

INSIGHT INTO SEQUENCE-STRUCTURE-FUNCTION RELATIONSHIP OF *CATHARANTHUS ROSEUS* RNA BINDING PROTEIN USING *INSILICO* APPROACH

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Abstract: RNA binding protein regulates numerous aspects of RNA metabolism such as pre-mRNA processing, transport and translation. This study describes sequence-structure-function relationship between the *Catharanthus roseus* and their homologs plant species through computational approach. After using sequence analysis techniques, it was observed that only 11 plant species showed higher similarity with RNA binding protein of *C. roseus*. Also, multiple sequence alignment illustrate only two conserve regions between *C. roseus* and their respective homologs plant species. Hence, the structural molecular model of the RNA binding protein was developed through homology modeling using the software MODELLER (9v5). Using PROCHECK and VERIFY-3D, the energy of constructed models was minimized and qualities of each models were evaluated. The corresponding Ramachandran plot specify 93.70% amino acid residues were in the most favoured regions. Final predicted model structure was submitted to Protein Model Database having deposition number PM0080432.

Keywords: RNA binding protein; *Catharanthus roseus*, Homology modeling, RNA recognition motif

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