

10th International Congress on

STRUCTURAL BIOLOGY

October 18-19, 2018 Helsinki, Finland

Bioinformatics analysis of novel 18s ribosomal RNA genomic sequence of mentha spicata

Abdul Nasir, Adnan Akbar and Samina Shakeel
Quaid-I-Azam University, Pakistan

Ribosomal RNAs (rRNAs) are universally distributed and known for their functional equivalence among all the known organisms. Analysis of small- subunit rRNAs (16-18S rRNAs) can permit the accurate statistical measurement of a broad range of phylogenetic relationships due to highly conserved sequences. *Mentha spicata* (Spearment) is a Medicinal plant belongs to family Lamiaceae used in the treatment of fevers, bronchitis, chills, cramps, chronic gastritis and common cold. Different Bioinformatics tools i.e Mega5, T-coffee alignment, Pepstats, Signal P4.1, Pepwindow, NEBV 2.0 Cutter, NetPhos 2.0, SOPMA, Phyre2, BioEdit and Prosite, were used to identify Phylogeny, homology, Physiochemical properties, Signal peptide, Hydropathy Plot, Restriction mapping, Phosphorylation sites, secondary structure, Protein 3D structure, Nucleotide composition and Pattern recognition respectively.

Notes: