



Computational Analysis Of Unknown DNA Sequence Using Integrated Bioinformatics Tools



INTRODUCTION

The CFTR gene encodes an ATP-regulated chloride channel that maintains ion and fluid balance in epithelial tissues. It has specialized domains which enable controlled ion transport, essential for normal lung and pancreatic function.

DNA ANALYSIS

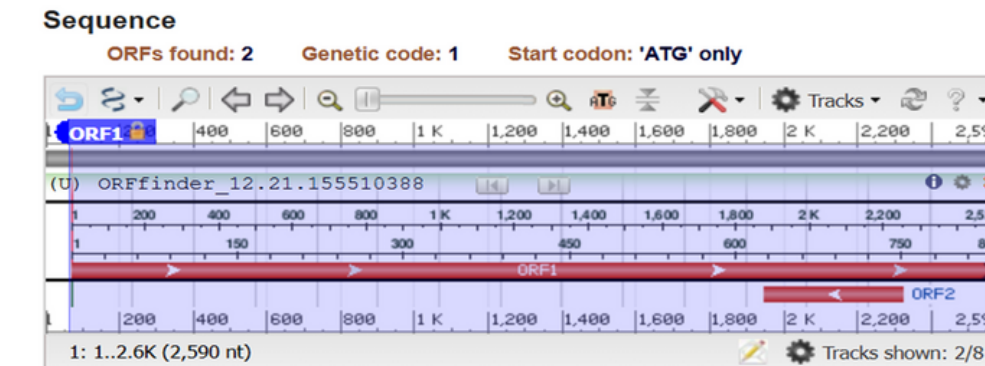
Descriptions	Graphic Summary	Alignments	Taxonomy
Sequences producing significant alignments			
Description	Scientific Name	Max Score	Total Score
Homo sapiens CF transmembrane conductance regulator (CFTR), mRNA	Homo s...	4783	4783
Human cystic fibrosis mRNA, encoding a pre...	Homo s...	4767	4767
Pan troglodytes CF transmembrane conductance...	Pan tro...	4745	4745

Homo sapiens CF transmembrane conductance regulator (CFTR), mRNA			
Sequence ID: NM_000492.4 Length: 6070 Number of Matches: 1			
Range 1: 1 to 2590			
Score	Expect	Identities	Gaps
4783 bits(2590)	0.0	2590/2590(100%)	0/2590(0%)
Query	1	GTAGTAGTCTTTGGCAATTAGAGAGCTTGAAGCCAGAGCGGCTTACGACAGGACCCAGCCAGC	60
Sbjct	1	GTAGTAGTCTTTGGCAATTAGAGAGCTTGAAGCCAGAGCGGCTTACGACAGGACCCAGCCAGC	60
Query	61	CCGAGAGACATGCAGAGTGCCTCTCGAAAAAGCCAGCGTTGTCTCCAACCTTTT	120
Sbjct	61	CCGAGAGACATGCAGAGTGCCTCTCGAAAAAGCCAGCGTTGTCTCCAACCTTTT	120
Query	121	CAGCTGACACAGACCAATTTTGAAGAAAGATACAGACAGCGCTTGAATTGTCAACAT	180
Sbjct	121	CAGCTGACACAGACCAATTTTGAAGAAAGATACAGACAGCGCTTGAATTGTCAACAT	180

blastn

The first hit represents fully annotated human CFTR mRNA sequence with 100% identity and coverage, making it the most accurate and biologically relevant match for the query

ORF FINDER



ORF 1 was selected because it is the longest continuous reading frame, containing a clear start and stop codon, making it the most likely to encode a functional protein

EXPASY

5'3' Frame 1
MQRSPLEKASVSKLFFSWTRPILRKGYRQRLSDIYQIPSVDSADNLSEKLEREWRELASKK
NPKLINALRRCFFWRFMFYGLFLYGEVTKAVQPLLGRITIASYDPDNKEERSIAIYLGIGLCIL
FIVRTLHLHPAIFGLHHIGQMRIAMFSLIYKTKLSSRVLDKISIGQLVSLNNLNKFDEGL
ALAHFVWIAPLQVALIMGLIWELLQASAFCGLGFLIVLALFQAGLGRMMKYRQDRAGKISERLV
ITSEMIENIQSVKAYCWEAEKMIENLRQTEKLTTRKAAYVRYFNSSAFFSGFFVFLVSLPY
ALIKGILRKIFTTISFCIVLRMAVTRQFFWAVQTYWYDSLGAINKIQDFLQKQEKYKLTLEYNLTT
EVVMENVTAFWEEGFGELFEKAKQNNNRKTSNGDLSFFSNFSLGTPLVKDINFKIERGQLLA
VAGSTGAGKTSILMVMIGELEPSEGGIKHSGRISFCQSQFSWIMPGTIKENIFGVSYDEYRYSV
IKACQLEEDISKFAEKDNIVLGEGGITLSGGQRARISLARAVYKDADLYLLDSFPGYLDVLTKE
IFESCVCKLANKTRILVTSKMEHLKKADKILLHGGSSYFYGTSELQNLQPDFSSKLMGCDSE
QDFSERRNSILTETLHRFSLLEGDAPVSWTETKKQSFQGTGEFGEKRKNSILNPINSIRKFSIVQ
KTPLOMNGIEEDSDEPLERRLSLVPDSEQGEAILPRISVISTGTPLQARRQSVNLMTSHVNOG
QNIHRKTTASTRKVSLAPQANLTEDIYSRRLSQETGLEISEEINEEDLKECFDDMESI

LOCALIZATION

Results of the k-NN Prediction

PSORT
k = 9/23
55.6 %: endoplasmic reticulum
22.2 %: vacuolar
11.1 %: nuclear
11.1 %: Golgi
>> prediction for 176664918422686 is end (k=9)

The protein is primarily localized to the ER, as indicated by its signal peptide, transmembrane domain, and ER-related predictions, suggesting it undergoes trafficking through the secretory pathway

DeepLoc

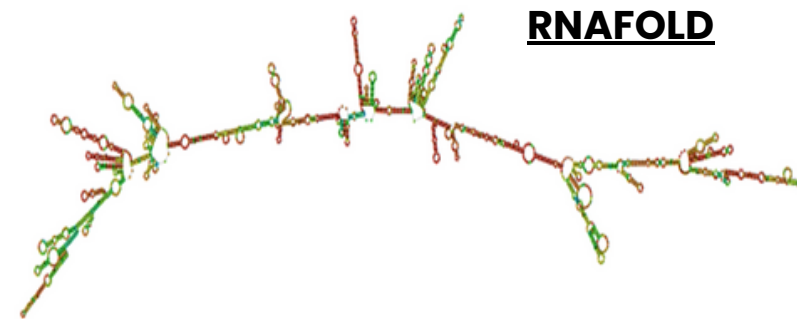
Sequence

Predicted localizations: Cell membrane, Lysosome/Vacuole

Predicted signals: Signal peptide, Transmembrane domain

Localization	Cytoplasm	Nucleus	Extracellular	Cell membrane	Mitochondrion	Plastid	Endoplasmic reticulum	Lysosome/Vacuole	Golgi apparatus	Peroxisome
Probability	0.0677	0.1588	0.0357	0.6748	0.1385	0.0196	0.4558	0.6736	0.4227	0.2516

RNA ANALYSIS

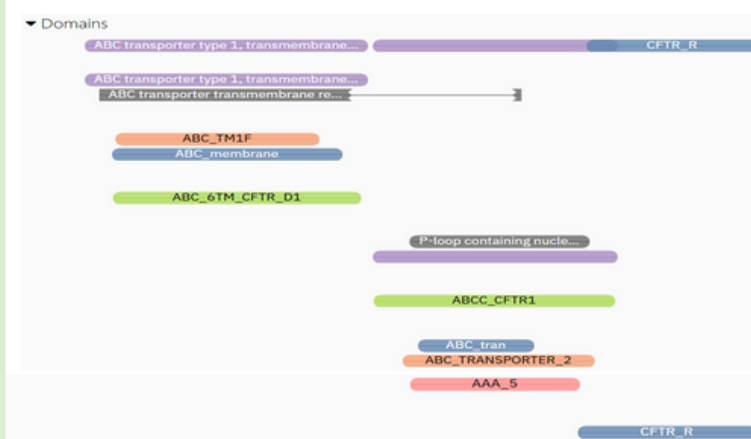


RNAFOLD

The RNA is thermodynamically stable due to its very low minimum free energy of -673.70 kcal/mol.

PROTEIN ANALYSIS

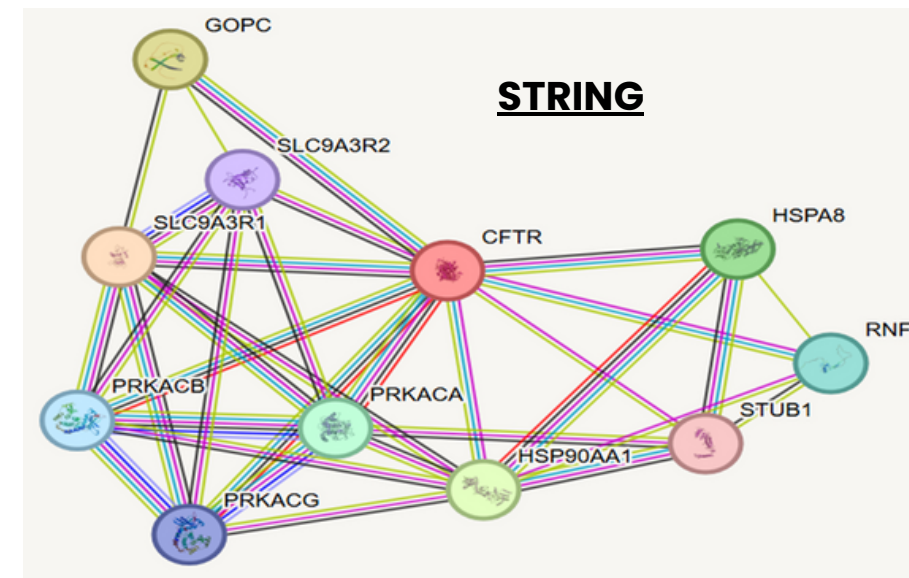
InterPro



ProtParam

No of AA	840
pI	8.67
MW	95883.04
II	43.06
AI	96.94

INTERACTIONS



PHYLOGENY

MSA

Query_18001 1 HQES PLEASVDELFPS--QTPLKADHQLLSDQVPSVDSADNLSEKLEREWRELASKK 60
Query_18002 1 ----CTPFFFFIIPPLKADHQLLSDQVPSVDSADNLSEKLEREWRELASKK 62
Query_18003 1 HQES PLEASVDELFPS--QTPLKADHQLLSDQVPSVDSADNLSEKLEREWRELASKK 60
Query_18004 1 HQES PLEASVDELFPS--QTPLKADHQLLSDQVPSVDSADNLSEKLEREWRELASKK 60
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