

A cDNA of putative chitinase from *Euglena gracilis*, designated EgChiA, encoded 960 amino acid residues, which is arranged from N-terminus in the order of signal peptide, glycoside hydrolase family 18 (GH18) domain, carbohydrate binding module family 18 (CBM18) domain, GH18 domain, CBM18 domain, and transmembrane helix. It is likely that EgChiA is anchored on the cell surface. The recombinant second GH18 domain of EgChiA, designated as CatD2, displayed optimal catalytic activity at pH 3.0 and 50 °C. The lower the polymerization degree of the chitin oligosaccharides [(GlcNAc)<sub>4-6</sub>] used as the substrates, the higher was the rate of degradation by CatD2. CatD2 degraded chitin nanofibers as an insoluble substrate, and it produced only (GlcNAc)<sub>2</sub> and GlcNAc. Therefore, we speculated that EgChiA localizes to the cell surface of *E. gracilis* and is involved in degradation of chitin polymers into (GlcNAc)<sub>2</sub> or GlcNAc, which are easily taken up by the cells.