Remorins are plant-specific proteins that may act as molecular scaffolds for signalling complexes during plant innate immunity and microbial invasion of host cells. Some members of this protein family associate with membrane rafts, are highly phosphorylated, can bind DNA and form filaments \textit{in vitro}. All remorins exhibit an evolutionary divergent N-terminal region and a conserved C-terminal region harbouring a predicted coiled-coil motif and a putative plasma membrane (PM) anchoring motif. Analyses of \textit{A. thaliana} Remorin AtREM1.3 structure by CD spectroscopy, limited proteolysis and MS mapping of resistant fragments indicate that its divergent N-terminal region is intrinsically disordered. Furthermore, formation of $\alpha$-helical structure is induced by increasing concentrations of TFE. In order to assess a possible role of intrinsic disorder in this protein we studied different truncation variants related to their ability to act as phosphorylation substrates for kinases involved in innate immune response, to form filaments, to bind DNA and to interact with nuclear localized Importin $\alpha$ isoforms in yeast-two-hybrid and Co-immunoprecipitation studies. We have localized the different AtREM1.3 truncation variants \textit{in planta} showing that the full-length protein localizes to the PM, while variants devoid of the PM anchoring motif localized to the cytoplasm and/or nucleus. Interestingly, co-expression of the full-length AtREM1.3 with Importin $\alpha$3 leads to co-localization in the nucleus. Here we discuss potential roles of intrinsically disordered AtREM1.3 inside the nucleus and its interaction with the nuclear import machinery.