | 1e15 | 27 | 1.80 |
| | 1ctn | 27 | 1.53 |
| *Lactococcus lactis* | 3ian | 27 | 2.74 |
| *Aspergillus fumigatus* | 1w9p | 27 | 1.56 |
| | 2y8v | 26 | 2.87 |
| *Vibrio harveyi* | 3b8s | 26 | 1.26 |
| *Yersinia entomophaga* | 3oa5 | 26 | 1.80 |
| *Bacteroides thetaiotaomicron* | 3co4 | 25 | 2.20 |
| *Coccidioides immitis* | 1d2k | 25 | 1.16 |
| *Arthrobacter tad20* | 1kfw | 24 | 1.52 |
| *Clonostachys rosea* | 3g6l | 23 | 1.25 |
| *Moritella marina* | 4hmc | 22 | 2.67 |
| *Bacillus cereus* | 3n15 | 22 | 2.67 |
| *Crocus vernus* | 3sim | 21 | 2.47 |

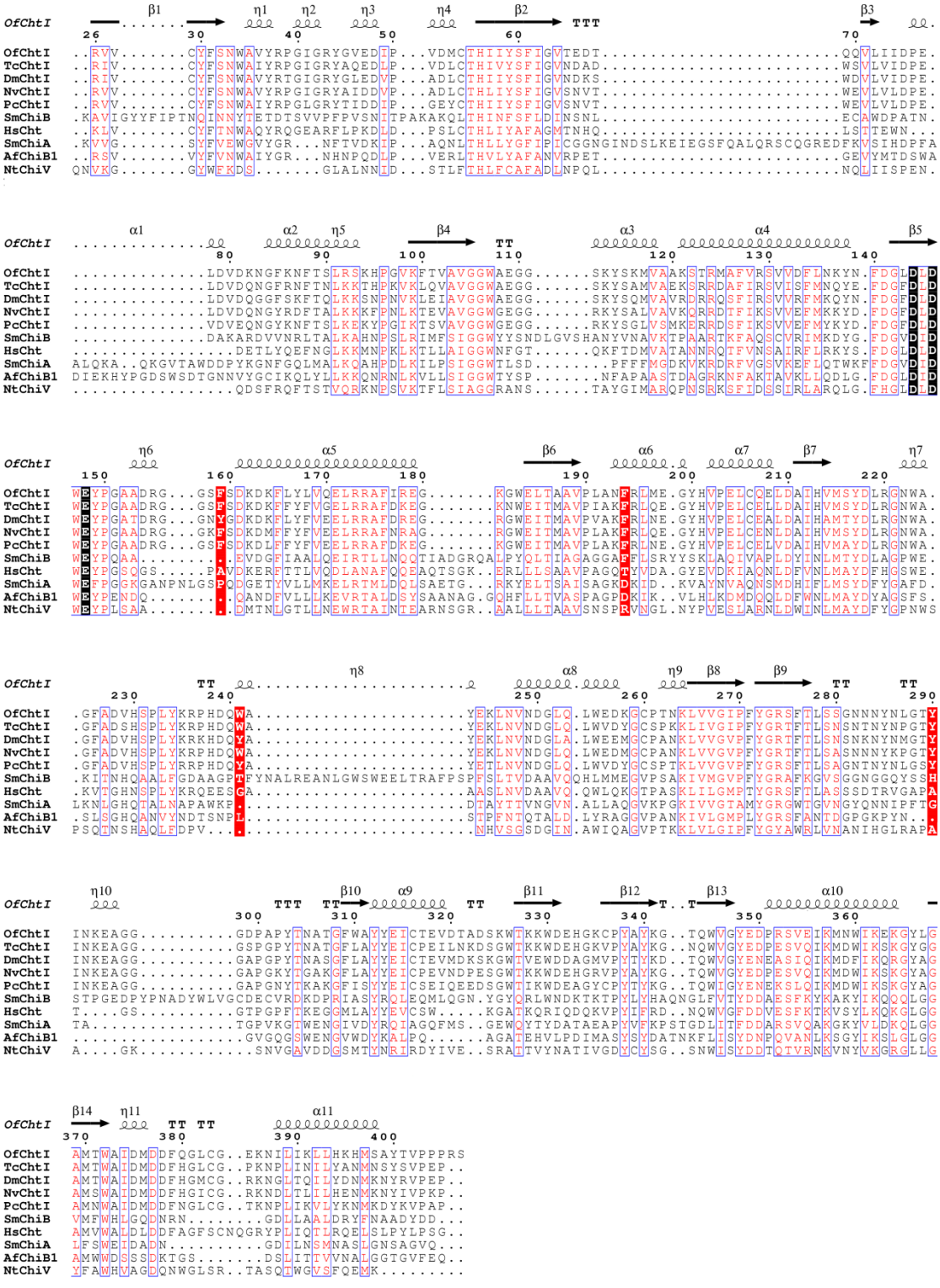


**Figure S1**

Structure-based sequence alignment of *Of*ChtI-CAD with other GH18 chitinases from various species. The insect Group I chitinases include *Of*ChtI from the lepidopteran insect *Ostrinia furnacalis* (Genbank ABB97081, PDB entry 3w4r), *Pc*ChtI from the hemipteran insect *Poophilus costalis* (Genbank AFW03959), *Nv*ChtI from the hymenopteran insect *Nasonia*

*vitripennis* (Genbank NP_001155084.1), *Tc*ChtI from the coleopteran insect *Tribolium castaneum* (Genbank AAV74190), and *Dm*ChtI from the dipteran insect *Drosophila melanogaster* (Genbank AAF54987). The other known chitinases include *Sm*ChiA (PDB entry 1ctn) and *Sm*ChiB (PDB entry 1e15) from *Serratia marcescens*, *Hs*Cht from *Homo sapiens* (PDB entry 1lg1), *Af*ChiB1 from *Aspergillus fumigatus* (PDB entry 1w9p), and *Nt*ChiV from *Nicotiana tabacum* (PDB entry 3alf). The secondary structure elements of *Of*ChtI-CAD are shown and labeled. The conserved catalytic residues are labeled with black background blocks. The four aromatic residues, which form a hydrophobic plane on the surface of *Of*ChtI-CAD, are highly conserved in the insect Group I chitinases but are absent in those from other species. They are labeled with red background blocks. The sequence alignment was generated by PROMALS3D (Pei *et al.*, 2008) and the picture was generated by ESPript (Gouet *et al.*, 2003).

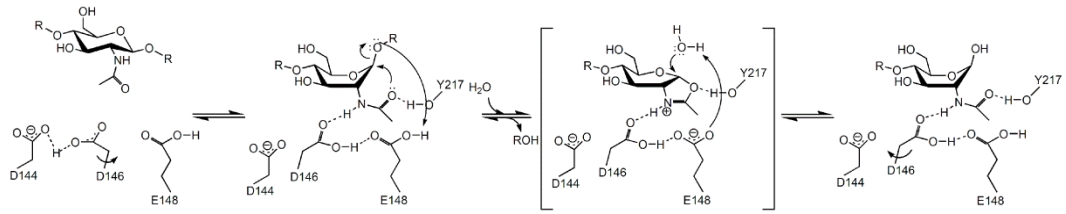


**Figure S2**

Proposed catalytic mechanism of family 18 chitinases, based on mechanism deduced by van Aalten *et al.* (2001).

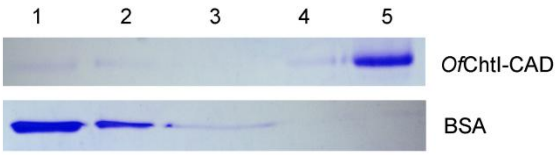


**Figure S3**

The binding of *Of*ChtI-CAD to crystalline α-chitin. The mixtures (50 µl) contained 10 µg *Of*ChtI-CAD and 1.0 mg crystalline α-chitin in 50 m*M* sodium phosphate buffer, pH 6.5. The mixtures were incubated at 303 K for 3 h and then centrifuged at 13 000*g* for 5 min. The supernatant was collected and the pellet was washed in 50 µl of 50 m*M* sodium phosphate buffer, pH 6.5, 50 m*M* sodium phosphate buffer, pH 6.5, containing 1*M* NaCl, and 0.1 *M* acetic

acid in turn. After centrifugation of each wash, the supernatants were collected. Finally, the pellet and all collected supernatants were subjected to 10% SDS-PAGE. Lane 1, unbound fraction; lane 2, wash fraction in 50 m*M* sodium phosphate; lane 3, wash fraction in 50 m*M* sodium phosphate containing 1*M* NaCl; lane 4, wash fraction in 0.1 *M* acetic acid; lane 5, bound fraction. BSA was used as a control.