

Supplementary file 2. Amino acid sequences of *bona fide* PAC domain proteins.

Originally, the accession numbers of the onekp database were of the following type: #onekp:WZYK_scaffold_2017325 Bazzania_trilobata. They have been simplified for more convenience, as follows: >YFGP_2017325_Bazzania_trilobata.

In the protein name, “.nd” means that the type of protein could not be determined because the amino acid sequence of the protein is not complete; “.1”, “.2”, “.3”, “.4” refers to the type of protein (see Figure 2).

Sequences in blue were not retained for the phylogenetic analysis because their percentage of identity with other PAC domain sequences of the same plant was higher than 85%.

Sequences in violet were not retained for phylogeny analysis because in some cases, only one/a few species were selected for a given plant family.

Sequences in brown were not retained because they were incomplete and it was not possible to predict either their sub-cellular localization or the presence of additional functional domains.

Marchantiophyta

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Isoetales

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