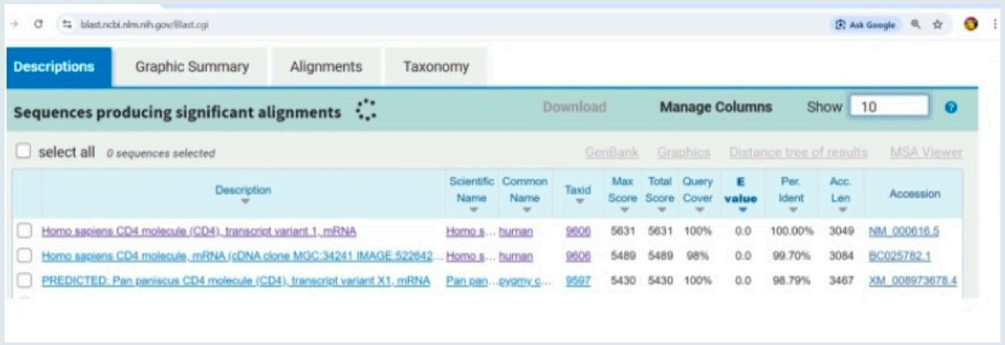
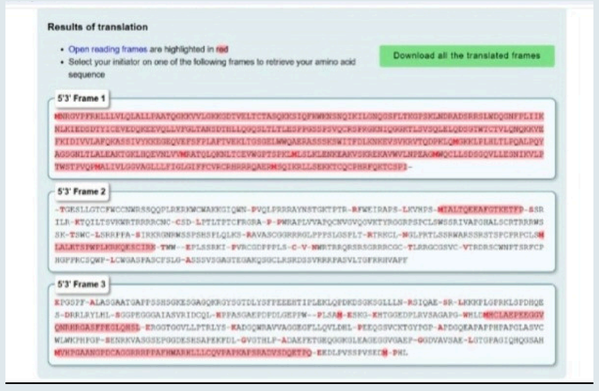
Computational Analysis of Unknown DNA Sequences Using Integrated Bioinformatics Tools

DNA ANALYSIS

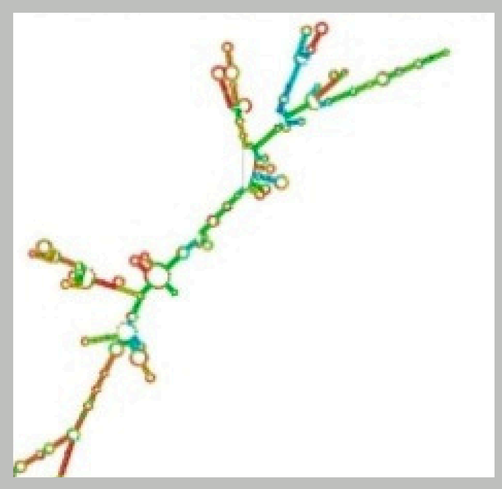


DNA>PROTEIN TRANSLATION FILE



ORF FINDER

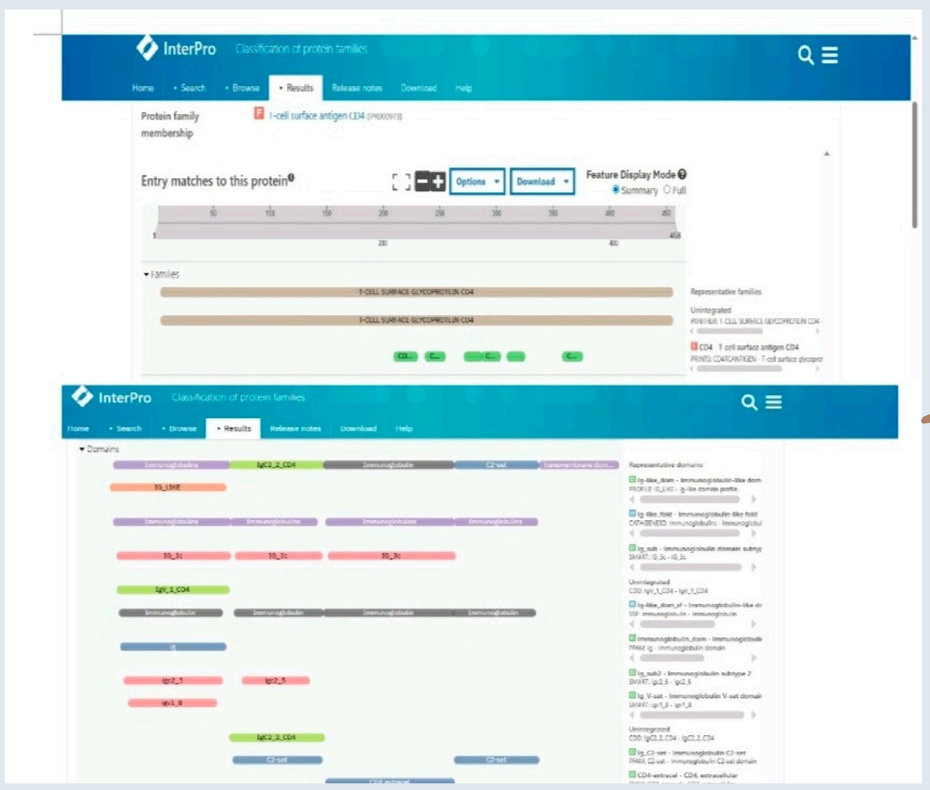
RNA ANALYSIS



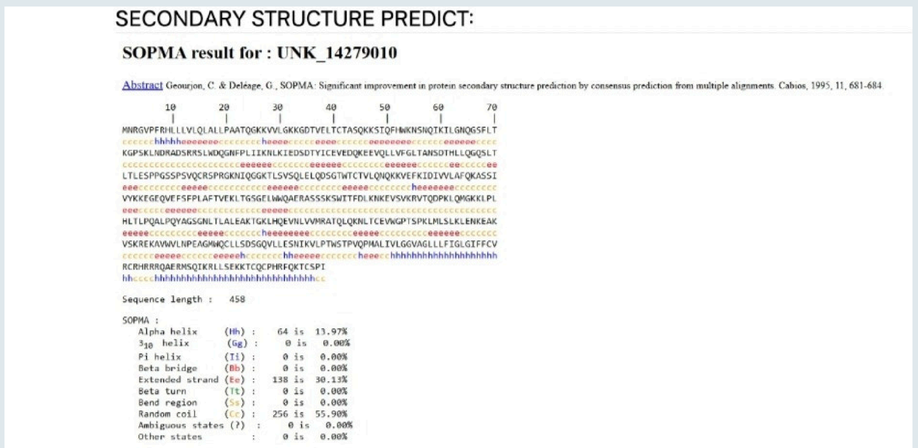
The RNA molecule is thermodynamically stable, as shown by the highly negative ensemble for free energy.
However, it is structurally flexible, with stability spread across multiple conformations rather than a single dominant structure.
This balance of stability and flexibility is often important for regulatory or functional RNAs

Protien Analysis

DOMAIN ARCHITECTURE



SECONDARY STRUCTURE PREDICT:



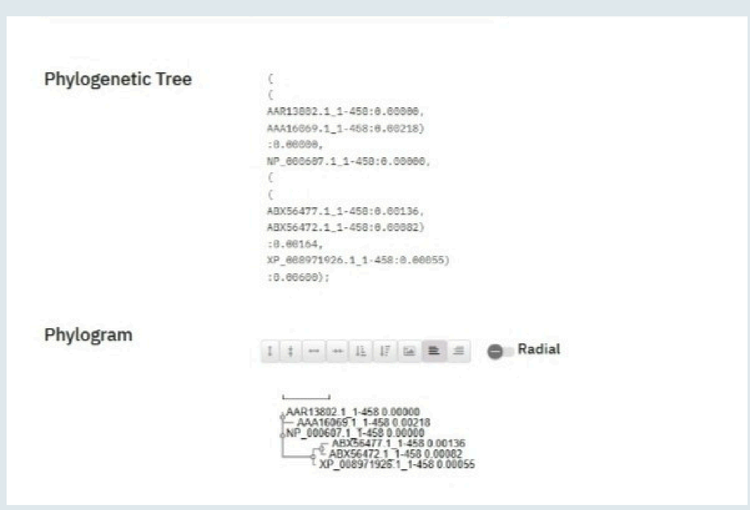
No. Of Amino Acids	464
Theoretical pI	9
Molecular weight	51980.67
Instability index	41.70
Aliphatic index	95.13
Grand average of hydropathicity (GRAVY)	0.236

FUNCTIONAL PREDICTION

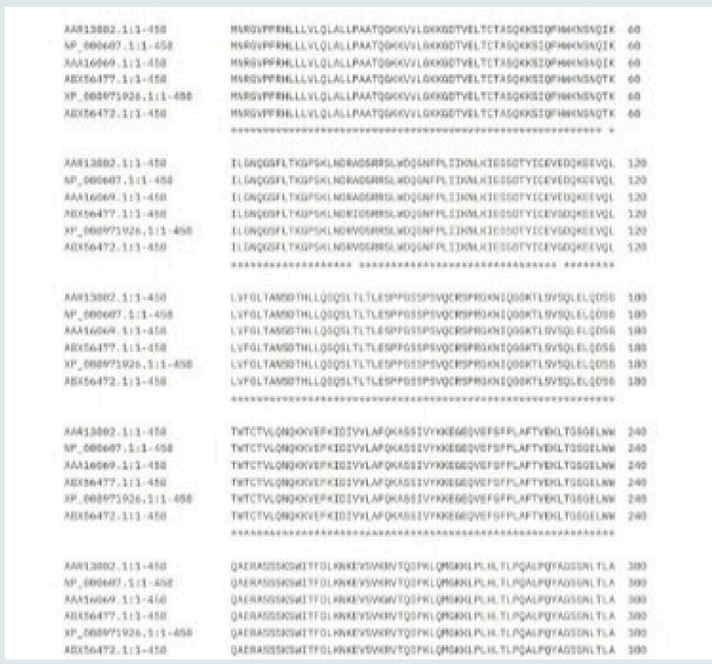
CD4 acts as a vital immune co-receptor that uses its four extracellular Immunoglobulin-like domains to bind MHC class II molecules and facilitate HIV-1 entry. Through its transmembrane anchor and cytoplasmic tail, it recruits the Lck kinase to the T-cell receptor complex, initiating the signaling necessary for T-cell activation and development. This domain architecture effectively bridges extracellular recognition with intracellular signal transduction to drive the adaptive immune response.

PHYLOGENETIC ANALYSIS

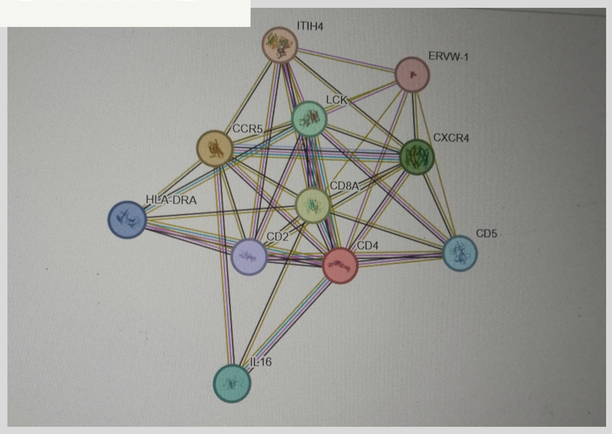
PHYLOGENETIC TREE



MULTIPLE SEQUENCE ALLIGNMENT BY CLUSTAL OMEGA



PROTIEN -PROTIEN INTERACTION ANALYSIS



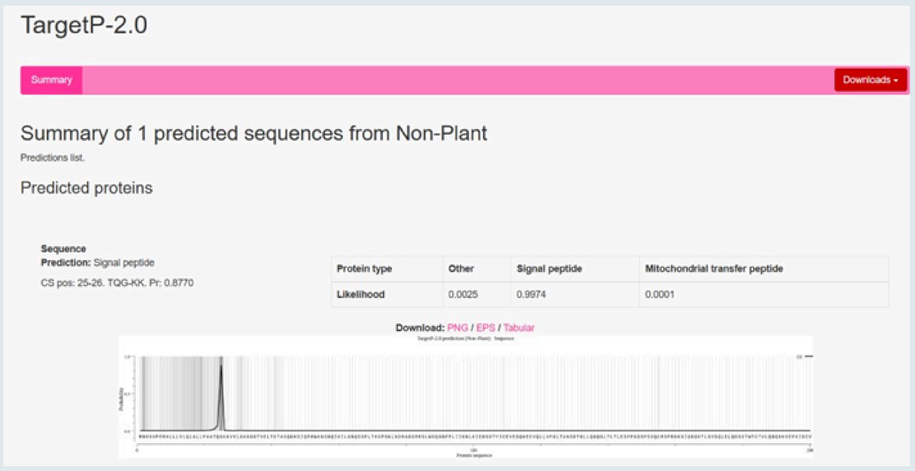
BIOLOGICAL SIGNIFICANCE

CD4 is a key co-receptor in adaptive immunity, linking the T-cell receptor to MHC II on antigen-presenting cells. By recruiting the kinase Lck, it lowers the activation threshold, enabling T-cells to respond to low antigen levels.
Clinically, CD4 is crucial as HIV binds CD4 via gp120, leading to CD4⁺ T-cell depletion and AIDS.

The CD4 phylogenetic tree highlights the close evolutionary bond between humans and bonobos, showing minimal genetic divergence from a recent common ancestor. Short branch lengths and alignment asterisks reflect strong purifying selection, preserving essential residues for MHC-II binding and immune signaling. This high conservation ensures the molecule remains functional as a critical co-receptor, while also serving as the primary gateway for HIV/SIV lentiviruses.

SUBCELLULAR LOCALIZATION PREDICTION

The 458 amino acid protein is a type I single-pass membrane protein with an Nterminal signal peptide, predicted to localize primarily to the endoplasmic reticulum, and likely trafficked via the secretory pathway. The C-terminal cytoplasmic tail may mediate interactions or intracellular trafficking, while no significant nuclear or mitochondrial targeting is predicted



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