

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.

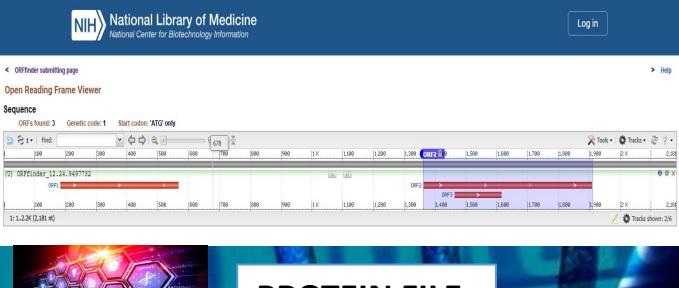
NCBI BLASTN Alignment

The screenshot shows the R F finder web interface with the following details:

- Descriptions**, **Graphic Summary**, **Alignments**, **Taxonomy** buttons at the top.
- Sequences producing significant alignments** search bar.
- Download**, **Select columns**, **Show** dropdowns.
- Results Table:**

Description	Scientific Name	Max Score	Total Score	Query Cover	E value	Pearl	Acc	Len	Accession
Mus musculus beta-globin complex gene (b6, b1, b5 and b7 genes, b6.2 and b6.3 pseudogenes)	Mus musculus	6593	6593	100%	0.0	100.00%	5588	Y41061.1	
Mus musculus hemoglobin, activating region (Hb6-6c) on chromosome 7	Mus musculus	6107	6107	100%	0.0	97.57%	2490	NG_455030.1	
Mus musculus BAC clone RP24-3596K1 from chromosome 7 complete sequence	Mus musculus	6107	6107	100%	0.0	97.57%	185661	AC72353.3	
Mus musculus BAC clone RP24-3440C1 from chromosome 7 complete sequence	Mus musculus	6107	6107	100%	0.0	97.57%	190325	AC751116.3	
Paromyscus leucopus beta-globin gene cluster, partial sequence	Peromyscus leucopus	366	366	20%	1e-95	76.83%	17951	EU553331.1	
Paromyscus maniculatus beta-globin gene cluster, complete sequence	Peromyscus maniculatus	366	366	20%	1e-95	76.92%	101092	EU704642.1	
Mus musculus Y-globin gene, complete cds	Mus musculus	185	185	3%	4e-41	96.49%	1753	MG56761.1	
- MSA Viewer** button.
- ORF Map** visualization on the right.

ORF Map



PROTEIN FILE

ORF2 (181 aa) Display ORF as... Mark

```
>1c1|ORF2
MTLLAALTQMTWWLNFKLVLETGVRHNGVWNRLHVCPRWSRAQAFPCRS
RRRPLPKGRRSPGKYYKRFLSQNRFYIIISIILIIIFLLLIVHDYVSA
TSHRQVQWCTIMTVSNTQGKSKLDLFLIFLIFMLLAFFFANLDLVIQELE
EVGGNEELDKESRIIKSYKKASGSGSSSSS
```

ORF 2 is selected because this is the longest ORF, it starts with ATG and shows homology to known functional proteins.

RNAfold WebServer

Annotated mRNA structure

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. A note on base-pairing
Hes: The structure below is colored by base-pairing probabilities; the unpaired regions the color denotes the probability of being unpaired.

MFE secondary structure

Centroid secondary structure

Sequence displacement
 ● Plain Sequence
 ○ No Sequence

Other display options
 ■ Minimally paired structures
 □ Mutual entropy
 ○ None

0 0.2 0.4 0.6 0.8 1

Sequence displacement
 ● Plain Sequence
 ○ No Sequence

Other display options
 ■ Minimally paired structures
 □ Mutual entropy
 ○ None

0 0.2 0.4 0.6 0.8 1

Find a scatterplot representation of the MFE structure, the thermodynamic ensemble of RNA structures, and the centroid structure. Additionally we present the positional entropy for each position. An [OPTIONAL] (OPTIONAL) (OPTIONAL).

STABILITY

Height

Energy

0 10 20 30 40 50 60 70 80

0 500 1000 1500 2000 2500 3000 3500

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

PSORT:

Icl_ORF2

Predicted localizations: Endoplasmic reticulum

Predicted signals: Signal peptide

Localization	Cytoplasm	Nucleus	Extracellular	Cell membrane	Mitochondrion	Plastid	Endoplasmic reticulum	Lysosome/Vesicle	Golgi apparatus	Peroxisome
Probability	0.3310	0.0800	0.1820	0.1521	0.0081	0.0332	0.0473	0.1907	0.2033	0.0401

Sorting Signal Importance: Computed: PhD CSV
Icl_ORF2
Predicted Signals: Signal peptide

Sequence signal importance

Sequence position

Found device of type cuda: NVidia L405 Loading model... Running ProfTTS on device of type cuda: NVidia L405 Model loaded in 13.9s Model run time: 2.78s Finished prediction in 24.6ms

Instability index:
Instability index (II) is computed to be 54.59
which classifies the protein as unstable.

hydropathicity (GRAVY): 0.004

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%.

Domains

The screenshot shows the InterPro Domains classification interface. At the top, there's a navigation bar with links for Home, Search, Browse, Results, Release notes, Download, and Help. The main title "Domains" is prominently displayed. On the left, there's a sidebar with the InterPro logo and a "Classification of protein families" section. Below that, there are tabs for "Protein family membership" and "None predicted". A search bar is located at the top right. The main content area displays "Entry matches to this protein" with a search bar and a zoom range from 0 to 100. Below this, there's a "Feature Display Mode" section with "Summary" and "Full" options. A "Domains" section is expanded, showing a horizontal bar representing the protein sequence with colored segments indicating domain presence. A legend below defines the colors: grey for Coiled-Coil, Signal Peptides, and Transmembrane Regions; red for Alpha-helices; blue for Beta-sheets; green for Beta-turns; and orange for Other structural features. To the right of the sequence bar, there's a "Representative domains" section listing "Unpredicted" and "DYN1NBD1 (255428.28.105.30)". A detailed legend for "Predicted regions of membrane binding" is provided, listing various domain types and their characteristics.

MSA

Accession	Description
Icti00001	CAF202793 Icti0001 ununamed protein [Thraupis episcopus]
Icti00002	DAA93360 Icti0002 hypothetical protein XXV [Thraupis episcopus thalassina]
Icti00003	KAF25264 Icti0003 hypothetical protein [Thraupis episcopus cretacea]
Icti00004	CAC03030 Icti0004 hypothetical protein [Thraupis episcopus]
Icti00005	NP_194900 Icti0005 hypothetical protein 1 [Thraupis episcopus]
Icti00006	KAF25270 Icti0006 hypothetical protein 1 [Thraupis episcopus thalassina]
Icti00007	Icti0007 hypothetical protein 2 [Thraupis episcopus cretacea]

phylogenetic tree

The figure displays a phylogenetic tree on the left and a Clustal Omega multiple sequence alignment on the right. The phylogenetic tree shows relationships between various sequences, with branch lengths indicated by numbers. The Clustal Omega alignment shows the sequence for each node, with gaps represented by dashes. A DNA double helix icon is also present.

The tree splits early into two main lineages: The Upper Clade: This includes a large cluster of sequences such as CAH2077952.1, NP_194300.1, and KAF2532463.1. The Lower Clade: This includes the sequences at the bottom, such as CAD53290852.1 and OAO97586.1. 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 OAO97586.1) 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

The figure displays a network graph of protein interactions. Nodes represent proteins: ZDS1 (blue), BETA-CHASSE_2 (light blue), CYP97A3 (yellow), CYP97B3 (pink), VDE1 (red), and ZEP (green). Edges represent interactions, colored by type: green for co-expression, purple for binding, red for phosphorylation, blue for protein-DNA interaction, and yellow for localization. The network shows complex interactions between ZEP and other proteins, with ZEP having the highest degree of connectivity.

The proteins are mainly involved in Carotenoid metabolic process,Carotenoid biosynthetic process,Terpenoid metabolic process,Terpenoid biosynthetic process,Xanthophyll metabolic process.Molecular fuctions include of these proteins include Oxidoreductase activity,Iron ion binding,Oxidoreductase activity,acting on paired donors,Monoxygenase activity,Catalytic activity.The cellular components that are involved in these function include chloroplast,plastid envelope, chloroplast envelope,Chloroplast