



Computational analysis of a predicted Patatin-Like Protein from Solanum Lycopersicum

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RNA analysis

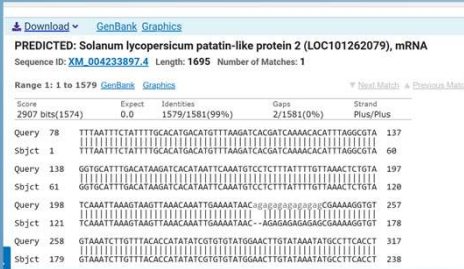
INTRODUCTION

Bioinformatics enables functional annotation of unknown DNA sequences using computational tools. In this study, an unknown DNA sequence was analyzed through an integrated pipeline to identify its gene, mRNA features, protein properties, evolutionary relationships, and interaction networks.

DNA sequence analysis

Gene identified by given sequence is Patatin- Like Protein 2 From Solanum Lycopersicum

BLASTn result



The Patatin-like protein 2 (508 aa) shows an instability index of 52.93, which is above the threshold of 40, indicating that the protein is predicted to be unstable in vitro. Although it has a moderately high aliphatic index (66.55)—suggesting reasonable thermal tolerance—the high instability index dominates the prediction. The basic pI (8.95) conditions

Subcellular Location

UniProt Annotation GO Annotation

Vacuole Automatic Annotation

Keywords

Cellular component

#Vacuole Automatic Annotation

Phylogenetic analysis

Phylogenetic Tree

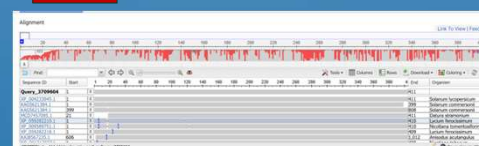


• All sequences cluster into a single clade, indicating a shared common ancestor.

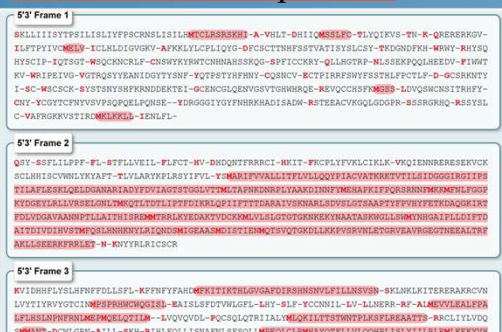
• XP_004233945.1 and KAG5621384.1 are the most closely related, showing minimal divergence.

• KAJ8567235.1 is the most divergent, suggesting greater evolutionary distance.

MSA



DNA translation profile

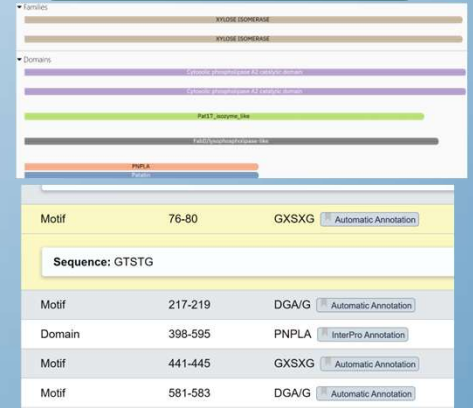


GC content and repeats

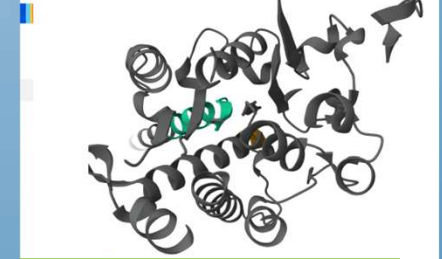
Total count, all bases:	1658
Adenine (A) count:	530
Thymine (T) count:	499
Guanine (G) count:	323
Cytosine (C) count:	306
%G-C content:	37.9

Protein Analysis

No of amino acids 508
Theoretical pI 8.95
Molecular weight 59265.39
Aliphatic index 66.55
Instability index 52.93



Secondary structure



Protein-protein interactions



Patatin-like protein 2 (PLP2) is a phospholipase that hydrolyzes membrane phospholipids into lipid signaling molecules. It plays roles in lipid metabolism, cellular stress responses, and inflammatory processes. In plants and microbes, PLP2 homologs are involved in defense against pathogens. Dysregulation of PLP2 can affect metabolic and inflammatory disorders, making it a target for biochemical research.

CONCLUSION

Computational analysis indicates that the predicted *patatin-like protein from *Solanum lycopersicum* is a conserved functional protein. Phylogenetic analysis places it closer to **plant and higher eukaryotic homologs, supporting a **shared evolutionary origin. The presence of conserved regions typical of patatin-like phospholipases suggests a role in **lipid metabolism and stress-related signaling. Overall, the in-silico results support its **biological relevance and evolutionary conservation, providing a strong basis for future **experimental validation.

References

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