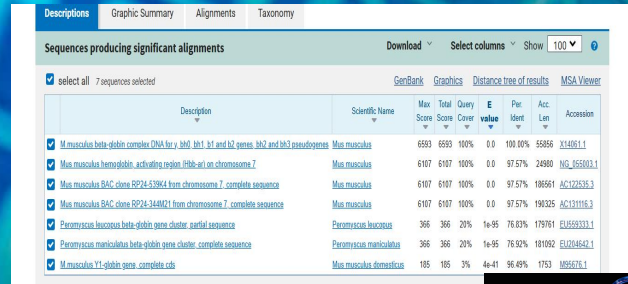
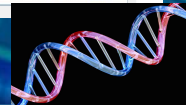


Protein:Ycf1 is a core subunit of the TIC (Translocon on the Inner Chloroplast membrane) complex. It acts as a channel or "scaffold" that helps pull proteins from the outside of the chloroplast into the internal stroma.

## NCBI BLASTN Alignment



## ORF Map

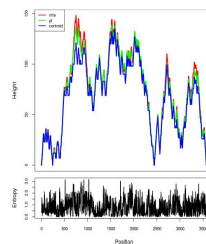


RNAfold WebServer

## Annotated mRNA structure



Here you find a printable post representation of the mRNA structure, the thermodynamic ensemble of RNA structures, and the centroid structure. Additionally we present the postorder entry for each position. (download as [GZIP][PDF][IMAGE] [PNG][PDF][PDF])



## STABILITY

The "height" at a given position corresponds to the number of base pairs enclosing that position. Stable regions form high "mountains" (many nested base pairs), while less stable or single-stranded regions form "valleys". Regions with low positional entropy are consistently paired or unpaired in most probable structures, indicating a rigid, stable local structure. Regions with high positional entropy are flexible, potentially alternating between paired and unpaired states, suggesting less stable areas that might be more susceptible to enzymatic degradation. We can identify stable, highly structured regions (low entropy, high mountain ranges) and less stable, flexible regions (high entropy, low or fluctuating mountain ranges), which collectively inform the overall stability and potential degradation sites of the mRNA molecule.

## ProtParam

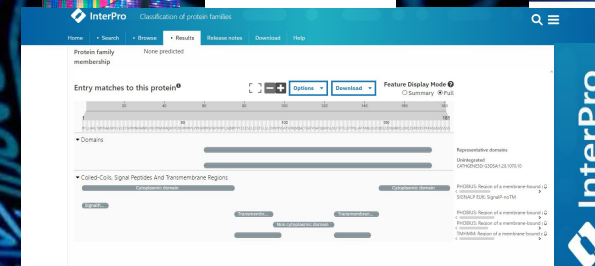
## Protein properties

Number of amino acids: 181  
Theoretical pI: 10.50  
Molecular weight: 21221.92

stability index:  
e instability index (II) is computed to be 54.59  
is classifies the protein as unstable.

iphatic index: 100.17  
and average of hydropathicity (GRAVY): 0.004

## Domains



This protein is likely a membrane-anchored receptor or adhesion molecule. It has a surface-exposed domain (the CATH-Gene3D region) that probably interacts with extracellular molecules or other cells. It is anchored in the membrane by transmembrane helix. It has intracellular (cytoplasmic) tails that might be involved in transmitting signals into the cell or anchoring the protein to the internal cytoskeleton.

## Localization Prediction



## Results of the k-NN Prediction

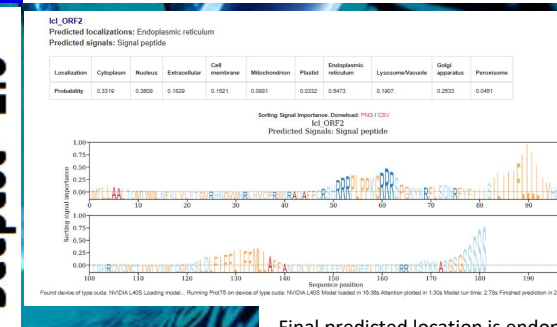
k = 9/23

55.6 %: endoplasmic reticulum  
44.4 %: mitochondrial

>> prediction for 176650784722689 is end (k=9)

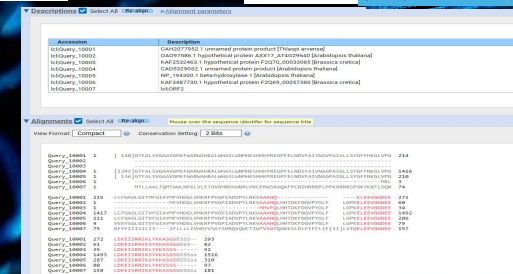
PSORT:

DeepLoc - 2.0



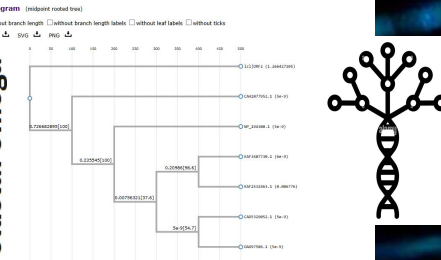
Final predicted location is endoplasmic reticulum as results from DeepLoc indicate highest probability of 0.5473 for it and results from PSORT also mention highest percentage for endoplasmic reticulum that is 55.6%.

## MSA



## Phylogenetic tree

## Clustal Omega



The tree splits early into two main lineages: The Upper Clade: This includes a large cluster of sequences like CAH2077952.1, NP\_194300.1, and KAF2532463.1. The Lower Clade: This includes the sequences at the bottom, such as CAD53290852.1 and OA097586.1. KAF3487730.1 and KAF2532463.1 appear to be sister taxa, meaning they share a more recent common ancestor with each other than with any other sequence in the tree. The long horizontal branches (like the one leading to OA097586.1) indicate a significant amount of unique evolutionary change or genetic divergence that occurred in that specific lineage after it split from its relatives.

## Interaction Map

