

A phylogenetic tree of HyPRP sequences rooted using the *Arabidopsis thaliana* AtLTP2 (At2g38530) sequence as outgroup. NJ (top) and ML (bottom) bootstrap values above 50 % are shown at branches of the tree (constructed by the NJ method using Treecon). The outgroup sequence was added manually to the alignment of HyPRP sequences, using the invariant cysteine positions and published 8CM domain alignments as a guide. The tree was then calculated from a subset of HyPRP sequences from Figure 4, selected in order to keep representatives of all branches with a significant support in trees constructed using both NJ and ML method; in addition, several sequences whose inclusion would have introduced gaps in the alignment and thus reduced the amount of usable data have been excluded. HyPRPs with long N-terminal domains are marked in **bold**, the clade of C-type HyPRPs is boxed. Bootstrap values in **blue** correspond to an otherwise identical tree calculated after omission of the outlier sequences with long N-terminal domains (also shown in **blue**, ML values from only 100 replicates), indicating that these probably rapidly evolving sequences were responsible for most of the uncertainty in the delimitation of the C-type clade.

