



Bioinformatics Poster

Introduction:

Cystic Fibrosis gene in humans encoding transmembrane conductance regulator that acts as vital component for maintaining respiratory and gastrointestinal health

Accession ID: M28668.1

Hit 1:

Accession: M28668.1
Identity: 100%
E value: 0.0

Description: Human cystic fibrosis mRNA, encoding a presumed transmembrane conductance regulator (CFTR).

Hit 2

Accession: NM_000492.4
Identity: 100%
E value: 0.0

Description: Homo sapiens CF transmembrane conductance regulator (CFTR), mRNA.

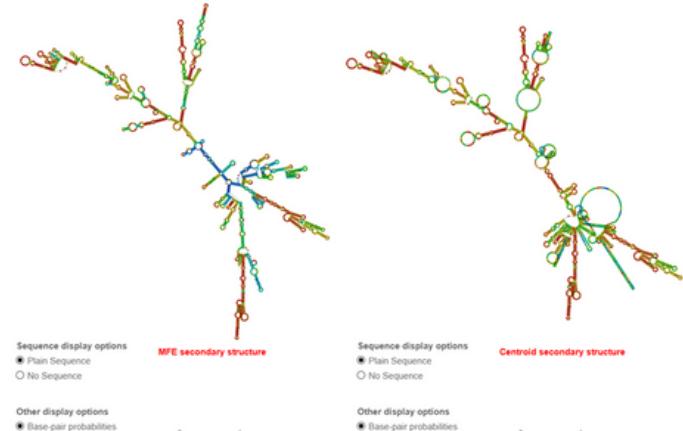
Hit 3

Accession: XM_055114832.2
Identity: 99.64%
E value: 0.0

Description: PREDICTED: Pan paniscus CF transmembrane conductance regulator (CFTR), mRNA.

RNA Fold Image

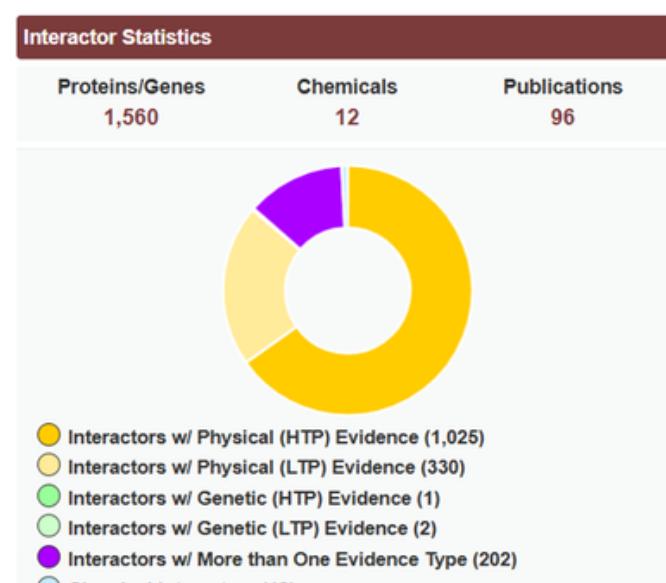
Graphical output
You may look at the interactive drawing of the MFE structure below. If you do not see the interactive drawing and you are using Internet Explorer, please install the Adobe SVG plugin.
pairing probabilities: The structure below is colored by base-pairing probabilities. For unpaired regions the color denotes the probability of being unpaired.



Explanation of Stability

The RNAfold WebServer analysis reveals two primary conformations: the Minimum Free Energy (MFE) structure, which represents the most thermodynamically stable state, and the Centroid structure, which reflects the overall Boltzmann ensemble. The complex branched folding—characterized by numerous hairpins and multiloops—is color-coded by base-pairing probability, with red regions indicating high confidence. This intricate structural arrangement suggests a highly stable and functional RNA molecule capable of complex regulatory interactions.

STRING Interaction Map



Evolutionary Relationship:

The phylogenetic tree illustrates high evolutionary conservation of the human CFTR protein, showing a monophyletic group with close mammalian homologs like NP_001007144.1. While some lineages exhibit greater divergence, the overall tight clustering and short branch lengths across species signify that the CFTR protein's core structural framework is under strong selective pressure to maintain its vital biological functions.

Conclusion:

The analysis confirms that the identified 552-amino acid protein is a critical regulator of cellular ion homeostasis and mucus hydration. Our findings highlight that the protein's correct folding and localization to the apical plasma membrane are essential for preventing the obstructive secretions characteristic of Cystic Fibrosis. Furthermore, the high degree of evolutionary conservation observed across mammalian lineages underscores the vital biological importance of the CFTR structural framework. Ultimately, this ORF represents a central functional hub necessary for maintaining human physiological balance.

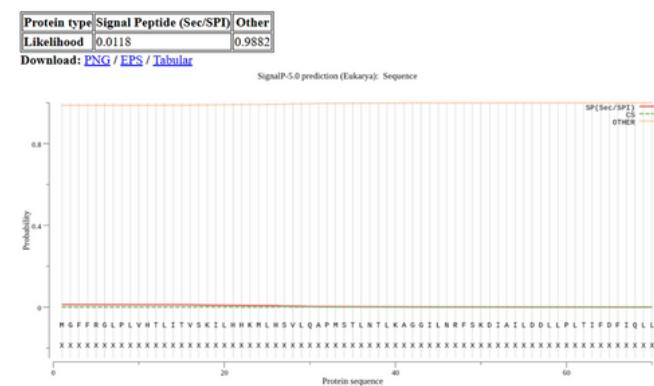
ORF Map



Reason for selecting Final ORF

ORF1 was selected as the most likely functional gene because it is significantly longer than other candidates, spanning 1,659 nucleotides and 552 amino acids. This length minimizes the probability of it occurring by random chance and suggests a robust protein-coding sequence. Additionally, ORF1 exhibits high coding density, occupying the majority of the 2,240 nt sequence on the primary positive strand. By starting with a standard 'ATG' codon and maintaining a continuous reading frame without premature stops, it fulfills the structural requirements of a functional gene, whereas shorter, nested ORFs are likely non-coding biological "noise."

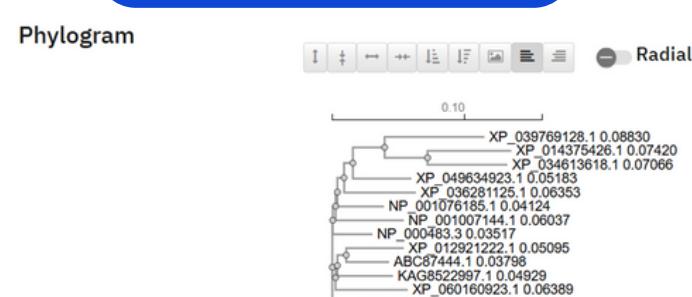
Subcellular Localization



Justification of Predicted Location:

Based on the sequence analysis of the 552-amino acid ORF1, the protein is predicted to be localized at the Apical Plasma Membrane of epithelial cells. This location is justified by the presence of hydrophobic alpha-helices within the Transmembrane Domain (TMD1), which facilitate insertion into the lipid bilayer. After being synthesized in the Endoplasmic Reticulum and processed through the Golgi apparatus, the protein is trafficked via vesicles specifically to the apical surface facing the duct lumen. This positioning is essential for its functional role in chloride ion transport and the maintenance of osmotic balance in the lungs and digestive tract.

Phylogenetic Tree



DNA-> Protein translation file

Sequence 1: NT_000014.11:1123252-1123252
Sequence 2: NT_000014.11:1123252-1123252
Sequence 3: NT_000014.11:1123252-1123252
Sequence 4: NT_000014.11:1123252-1123252
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