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*.

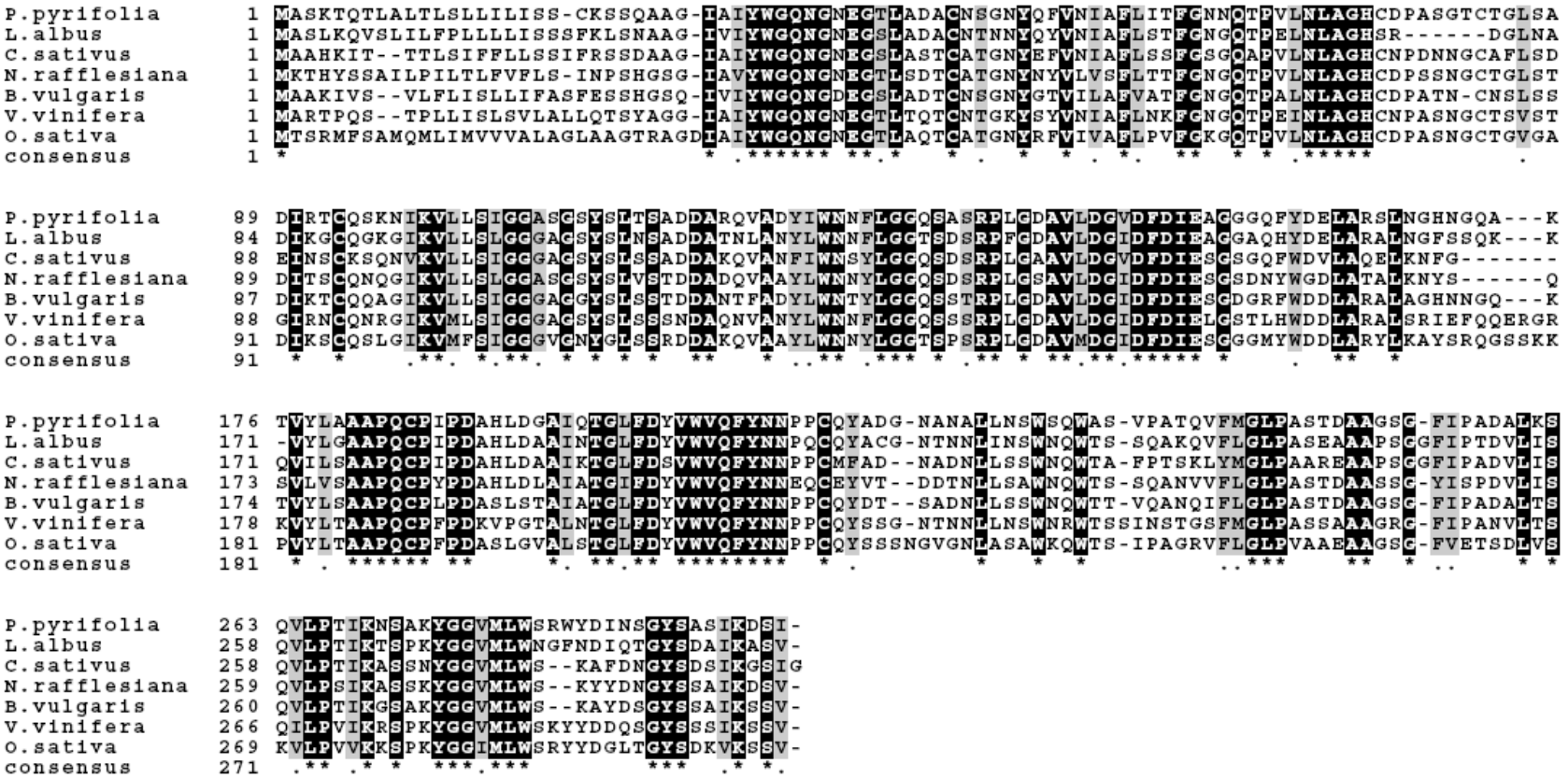
P.pyrifolia
L.albus
C.sativus
N.rafflesiana
B.vulgaris
V.vinifera
O.sativa
consensus

Fig. S1