

Functional characterization of a class III acid endochitinase from the traps of the carnivorous pitcher plant genus, *Nepenthes*

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Fig. S1. Amino acid sequence alignment of endochitinases from various species. The amino acid sequence alignment and the deduced consensus sequence was generated using Clustal X involving the plant species *Pyrus pyrifolia*; *Lupinus albus*; *Cucumis sativus*; *Nepenthes rafflesiana*; *Beta vulgaris*; *Vitis vinifera*; *Oryza sativa*.

