In silico analysis of proteins of *Curcuma aromatica* Salisb

K.Mahalakshmi

Department of Biotechnology, Faculty of Science and Humanities
SRM University, Kattankulathur-603203

Abstract: From ancient times, many scientists have been exploring the nature, specifically plants to discover novel drugs which are used to treat various diseases. *Curcuma aromatica* Salisb. Commonly known as Wild Turmeric is indulged in treatment of various diseases related to skin, cardiovascular and respiratory system. So the medicinal plants have a promising role in to prevent and as well as to cure the diseases. In this study three proteins of *Curcuma aromatica* were analysed using different bioinformatics tools. By using the tools like protparam (Expasy), SOPMA, SOSUI, TMHMM, structural predictions and functional characterisation were done. The primary information like molecular weight, pI etc., were obtained by protparam and the secondary structures like alpha helix, beta strand were obtained by SOPMA. Transmembrane proteins were identified by SOSUI and TMHMM. Homology modelling was done using swiss model and finally Rasmol was used to visualise the tertiary structure of the proteins.
Keywords: *Curcuma aromatica*, Expasy, Swiss model, Rasmol.

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