

IN SILICO DOMAIN IDENTIFICATION AND SUBCELLULAR LOCALIZATION OF PEANUT ALLERGEN PROTEIN SEQUENCES

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The peanut (*Arachis hypogaea* L.) is one of the most cultivated oleaginous plant in the world despite some allergic reactions. In this work, proteins allergen sequences of *A. hypogaea* L. were collected from NCBI, and studied by domains identification (Pfam database) and subcellular localization tools (WolfPsort and MultiLoc). Four different domains were identified: Tryp_alpha_amyl (TAA), Cupin 1(C1), Profilin (PF) and Bet_v_I (BV). The TAA domain is found in Ara h 6 sequences and it's composed by the alpha tripsin amylase inhibitors. C1 domain is found in Ara h 1, 3 and 4 sequences and represents the conserved barrel domain of the 'cupin' super family. The PF domain is found in Ara h 5 and represents a small eukaryotic protein that binds the monomeric actin and BV domain, found in Ara h 8 and it's considered the major birch pollen antigen. The peanut sequences with TAA domain were predicted as extracellular, as *Glycine max* and *Medicago truncatula* L. Sequences with PF and BV domains were predicted as cytoplasm, as well as in legume model plants. However, C1 domain were related to vacuolar localization. Both subcellular prediction tools presented similar results. These results could help to understand allergen protein interactions, function and metabolic pathways.

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